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OM protein - protein search, using sw model

Run on: August 5, 2005, 14:08:08 ; Search time 45 Seconds
(without alignments)
1877.839 Million cell updates/sec

Title: US-10-053-758-225
Perfect score: 5961
Sequence: 1 MFRAPRCRAVRSLLRSHYRE.....TALEAANPALPSDFKTLTD 1132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA*
1: /cgn2_6/ptodata/1/1aa/5A COMB.pcp:*
2: /cgn2_6/ptodata/1/1aa/5B COMB.pcp:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5961	100.0	1132	3	US-08-851-843A-225
2	5961	100.0	1132	3	US-08-974-549A-2
3	5961	100.0	1132	3	US-08-854-050-225
4	5961	100.0	1132	3	US-09-430-323-225
5	5961	100.0	1132	3	US-09-128-354-2
6	5961	100.0	1132	4	US-09-675-321-2
7	5961	100.0	1132	4	US-09-052-919-2
8	5961	100.0	1132	4	US-08-912-951-2
9	5961	100.0	1132	4	US-09-402-181B-2
10	5961	100.0	1132	4	US-09-721-456-2
11	5961	100.0	1132	4	US-09-953-052-2
12	5961	100.0	1132	4	US-09-042-460-3
13	5961	100.0	1132	4	US-09-949-016-6326
14	5961	100.0	1154	4	US-08-974-549A-611
15	5961	100.0	1154	4	US-08-912-951-323
16	5961	100.0	1154	4	US-09-402-181B-611
17	5961	100.0	1154	4	US-09-721-456-611
18	5961	100.0	1189	3	US-08-974-549A-613
19	5961	100.0	1189	4	US-08-912-951-325
20	5961	100.0	1189	4	US-09-402-181B-613
21	5961	100.0	1189	4	US-09-721-456-613
22	5961	100.0	1200	3	US-08-974-549A-612
23	5961	100.0	1200	4	US-08-912-951-324
24	5961	100.0	1200	4	US-09-402-181B-612
25	5961	100.0	1200	4	US-09-721-456-612
26	5961	100.0	1285	3	US-08-974-549A-600
27	5961	100.0	1285	4	US-08-912-951-314

28 5961 100.0 1285 4 US-09-402-181B-600
29 5961 100.0 1285 4 US-09-721-456-600
30 5952 99.8 1132 3 US-08-974-549A-344
31 5952 99.8 1132 4 US-09-402-181B-344
32 5952 99.8 1132 4 US-09-721-456-344
33 5952 99.8 1407 3 US-08-974-549A-628
34 5952 99.8 1407 4 US-08-912-951-334
35 5952 99.8 1407 4 US-09-402-181B-628
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37 5807 97.4 1193 4 US-09-949-016-11712
38 4052 68.0 807 3 US-08-974-549A-5
39 4052 68.0 807 4 US-08-912-951-5
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42 3819.5 64.1 1003 3 US-08-851-843A-217
43 3819.5 64.1 1003 3 US-08-974-549A-236
44 3819.5 64.1 1003 3 US-08-854-050-217
45 3819.5 64.1 1003 3 US-09-430-323-217

ALIGNMENTS

RESULT 1

US-08-851-843A-225
; Sequence 225, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION
; APPLICANT: Cecchi, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; NUMBER OF INVENTION: No. 6093809el Telomerase
; TITLE OF INVENTION: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 225:

Sequence 600, App
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Sequence 344, App
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Sequence 344, App
Sequence 628, App
Sequence 334, App
Sequence 628, App
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Sequence 5, Appli
Sequence 5, Appli
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Sequence 336, App
Sequence 217, App
Sequence 217, App

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-851-843A-225

Query Match 100.0%; Score 5961; DB 3; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCVAVSLARSHYREVLPVPLATFVRRLGPGQWRVQORGDPAARALVAQCLVCPV 60
Db 1 MPRAPRCVAVSLARSHYREVLPVPLATFVRRLGPGQWRVQORGDPAARALVAQCLVCPV 60

Qy 61 DARPPPAAPSPQVSCLEKELVARVQLRCERGAKNVLAFAFGFALLDGGAGGPEAFTTSVR 120
Db 61 DARPPPAAPSPQVSCLEKELVARVQLRCERGAKNVLAFAFGFALLDGGAGGPEAFTTSVR 120

Qy 121 SYLNTVTDALRGSGAWGLLRRVGDVVLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLNTVTDALRGSGAWGLLRRVGDVVLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy 181 ATOARPPHAGPRRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGASRLPLPKRPR 240
Db 181 ATOARPPHAGPRRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGASRLPLPKRPR 240

Qy 241 GAAPEPERTVPGQSWAHPTGRPSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 300
Db 241 GAAPEPERTVPGQSWAHPTGRPSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 300

Qy 301 QOHAGPSTSRPRPMDTPCPVVAETKHYFLYSSGDKQLRPSFLSSRLPSLTGARRL 360
Db 301 QOHAGPSTSRPRPMDTPCPVVAETKHYFLYSSGDKQLRPSFLSSRLPSLTGARRL 360

Qy 361 VETFLGSRPMWGTRELPLRPLORYWOMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETFLGSRPMWGTRELPLRPLORYWOMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy 421 PAAGVCAREKPGQSWAPEEDTDPRRLVQLLRQHSPPWQYGVFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSWAPEEDTDPRRLVQLLRQHSPPWQYGVFVRACLRLVPPGLWGS 480

Qy 481 RHNERFLRNTKXTISLGKHAHLSQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERFLRNTKXTISLGKHAHLSQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540

Qy 541 LAKFLHLMMSVYVVELLRSFFVTETTFQKNRLEFFYRKSVMSKLSQIGIROHLKRVOLRE 600
Db 541 LAKFLHLMMSVYVVELLRSFFVTETTFQKNRLEFFYRKSVMSKLSQIGIROHLKRVOLRE 600

Qy 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMMDYVVGARTFRREKRAERLTSRVKA 660
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Qy 661 LFSVLNTERARRPGLGASVLGLDDIHRAWTFVLRVRAQDPPPELFFVKVDVTGAVDTI 720
Db 661 LFSVLNTERARRPGLGASVLGLDDIHRAWTFVLRVRAQDPPPELFFVKVDVTGAVDTI 720

Qy 721 PQDLRTEVIASIIKPONTYCVRRVAVQKAHGHVRKAFKSHVSTLTDLPQYMQFVAHL 780
Db 721 PQDLRTEVIASIIKPONTYCVRRVAVQKAHGHVRKAFKSHVSTLTDLPQYMQFVAHL 780

Qy 781 QETSPLRDAVIEQSSSLNEASSGLFDVFLRFMCHAVIRGKSVYVQCGIPQSSILSTL 840
Db 781 QETSPLRDAVIEQSSSLNEASSGLFDVFLRFMCHAVIRGKSVYVQCGIPQSSILSTL 840

Qy 841 LCSICYGDMENKLFAGIRRDGLLRVDDFLVLTPLTHAKTFTLTVRGVPEYGCVVNL 900
Db 841 LCSICYGDMENKLFAGIRRDGLLRVDDFLVLTPLTHAKTFTLTVRGVPEYGCVVNL 900

Qy 901 RKTVMNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTTRTLEVQSDYSYARTSTRASLTF 960
Db 901 RKTVMNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTTRTLEVQSDYSYARTSTRASLTF 960

; Sequence 2, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-00261005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-549A-2

Query Match 100.0%; Score 5961; DB 3; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 DARPPAAPSPFQVSLKELVARVQLRCERCAKNVLAFFGALLDGAAGGPEAFTTSVR 120

QY 121 SYLPTNTVDALRGSGAWGLLRVDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPTNTVDALRGSGAWGLLRVDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASPRRLGRCERAWNSHREAGVPLGLPAGARRRGGASRSPLPKRRR 240
DB 181 ATQARPPPHASPRRLGRCERAWNSHREAGVPLGLPAGARRRGGASRSPLPKRRR 240

QY 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVVSPPARPAEATSLEGALSGTRHSHPSVG 300
DB 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVVSPPARPAEATSLEGALSGTRHSHPSVG 300

QY 301 RQHAGPSTSHPPRPWDTPCPVVAETHKFLYSSGDKQLRPSFLLSLPSLTGARRL 360
DB 301 RQHAGPSTSHPPRPWDTPCPVVAETHKFLYSSGDKQLRPSFLLSLPSLTGARRL 360

QY 361 VETIFLGRPMWPGTPRRLPLRQYQWNRPLFLLELGNHQAOCYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGRPMWPGTPRRLPLRQYQWNRPLFLLELGNHQAOCYGVLLKTHCPLRAAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSHPQVYGFVRACLRLVPPGLWGS 480
DB 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSHPQVYGFVRACLRLVPPGLWGS 480

QY 481 RHNERFLNTKKFISLGHAKLSLOELTKWMSVRDCAWLRRSPGVGCVPAEHLRBEI 540
DB 481 RHNERFLNTKKFISLGHAKLSLOELTKWMSVRDCAWLRRSPGVGCVPAEHLRBEI 540

QY 541 LAKFLHMLSVVVBLLRSFFVTTTQKNLFFYKSVMSKLSIGIRQLHKEVQLRE 600
DB 541 LAKFLHMLSVVVBLLRSFFVTTTQKNLFFYKSVMSKLSIGIRQLHKEVQLRE 600

QY 601 LSEAEVQHQREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVA 660
DB 601 LSEAEVQHQREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVA 660

QY 661 LPSVLYNERARPGLLGASVLGLDDIHRARTFVLIRVAQDPPPELYFVKVDVTGAYDTI 720
DB 661 LPSVLYNERARPGLLGASVLGLDDIHRARTFVLIRVAQDPPPELYFVKVDVTGAYDTI 720

QY 721 PODRLTEVASTIIPQNTYCVRRYAVQKAAHGHVKA PKSHVSTLTDLQPYMRQFVAHL 780
DB 721 PODRLTEVASTIIPQNTYCVRRYAVQKAAHGHVKA PKSHVSTLTDLQPYMRQFVAHL 780

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RESULT 3

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US-08-854-050-225
; Sequence 225, Application US/08854050
; Patent No 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.

```

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QY 781 QETSPLRDAVVEIOSSSLNEASSGLFDVFLRFMCHHAVRIRKSVQCOGIPQGSILSTL 840
DB 781 QETSPLRDAVVEIOSSSLNEASSGLFDVFLRFMCHHAVRIRKSVQCOGIPQGSILSTL 840

QY 841 LCSLCYGDMEKLFAGIRDDGLLRLVDDFLVTPHLTHAKTFLRTLYRGVPEYCVVNL 900
DB 841 LCSLCYGDMEKLFAGIRDDGLLRLVDDFLVTPHLTHAKTFLRTLYRGVPEYCVVNL 900

QY 901 RKTVVNFEVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSIRASLTF 960
DB 901 RKTVVNFEVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSIRASLTF 960

QY 961 NRGFKAGRNMRKLFVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHACVQLP 1020
DB 961 NRGFKAGRNMRKLFVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHACVQLP 1020

QY 1021 FHQQWKNPTFFLRVISDTASLCYSILKAKWAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
DB 1021 FHQQWKNPTFFLRVISDTASLCYSILKAKWAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080

QY 1081 KLTRHRTVTVPLLGSLRTAQTLRSKLPCTTTLTALEAAANPALPSDFKTILD 1132
DB 1081 KLTRHRTVTVPLLGSLRTAQTLRSKLPCTTTLTALEAAANPALPSDFKTILD 1132

```

REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-854-050-225

Query Match 100.0%; Score 5961; DB 3; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	MPRAPRCRAVRLSHRYREVLPLATFVRRLLGPGQWRLVQRGDPAAPRALVAQCLVCPW	60
QY	61	DARPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDGAAGGPEAFTTSVR	120
DB	61	DARPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDGAAGGPEAFTTSVR	120
QY	121	SYLNTVTDALRGSGAWGLLRRVDDVLLVHLLARCALFVLVAPSCAYQVCGPLYQLGA	180
DB	121	SYLNTVTDALRGSGAWGLLRRVDDVLLVHLLARCALFVLVAPSCAYQVCGPLYQLGA	180
QY	181	ATQARPPPHASGPRRLCERAWNHSVREAGVPLGLPAPGARRRGGSASRLPLPKPRR	240
DB	181	ATQARPPPHASGPRRLCERAWNHSVREAGVPLGLPAPGARRRGGSASRLPLPKPRR	240
QY	241	GAAPERTPVQGSWAHPGTRGSDRGFCVWSPARPAEATSLGALSCTRSHPSVG	300
DB	241	GAAPERTPVQGSWAHPGTRGSDRGFCVWSPARPAEATSLGALSCTRSHPSVG	300
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QY	361	VETIFLGSRPWMPGTPRLPRLPQRYQWMLPFLLELGNHAQCPYGVLLKTHCPRAAVT	420
DB	361	VETIFLGSRPWMPGTPRLPRLPQRYQWMLPFLLELGNHAQCPYGVLLKTHCPRAAVT	420
QY	421	PAAGVCAREKPGQSVAAPEEDTPRLVQLLRQHSSFPQVYGFVRACLRRLVPPGLWS	480
DB	421	PAAGVCAREKPGQSVAAPEEDTPRLVQLLRQHSSFPQVYGFVRACLRRLVPPGLWS	480
QY	481	RHNERFLNNTKFTISLGHAKLSLOELTWKMSVRDCAWLRSQVGCVPAAEHLREEI	540
DB	481	RHNERFLNNTKFTISLGHAKLSLOELTWKMSVRDCAWLRSQVGCVPAAEHLREEI	540
QY	541	LAKFLHLMVSVVVELLSFFVYVTTTQKNRLFFYKSVMSKLSQSIGIRHKLKRVQRE	600
DB	541	LAKFLHLMVSVVVELLSFFVYVTTTQKNRLFFYKSVMSKLSQSIGIRHKLKRVQRE	600
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DB	601	LSEAEVROHREARPALTSRLRFPKPDGLRPIVNMDDVVGARTFRREKRAERLTSRVKA	660
QY	661	LPSVLNYERARRPGLGSLVGLDDIHRAWTFVLVRAQDPPPELYFVKVDTVTGAYDTI	720
DB	661	LPSVLNYERARRPGLGSLVGLDDIHRAWTFVLVRAQDPPPELYFVKVDTVTGAYDTI	720
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QY	781	QETSPRLDAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRKGSYVQCQGIPOQSILSTL	840
DB	781	QETSPRLDAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRKGSYVQCQGIPOQSILSTL	840

QY	841	LCSLCYGDMENKLPAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLTRLVRGVPYGCVVNL	900
DB	841	LCSLCYGDMENKLPAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLTRLVRGVPYGCVVNL	900
QY	901	RKTVNFPEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVSQSDYSYARTSIRASLTF	960
DB	901	RKTVNFPEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVSQSDYSYARTSIRASLTF	960
QY	961	NRGFKAGNNRRKLPFVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVQLP	1020
DB	961	NRGFKAGNNRRKLPFVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVQLP	1020
QY	1021	FHOQVKNPTEFRLVISDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOMLCHOAFL	1080
DB	1021	FHOQVKNPTEFRLVISDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOMLCHOAFL	1080
QY	1081	KLTRHRYVYVPLGLSLRTAQTLSRKLPGTTLTALEAAANPALPSDFKTILD	1132
DB	1081	KLTRHRYVYVPLGLSLRTAQTLSRKLPGTTLTALEAAANPALPSDFKTILD	1132

RESULT 4

US-09-430-323-225
Sequence 225, Application US/09430323
Patent No. 6309867

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. 6309867el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/430,323

FILING DATE: 29-Oct-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 225:

SEQUENCE CHARACTERISTICS:

LENGTH: 1132 amino acids

TYPE: amino acid

; TOPOLOGY: linear									
; MOLECULE TYPE: protein									
; SEQUENCE DESCRIPTION: SEQ ID NO: 225:									
US-09-430-323-225									
Query Match 100.0%; Score 5961; DB 3; Length 1132;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	MPRAPRCRAVRSLLSHYREVLP	PLATFVRRLGPGQWRVLVQ	RGDPAAFRALVAQCLVCVPW	60				
Db	1	MPRAPRCRAVRSLLSHYREVLP	PLATFVRRLGPGQWRVLVQ	RGDPAAFRALVAQCLVCVPW	60				
Qy	61	DARPPAAPSPFQVSC	KLKELVARVLQRLCERGA	KNVLAFGFALLDGA	RGGPEAFTTSVR	120			
Db	61	DARPPAAPSPFQVSC	KLKELVARVLQRLCERGA	KNVLAFGFALLDGA	RGGPEAFTTSVR	120			
Qy	121	SYLPTNTVDALRGSG	ANGWLLLRVGGDVLV	HLARCALFVLVAP	SCAYQVCGPPLYQLGA	180			
Db	121	SYLPTNTVDALRGSG	ANGWLLLRVGGDVLV	HLARCALFVLVAP	SCAYQVCGPPLYQLGA	180			
Qy	181	ATQARPPPHASGPR	RLGRCERAWNHSVRE	AGVPLGLPAPGAR	RRGGSASRSLPLPKRPR	240			
Db	181	ATQARPPPHASGPR	RLGRCERAWNHSVRE	AGVPLGLPAPGAR	RRGGSASRSLPLPKRPR	240			
Qy	241	GAAPPERTPVQGS	WAHPGRTGSDRGFC	VVSPARPAEATS	LEGALSGTRHSHPSVG	300			
Db	241	GAAPPERTPVQGS	WAHPGRTGSDRGFC	VVSPARPAEATS	LEGALSGTRHSHPSVG	300			
Qy	301	ROHAGPSTSRPP	PPWTCPBPVYAE	TKHFLYSSGDK	EQLRPSLLSLRPSLTGARRL	360			
Db	301	ROHAGPSTSRPP	PPWTCPBPVYAE	TKHFLYSSGDK	EQLRPSLLSLRPSLTGARRL	360			
Qy	361	VETIFLGRPMW	GPTRLPQRYQW	MRPLFLELLGN	HAQCPYGVLLKTHCPLRAVT	420			
Db	361	VETIFLGRPMW	GPTRLPQRYQW	MRPLFLELLGN	HAQCPYGVLLKTHCPLRAVT	420			
Qy	421	PAAGVCAREK	PGSVAAPFEE	DDPRRLVQLLR	QHSSPWQVYGFVRAC	LRRLVPPGLWS	480		
Db	421	PAAGVCAREK	PGSVAAPFEE	DDPRRLVQLLR	QHSSPWQVYGFVRAC	LRRLVPPGLWS	480		
Qy	481	RHNERFLNTK	FKFISLGHAK	LSLOELTWMS	VRDCAWLRSPG	VCVPAAEHRLREI	540		
Db	481	RHNERFLNTK	FKFISLGHAK	LSLOELTWMS	VRDCAWLRSPG	VCVPAAEHRLREI	540		
Qy	541	LAKFLHLM	SVVVBELL	SFFVYTTTQ	KNLFFYKSVMS	KLOSIGIROHLKEVQRE	600		
Db	541	LAKFLHLM	SVVVBELL	SFFVYTTTQ	KNLFFYKSVMS	KLOSIGIROHLKEVQRE	600		
Qy	601	LSEAEVRQ	HREARPA	LLTSRLRFP	KPDGLRPIVNM	DYVVGARTPRR	KRAERLTSRVKA	660	
Db	601	LSEAEVRQ	HREARPA	LLTSRLRFP	KPDGLRPIVNM	DYVVGARTPRR	KRAERLTSRVKA	660	
Qy	661	LFSVLN	YERARRP	GLLGASV	LGDDIHR	AWRTFVLVRAQ	DDPPPELYFVKVDVTGAYDTI	720	
Db	661	LFSVLN	YERARRP	GLLGASV	LGDDIHR	AWRTFVLVRAQ	DDPPPELYFVKVDVTGAYDTI	720	
Qy	721	PODRLE	TVIASI	IKPNTY	CVRRYAVQ	KAHGHVKA	FKSHVSTLTDLPYMRQFVAHL	780	
Db	721	PODRLE	TVIASI	IKPNTY	CVRRYAVQ	KAHGHVKA	FKSHVSTLTDLPYMRQFVAHL	780	
Qy	781	QETSPL	RAVVTIEQ	SSLINE	ASSGLFDV	FLRPMCH	HAVIRGKSVVCCQGIPOGSILSTL	840	
Db	781	QETSPL	RAVVTIEQ	SSLINE	ASSGLFDV	FLRPMCH	HAVIRGKSVVCCQGIPOGSILSTL	840	
Qy	841	LCSLCY	GMENKLF	AGIRRD	GLLLRLV	DDFLVTP	HLTHAKTFLRTLVRGPEYGCVVNL	900	
Db	841	LCSLCY	GMENKLF	AGIRRD	GLLLRLV	DDFLVTP	HLTHAKTFLRTLVRGPEYGCVVNL	900	
Qy	901	RKTVNF	FEDEAL	GGTAF	QMPA	GLFPWC	GLLLDTRTLEVSQSYSSARTSIRASLTFF	960	
Db	901	RKTVNF	FEDEAL	GGTAF	QMPA	GLFPWC	GLLLDTRTLEVSQSYSSARTSIRASLTFF	960	

RESULT 5
US-09-128-354-2
; Sequence 2, Application US/09128354
; Patent No. 6337200
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 015389-003310US
; CURRENT APPLICATION NUMBER: US/09/128,354
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 08/851,843
; EARLIER FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: US 08/854,050
; EARLIER FILING DATE: 1997-05-09
; EARLIER APPLICATION NUMBER: US 08/911,312
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/912,951
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/915,503
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: WO PCT/US97/17885
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: US 08/974,549
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 08/974,584
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 09/052,864
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 1132
; ORGANISM: Homo sapiens
US-09-128-354-2

Query Match 100.0%; Score 5961; DB 3; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLSHYREVLP PLATFVRRLGPGQWRVLVQ | RGDPAAFRALVAQCLVCVPW | 60 || Db 1 MPRAPRCRAVRSLLSHYREVLP | PLATFVRRLGPGQWRVLVQ | RGDPAAFRALVAQCLVCVPW | 60 |
Qy 61 DARPPAAPSPFQVSC	KLKELVARVLQRLCERGA	KNVLAFGFALLDGA	RGGPEAFTTSVR 120
Db 61 DARPPAAPSPFQVSC	KLKELVARVLQRLCERGA	KNVLAFGFALLDGA	RGGPEAFTTSVR 120
Qy 121 SYLPTNTVDALRGSG	ANGWLLLRVGGDVLV	HLARCALFVLVAP	SCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVDALRGSG	ANGWLLLRVGGDVLV	HLARCALFVLVAP	SCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPR	RLGRCERAWNHSVRE	AGVPLGLPAPGAR	RRGGSASRSLPLPKRPR 240
Db 181 ATQARPPPHASGPR	RLGRCERAWNHSVRE	AGVPLGLPAPGAR	RRGGSASRSLPLPKRPR 240
Qy 241 GAAPPERTPVQGS	WAHPGRTGSDRGFC	VVSPARPAEATS	LEGALSGTRHSHPSVG 300

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Db 241 GAAPEPRTVQGSWAHPGTRGSDRGFCVSPAPAEATSLGALSSTRHSHPVG 300
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Db 301 ROHAGPSTSRPRPMDTPCPVVAETKHFYSSGDKQELRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKQGSVAAPAEEDTDPRRLVQLLRQHSPPQVYGFVRACLRLVPGLWGS 480
Db 421 PAAGVCAREKQGSVAAPAEEDTDPRRLVQLLRQHSPPQVYGFVRACLRLVPGLWGS 480
Qy 481 RHNERRFLRNTKXFIISLGKHAKLSLQELTWKMSVRDCAWLRSPGVCPVAAEHLREEI 540
Db 481 RHNERRFLRNTKXFIISLGKHAKLSLQELTWKMSVRDCAWLRSPGVCPVAAEHLREEI 540
Qy 541 LAKFLHLMVSVYVVELLRSPFYVTTTFOKNRLFYRKSVMSKLSQIGIRQHLKRVOLRE 600
Db 541 LAKFLHLMVSVYVVELLRSPFYVTTTFOKNRLFYRKSVMSKLSQIGIRQHLKRVOLRE 600
Qy 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVA 660
Db 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVA 660
Qy 661 LFSVLNVERARRPGLLGASVLGLDDIHRAMRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRAMRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
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Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLPYMRQFVAHL 780
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Db 781 QETSPURDAVIEQSSSLNEASSGLFDVLRFMCHHAVIRGKSVYVOCQIGPQSGIISLTL 840
Qy 841 LCSLCYGD MENKLFAGIRRDGLLRLVDLFLTPHLLTHAKTFLTLTVRGVPEYGCVVNL 900
Db 841 LCSLCYGD MENKLFAGIRRDGLLRLVDLFLTPHLLTHAKTFLTLTVRGVPEYGCVVNL 900
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Db 901 RKTWNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLLEVSQSDYSYARTSIRASLTF 960
Qy 961 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020
Db 961 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP 1020
Qy 1021 FHQQWKNTPFRLVISTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVOWLCHQAPLL 1080
Db 1021 FHQQWKNTPFRLVISTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVOWLCHQAPLL 1080
Qy 1081 KLTHRRVTYVPLGLSLRPAOTOLSKRLPGTTLTALEAANPALPSDFKTILD 1132
Db 1081 KLTHRRVTYVPLGLSLRPAOTOLSKRLPGTTLTALEAANPALPSDFKTILD 1132
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RESULT 6

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US-09-675-321-2
; Sequence 2, Application US/09675321
; Patent No. 6440735
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; TITLE OF INVENTION: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/09/675.321
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
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; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-675-321-2
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Query Match 100.0%; Score 5961; DB 4; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAPRALVAQCLVCVPM 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAPRALVAQCLVCVPM 60
Qy 61 DARPPPAAPSFQVSCIKELVARVLQRLCERGAKNVLAFCGALLDGGAGGPPAFTTSVR 120
Db 61 DARPPPAAPSFQVSCIKELVARVLQRLCERGAKNVLAFCGALLDGGAGGPPAFTTSVR 120
Qy 121 SYLPTVTVDALRGSGAWGLLLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTVTVDALRGSGAWGLLLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPHAGSPRRRLGRCERAWNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKRPR 240
Db 181 ATQARPPHAGSPRRRLGRCERAWNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKRPR 240
Qy 241 GAAPERTPVGQSWAHPCRTGSDRGFCVSPAPAEATSLGALSSTRHSHPVG 300
Db 241 GAAPERTPVGQSWAHPCRTGSDRGFCVSPAPAEATSLGALSSTRHSHPVG 300
Qy 301 ROHAGPSTSRPRPMDTPCPVVAETKHFYSSGDKQELRPSFLSSLRPSLTGARRL 360
Db 301 ROHAGPSTSRPRPMDTPCPVVAETKHFYSSGDKQELRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKQGSVAAPAEEDTDPRRLVQLLRQHSPPQVYGFVRACLRLVPGLWGS 480
Db 421 PAAGVCAREKQGSVAAPAEEDTDPRRLVQLLRQHSPPQVYGFVRACLRLVPGLWGS 480
Qy 481 RHNERRFLRNTKXFIISLGKHAKLSLQELTWKMSVRDCAWLRSPGVCPVAAEHLREEI 540
Db 481 RHNERRFLRNTKXFIISLGKHAKLSLQELTWKMSVRDCAWLRSPGVCPVAAEHLREEI 540
Qy 541 LAKFLHLMVSVYVVELLRSPFYVTTTFOKNRLFYRKSVMSKLSQIGIRQHLKRVOLRE 600
Db 541 LAKFLHLMVSVYVVELLRSPFYVTTTFOKNRLFYRKSVMSKLSQIGIRQHLKRVOLRE 600
Qy 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVA 660
Db 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVA 660
Qy 661 LFSVLNVERARRPGLLGASVLGLDDIHRAMRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRAMRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
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Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLPYMRQFVAHL 780
Qy 781 QETSPURDAVIEQSSSLNEASSGLFDVLRFMCHHAVIRGKSVYVOCQIGPQSGIISLTL 840
Db 781 QETSPURDAVIEQSSSLNEASSGLFDVLRFMCHHAVIRGKSVYVOCQIGPQSGIISLTL 840
Qy 841 LCSLCYGD MENKLFAGIRRDGLLRLVDLFLTPHLLTHAKTFLTLTVRGVPEYGCVVNL 900
Db 841 LCSLCYGD MENKLFAGIRRDGLLRLVDLFLTPHLLTHAKTFLTLTVRGVPEYGCVVNL 900
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Db 841 LCSLCYGMENKLFAGIRDRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGVVNL 900
Qy 901 RKTUVNFPVEDALGTAQVQMPAHLGFWCGLLDTRTLEVOSSDYSSVARTSIRASLTF 960
Db 901 RKTUVNFPVEDALGTAQVQMPAHLGFWCGLLDTRTLEVOSSDYSSVARTSIRASLTF 960
Qy 961 NRGFKAGNRMRKLGVLRLKCHSLFLDLQVNSLOTVCVTNIYKILLQAYRPHACVLOLP 1020
Db 961 NRGFKAGNRMRKLGVLRLKCHSLFLDLQVNSLOTVCVTNIYKILLQAYRPHACVLOLP 1020
Qy 1021 FHOQVWKNPTFFLRVISTASLCYILKAKNAGMSLGAAGPLPSEAVOMLCHOAELL 1080
Db 1021 FHOQVWKNPTFFLRVISTASLCYILKAKNAGMSLGAAGPLPSEAVOMLCHOAELL 1080
Qy 1081 KLTRHRTVYVPLGSLRTAQTLRSKLPFGTTTLTALEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRTVYVPLGSLRTAQTLRSKLPFGTTTLTALEAAANPALPSDFKTILD 1132

RESULT 7
US-09-052-919-2
; Sequence 2, Application US/09052919
; Patent No. 6444650
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Antisense Compositions for Detecting and
; TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,919
; FILING DATE: 31-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,549
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,584
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 015389-003600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-052-919-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCARVRSLLRSHYREVLPLATFVRRLGPGQWRVLRVQGDPAAPRALVAQCILVCVPM 60
Db 1 MPRAPRCARVRSLLRSHYREVLPLATFVRRLGPGQWRVLRVQGDPAAPRALVAQCILVCVPM 60
Qy 61 DARPPAAPSPRQVSCIKELVARVLQRLCERGAKNVLAFGFALLDARGGPPFAFTTSVR 120
Db 61 DARPPAAPSPRQVSCIKELVARVLQRLCERGAKNVLAFGFALLDARGGPPFAFTTSVR 120
Qy 121 SYLENTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLENTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
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Db 181 ATOARPPPHASGPRRLGRCERAWNHSVREACVPLGLPAPGARRRGSSASRSIPLPKRRR 240
Qy 241 GAPEPERTPVQGSWAHPGRTGRGFCVSPARPAEATSLGALSCTRHSHPVSG 300
Db 241 GAPEPERTPVQGSWAHPGRTGRGFCVSPARPAEATSLGALSCTRHSHPVSG 300
Qy 301 ROHAGPPSTRPPRPMDTTPCPVYAEKHPLYSGGKEQLRPSFLSSLPSTGARRL 360
Db 301 ROHAGPPSTRPPRPMDTTPCPVYAEKHPLYSGGKEQLRPSFLSSLPSTGARRL 360
Qy 361 VETIFLGSRPMPGTPRRLPRLPORYQWMLPFLLELLGNHAQCYPVGLLTKHCPRAAVT 420
Db 361 VETIFLGSRPMPGTPRRLPRLPORYQWMLPFLLELLGNHAQCYPVGLLTKHCPRAAVT 420
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Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQVYGVFVACLRRLVPPGLWGS 480
Qy 481 RHNERFRINTKFPISLGKIAKLSLOELTWKMSVRDCAWLRSPGVGCVPAEHLRBEI 540
Db 481 RHNERFRINTKFPISLGKIAKLSLOELTWKMSVRDCAWLRSPGVGCVPAEHLRBEI 540
Qy 541 LAKELHLMMSVYVVELLRSFYVTETTFQKNRLFYKSVMSKLOSTGIROHLKRVQRE 600
Db 541 LAKELHLMMSVYVVELLRSFYVTETTFQKNRLFYKSVMSKLOSTGIROHLKRVQRE 600
Qy 601 LSEAEVRQHRREARPALLTSLRFLPKPDGLRPIVNMMDYVVGARTFRREKRAERLTSRVKA 660

Db 601 LSEAEVROHREARPPALLTSRLRFLPKPDGLRPIVMDYVVGARTFRREKRAERTLSRKA 660
Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRARTFVLVRVRAQPPPELYFKVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRARTFVLVRVRAQPPPELYFKVKVDVTGAYDTI 720
Qy 721 PQDLRLTEVIASIIKPNQTYCYRRYAVVQKAAGHVRKAFKSHVSTLTDLQYMRQFVAHL 780
Db 721 PQDLRLTEVIASIIKPNQTYCYRRYAVVQKAAGHVRKAFKSHVSTLTDLQYMRQFVAHL 780
Qy 781 QETSLRDAVIEQSSSINEASSGLFDVFLRFPMCHAVIRKGSYVQCGIPQGSII STL 840
Db 781 QETSLRDAVIEQSSSINEASSGLFDVFLRFPMCHAVIRKGSYVQCGIPQGSII STL 840
Qy 841 LCSLCYGMENKLFAGIRRDGLLRLLRVDVFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRRDGLLRLLRVDVFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
Qy 901 RKTWNFFVEBALGCTAFVQMPAHGLPPWCGLLLDTRTLEVOQSDYSSYARTSIRASLTF 960
Db 901 RKTWNFFVEBALGCTAFVQMPAHGLPPWCGLLLDTRTLEVOQSDYSSYARTSIRASLTF 960
Qy 961 NRGFKAGNMRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVILQLP 1020
Db 961 NRGFKAGNMRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVILQLP 1020
Qy 1021 FHQQWKNTFFLRVISDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQQWKNTFFLRVISDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTHRVTVYVPLLSRLTAQTLQRKLPGLTTLTALEAANPALPSDFKTIILD 1132
Db 1081 KLTHRVTVYVPLLSRLTAQTLQRKLPGLTTLTALEAANPALPSDFKTIILD 1132

RESULT 8

US-08-912-951-2
; Sequence 2, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-912-951-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPVPLATEFVRLPGQWRLVQGPAAFRALVAOCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPVPLATEFVRLPGQWRLVQGPAAFRALVAOCLVCVPW 60

Qy 61 DARPPPAAPSFQVSCIKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
Db 61 DARPPPAAPSFQVSCIKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

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Db 181 ATQARPPPHASGPRRLRGCEANWHSVREAGVPLGLPAPGARRRGGSASRSLPLPKPRR 240

Qy 241 GAAPEPRTVGGQSWAHPORTRGPSDRGFCVVSPPAPAEATSLGALSCTRHSHPVG 300
Db 241 GAAPEPRTVGGQSWAHPORTRGPSDRGFCVVSPPAPAEATSLGALSCTRHSHPVG 300

Qy 301 ROHHAGPSTSRPPRMDTFCPPVYAEKFLYSSGDKQLRPSFLLSSLRPSLTGARRL 360
Db 301 ROHHAGPSTSRPPRMDTFCPPVYAEKFLYSSGDKQLRPSFLLSSLRPSLTGARRL 360

Qy 361 VETIFLGSREPMFGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCFLRAAVT 420
Db 361 VETIFLGSREPMFGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCFLRAAVT 420

Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRLVQLLRQHSPPQWYGVFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEDTDPRLVQLLRQHSPPQWYGVFVRACLRLVPPGLWGS 480

Qy 481 RHNERFLRNTKKFISLGHAKLSLQELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
Db 481 RHNERFLRNTKKFISLGHAKLSLQELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540

Qy 541 LAKFLHMLMSVYVVELLSRFFVYTTTFQKNRLLFFRYKSVMSKIQSIGIRQHLKRVQURE 600
Db 541 LAKFLHMLMSVYVVELLSRFFVYTTTFQKNRLLFFRYKSVMSKIQSIGIRQHLKRVQURE 600

QY 601 LSEAEVQHQREARPAALLTSRLRPIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVQHQREARPAALLTSRLRPIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNBERARRPGLLGASVLGDDIHRAWRTPVLKRAQDPPPELYFKVVDVTCAYDTI 720
Db 661 LFSVLNBERARRPGLLGASVLGDDIHRAWRTPVLKRAQDPPPELYFKVVDVTCAYDTI 720
QY 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPTMRQFVAHL 780
Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPTMRQFVAHL 780
QY 781 QTSPLRDVAVTEQSSLINEASGLFDVPLRPMCHHAVIRKSVYQCGIPIQSGSILSTL 840
Db 781 QTSPLRDVAVTEQSSLINEASGLFDVPLRPMCHHAVIRKSVYQCGIPIQSGSILSTL 840
QY 841 LCSLCYGDMEKLFAGIRDDGLLRLVDDFLAVTHTLTHAKTFLRTLVGRVPEYGCNVNL 900
Db 841 LCSLCYGDMEKLFAGIRDDGLLRLVDDFLAVTHTLTHAKTFLRTLVGRVPEYGCNVNL 900
QY 901 RKTVNVFVEDEALGTAFAVQMPAHGLFPWCGLLDDTRTLEVSQSYSSVARTSIRASLTF 960
Db 901 RKTVNVFVEDEALGTAFAVQMPAHGLFPWCGLLDDTRTLEVSQSYSSVARTSIRASLTF 960
QY 961 NRGFKAGRNMRKLFQVLRKCHSLFLDLQVNSLOTVCNTNIYKILLQAYRHFACVLQLP 1020
Db 961 NRGFKAGRNMRKLFQVLRKCHSLFLDLQVNSLOTVCNTNIYKILLQAYRHFACVLQLP 1020
QY 1021 FHQQVWKQNTPTFLRVISDTASICYSLKAKNAGMSLGAKGAGPLPSEAVOMLCHOAFL 1080
Db 1021 FHQQVWKQNTPTFLRVISDTASICYSLKAKNAGMSLGAKGAGPLPSEAVOMLCHOAFL 1080
QY 1081 KLTRHRVTYVPLGLSLRTAQTLQSLRKLPGTTLTALAAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLGLSLRTAQTLQSLRKLPGTTLTALAAAANPALPSDFKTILD 1132

RESULT 9

US-09-402-181B-2
; Sequence 2, Application US/09402181B
; Patent No. 6610839

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/402,181B

APPLICATION NUMBER: US/09/402,181B

FILING DATE: 29-Sep-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1132 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-402-181B-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MPAPRCBAVSLRSHYREVLPATFVRRLGPOGWRIVQGRDPAAFALVAQCLVCPWM 60

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QY 121 SYLNTVTDALRGSGANGLLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPYQLGA 180
Db 121 SYLNTVTDALRGSGANGLLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPYQLGA 180

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Db 181 ATOARPPPHASGPRRLGCEANWHSVEAGVPLGAPAGARRGGSASRSIPLPKRRR 240

QY 241 GAAPEPERTVQGSWAHPGTRGSPDRGFCVSPARPAEATSLGALSGRHSHPSVG 300
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Db 301 ROHAGPESTSRPRPMDTPCPVYAEATKHFYLSGDKQLRPSFLLSLRPSLTGARRL 360

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Db 361 VETIFLGSRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420

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Db 481 RHNERRFLRNTKTFISLGKHAQLSLQELTWKMSVRDCAWLRSPGVCPVAAEHLRBEI 540

QY 541 LAKFLHMLSVYVVELLRSPFFVTETTPQKRLFFYRKSVMSKLOSIGIROHLKRVQRE 600
Db 541 LAKFLHMLSVYVVELLRSPFFVTETTPQKRLFFYRKSVMSKLOSIGIROHLKRVQRE 600

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Qy 601 LSEAEVROHREARPALLTSRLRFIPKPDGLRPIVNMDDVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVROHREARPALLTSRLRFIPKPDGLRPIVNMDDVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNYSERARRPGLLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYSERARRPGLLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVVRKAFKSHVSTLTDLQPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVVRKAFKSHVSTLTDLQPYMRQFVAHL 780
Qy 781 QETSLRDAVTEQSSSINEASSGLFDVFLRPMCHHVRIRGKSVQCGIPQGSILSTL 840
Db 781 QETSLRDAVTEQSSSINEASSGLFDVFLRPMCHHVRIRGKSVQCGIPQGSILSTL 840
Qy 841 LCSLCYGMENKLFAGIRDDGLLRVDDFLVTPHLTHAKTFLTLVRGVPEYGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRDDGLLRVDDFLVTPHLTHAKTFLTLVRGVPEYGCVVNL 900
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Qy 961 NRGFKAGNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNLYKILLQAYRHFACVLQLP 1020
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Qy 1021 FHQQVWKNPFTFLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQQVWKNPFTFLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTHRRVTVPLGLSLRTAQQLSKPLPGTTLTALAAAANPALPSDFKTLID 1132
Db 1081 KLTHRRVTVPLGLSLRTAQQLSKPLPGTTLTALAAAANPALPSDFKTLID 1132
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RESULT 10

US-09-721-456-2

Sequence 2, Application US/09721456

Patent No. 6617110

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456

FILING DATE: 22-Nov. 6617110-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

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;
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-721-456-2

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Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRLGPOGWRVLVQGDPAAPFALVAQCLVCPW 60
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Db 61 DARPPPAAPSPROVSCLELVARVLQRLCERGANVLAFGFALLDARGGPEAFTTSVR 120
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Db 301 RQHHAGPSTSRPPRPMWDTFCPPVYATKHFLLYSSGDKQLRPSFLSSLRPSLTGARRL 360
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Db 361 VETIFLGSRRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVOLLROHSSPWQVYGFVACLRRLVPPGLMGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVOLLROHSSPWQVYGFVACLRRLVPPGLMGS 480
Qy 481 RHNERRFLRNTKPFISLGKHAQSLQBLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERRFLRNTKPFISLGKHAQSLQBLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

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QY 541 LAKELHLMVSVVWELLRSFFVYVTTTFOKNRLFFYRKSVWKSQSIGIRQHLKRVQURE 600
 Db 541 LAKELHLMVSVVWELLRSFFVYVTTTFOKNRLFFYRKSVWKSQSIGIRQHLKRVQURE 600
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 Db 601 LSEAEVRQREARPAALLTSRLRAPIPKPDGLRPIVMDYVVGARTFRREKRAERLTSRVKA 660
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 Db 661 LFSVLNYERARPGLLGASVLGLDDIHRAMRTFVLKRAQDPPPELYFKVDVDTGAYDTI 720
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 Db 961 NRGFKAGNMRRLKFGVLRKCHSLFDLQVNSLOTCTNIYKILLQAYRHACVLOLP 1020
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 Db 1021 FHQQWKNPTFLRVIDSTASICYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
 QY 1081 KLTHRVTVYVLLGLSLRTAQOLSKLPCTTTLTALAAANPALPSDFKTILD 1132
 Db 1081 KLTHRVTVYVLLGLSLRTAQOLSKLPCTTTLTALAAANPALPSDFKTILD 1132

RESULT 11

US-09-953-052-2
 ; Sequence 2, Application US/09953052
 ; Patent No. 6627619
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; Lingner, Joachim
 ; Nakamura, Toru
 ; Chapman, Karen B.
 ; Morin, Gregg B.
 ; Harley, Calvin B.
 ; Andrews, William H.
 ;
 ; TITLE OF INVENTION: Antisense Compositions for Detecting and
 ; Inhibiting Telomerase Reverse Transcriptase
 ;
 ; NUMBER OF SEQUENCES: 72
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/953,052
 ; FILING DATE: 14-Sep-2001
 ; CLASSIFICATION: <Unknown>
 ;
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/052,919
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/974,549
 FILING DATE: 19-NOV-1997
 APPLICATION NUMBER: US 08/974,584
 FILING DATE: 19-NOV-1997
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Parent, Annette S.
 REGISTRATION NUMBER: 42,058
 REFERENCE/DOCKET NUMBER: 015389-00360005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-953-052-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPAPRCRAVRSLLRSHYREVLPVPLATFVRRLGPGQWRVLRQGDPAAFRALVAQCVCVPM 60
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 Db 61 DARPPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEAFTTSVR 120
 QY 121 SYLNTVTDALRGSGAWGLLRLRVGDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 Db 121 SYLNTVTDALRGSGAWGLLRLRVGDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 QY 181 ATQARPPPHASGPRRLGCRANWHSVREACVPLGLPAGARRRGGSASRSIPLPKRRR 240
 Db 181 ATQARPPPHASGPRRLGCRANWHSVREACVPLGLPAGARRRGGSASRSIPLPKRRR 240
 QY 241 GAAPEPERTVPGQSWAHPGTRGPGSDRGFCVSPARPAAEATSLLEGALSSTRHSPSVG 300
 Db 241 GAAPEPERTVPGQSWAHPGTRGPGSDRGFCVSPARPAAEATSLLEGALSSTRHSPSVG 300
 QY 301 RQHAGPPSTSRPPRPMDTPCPVYAEKHFLLYSQDKEQLRPSFLJSSLPSTGARRL 360
 Db 301 RQHAGPPSTSRPPRPMDTPCPVYAEKHFLLYSQDKEQLRPSFLJSSLPSTGARRL 360
 QY 361 VETIFLGSRRPMPGTPRRLPQRYQWQMRPLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
 Db 361 VETIFLGSRRPMPGTPRRLPQRYQWQMRPLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
 QY 421 PAAGVCAREKPGQSWAAPEEDTDPRRLVQLLRQHSSPQVYGFVRACLRLVPPGLWGS 480

Db 421 PAAGVCAEKEQGSVAAREEEDTDPRRLVQLLRQHSSPQYVGFVRACLRRLVPPGLNGS 480
Qy 481 RHNERFLRNTKFTSLGKHAKLSIQELTWKMSVRDCAWLRSPGVCVPAAEHRLREI 540
Db 481 RHNERFLRNTKFTSLGKHAKLSIQELTWKMSVRDCAWLRSPGVCVPAAEHRLREI 540
Qy 541 LAKFLHLMMSVVVVELLSFFVTTTFFOKRLFFYKSVMSKLSQIGIROHLKRVQRE 600
Db 541 LAKFLHLMMSVVVVELLSFFVTTTFFOKRLFFYKSVMSKLSQIGIROHLKRVQRE 600
Qy 601 LSEAEVROHREARPAALLSRFLPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRKA 660
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Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPNQTYCVRRAVQKAAHGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPNQTYCVRRAVQKAAHGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
Qy 781 QETSLRDAVIEQSSSINEASSGLFDVFLRFMCHHAVIRGKSVQCGIPQGSILSTL 840
Db 781 QETSLRDAVIEQSSSINEASSGLFDVFLRFMCHHAVIRGKSVQCGIPQGSILSTL 840
Qy 841 LCSLCYGMENKLFAGIRRDGLLRLLVDLFTLPHLTHAKTFLTLVRGVPYGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRRDGLLRLLVDLFTLPHLTHAKTFLTLVRGVPYGCVVNL 900
Qy 901 RKTUVNFEDEALGGTAFVQMPAHGLFPWCGLLDTTLEVSQSDYSYARTSIRASLTF 960
Db 901 RKTUVNFEDEALGGTAFVQMPAHGLFPWCGLLDTTLEVSQSDYSYARTSIRASLTF 960
Qy 961 NRGFKAGNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Qy 1021 FHQVKNKPTFLRVLSTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAPLL 1080
Db 1021 FHQVKNKPTFLRVLSTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAPLL 1080
Qy 1081 KLTHRVTVVPLGLSLRTAQTLSKLPCTTLTALAAANPALPSDFKTILD 1132
Db 1081 KLTHRVTVVPLGLSLRTAQTLSKLPCTTLTALAAANPALPSDFKTILD 1132

RESULT 12

US-09-042-460-3

; Sequence 3, Application US/09042460

; Patent No. 6767719

; GENERAL INFORMATION:

; APPLICANT: Morin, Gregg B.

; APPLICANT: Allsopp, Richard

; APPLICANT: Depinho, Ronald

; APPLICANT: Greenberg, Roger

; TITLE OF INVENTION: Mouse Telomerase Reverse Transcriptase

; NUMBER OF SEQUENCES: 101

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/042,460

; FILING DATE: 16-MAR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,549
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,584
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/979,742
; FILING DATE: 26-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 0153899-0031100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1132
; OTHER INFORMATION: /note="human telomerase reverse
; OTHER INFORMATION: transcriptase (hTERT)"
; US-09-042-460-3

Query Match 100.0%; Score 5961; DB 4; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLLGPOCWLVRGDDPAAFRALVAQCILVCVWP 60

Db 1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLLGPOCWLVRGDDPAAFRALVAQCILVCVWP 60

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Db 61 DARPPPAAPSPRQVSCILKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEFTTSVR 120


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QY 121 SYLNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPYQLGA 180
Db 121 SYLNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPYQLGA 180
QY 181 ATQARPPPHASGRRLRCERAWNSVREAGVPLGLPAGCARRRGSGASRSIPLPKRPR 240
Db 181 ATQARPPPHASGRRLRCERAWNSVREAGVPLGLPAGCARRRGSGASRSIPLPKRPR 240
QY 241 GAAPPERTPVQGGSWAHPTGRGSDRGFCVVSAPPAEATSLGALSGRHSHPSVG 300
Db 241 GAAPPERTPVQGGSWAHPTGRGSDRGFCVVSAPPAEATSLGALSGRHSHPSVG 300
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Db 301 ROHAGPSTSRPPRPMDTPCPVVAETKHFYLSGDKQLRPSFLLSRLPSLTGARRL 360
QY 361 VETIFLGRPMWPGTTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGRPMWPGTTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPOGSAVAPEEEDTDPRRLVOLLROHSSPMQVYGFVRACLRRLVPPGLMGS 480
Db 421 PAAGVCAREKPOGSAVAPEEEDTDPRRLVOLLROHSSPMQVYGFVRACLRRLVPPGLMGS 480
QY 481 RHNERFLRNTKFFISLGKHAHLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLRBEI 540
Db 481 RHNERFLRNTKFFISLGKHAHLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLRBEI 540
QY 541 LAKFLHLMVSVVVELLSRFFVYTTTQKNRLLFFYKSVWSKLSQSIGIRQHLKRVQRE 600
Db 541 LAKFLHLMVSVVVELLSRFFVYTTTQKNRLLFFYKSVWSKLSQSIGIRQHLKRVQRE 600
QY 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVA 660
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QY 661 LFSVLNVERARRPGLLGASVLGLDDIHRAWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRAWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
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Db 721 PODRLTEVIASIIKPONTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSPLRDVAVIEQSSSLEASSGLFDVFLRPMCHHAVIRGKSVVQCGIPQGSILSTL 840
Db 781 QETSPLRDVAVIEQSSSLEASSGLFDVFLRPMCHHAVIRGKSVVQCGIPQGSILSTL 840
QY 841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVEYCVVNL 900
Db 841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVEYCVVNL 900
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Db 901 RKTVVNFVEDEALGCTAFVQMPAHLFPWCGLLDTRTLEQSDSYSSYARTSIRASITF 960
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Db 961 NRGFKAGNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLLOAYRPHACVLOLP 1020
QY 1021 FHOQWKNTFFLRVISTASLCYSILKAKNAGMSLGAGAPLPSEAVOMLCHOAELL 1080
Db 1021 FHOQWKNTFFLRVISTASLCYSILKAKNAGMSLGAGAPLPSEAVOMLCHOAELL 1080
QY 1081 KLTHRVTVYVPLGSLRTAQQLSRKLPFGTTLTALAAANPALPSDFDKTILD 1132
Db 1081 KLTHRVTVYVPLGSLRTAQQLSRKLPFGTTLTALAAANPALPSDFDKTILD 1132

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RESULT 13
 US-09-949-016-6326
 ; Sequence 6326, Application US/09949016

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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6326
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6326

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Query Match 100.0%; Score 5961; DB 4; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 SYLNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPYQLGA 180
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QY 241 GAAPPERTPVQGGSWAHPTGRGSDRGFCVVSAPPAEATSLGALSGRHSHPSVG 300
Db 241 GAAPPERTPVQGGSWAHPTGRGSDRGFCVVSAPPAEATSLGALSGRHSHPSVG 300
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Db 361 VETIFLGRPMWPGTTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPOGSAVAPEEEDTDPRRLVOLLROHSSPMQVYGFVRACLRRLVPPGLMGS 480
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QY 541 LAKFLHLMVSVVVELLSRFFVYTTTQKNRLLFFYKSVWSKLSQSIGIRQHLKRVQRE 600
Db 541 LAKFLHLMVSVVVELLSRFFVYTTTQKNRLLFFYKSVWSKLSQSIGIRQHLKRVQRE 600
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Db 721 PODRLTEVIASIIKPNQTYCVRRAVAVQKAAGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
Qy 781 QETSPLRDAVIEQSSSINEASSGLFDVFLRPMCHHAVIRGKSVVOCQGIPOGSIILSTL 840
Db 781 QETSPLRDAVIEQSSSINEASSGLFDVFLRPMCHHAVIRGKSVVOCQGIPOGSIILSTL 840
Qy 841 LCSLCYGMENKLFAGIRRDGLLRLLRVDVFLVPHLTHAKTFLRTLVRGVPEYGCVVNL 900
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Qy 961 NRGFKAGNMRKLFGLVRLKCHSLFLLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
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Qy 1021 FHQQVWKNPFTFLRVIDSTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQQVWKNPFTFLRVIDSTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTHRVTVYVLLGSLRTAQTLQSLKPLGTTLTALAAANPALPSDFKTIILD 1132
Db 1081 KLTHRVTVYVLLGSLRTAQTLQSLKPLGTTLTALAAANPALPSDFKTIILD 1132
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RESULT 14

US-08-974-549A-611
Sequence 611, Application US/08974549A

Patent No. 6166178

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harlev, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

STREET: Townsend and Townsend and Crew LLP
CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A

FILING DATE: 19-NOV-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 611:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1154
OTHER INFORMATION: /note="fusion protein composed of hTERT
protein sequence, vector sequences, the
OTHER INFORMATION: Myc epitope and His6 tag"
US-08-974-549A-611

Query Match

Best Local Similarity 100.0%; Score 5961; DB 3; Length 1154;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 421 PAAGVCAREKFPQGSVAAPAEEDTDRRLVQLLRQHSFPQVYGFVRACLRRLVPPGLWS 480
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Db 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSSPMQVYGFVRACLRLRLLVPPGLMGS 480
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Db 481 RINERRFLNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREI 540
Qy 541 LAKFLHMLSVVVELLRSFFVYTTTFOKNRLFFYRKSVMSKLSQSIGIRQHLKRVOLRE 600
Db 541 LAKFLHMLSVVVELLRSFFVYTTTFOKNRLFFYRKSVMSKLSQSIGIRQHLKRVOLRE 600
Qy 601 LSEAEVROHREARPAALLTSLRBFIPKPDGLRPIVNDYVVGARTFREKRAERLTSRKA 660
Db 601 LSEAEVROHREARPAALLTSLRBFIPKPDGLRPIVNDYVVGARTFREKRAERLTSRKA 660
Qy 661 LFSVLNYERARPGILGASVLGLDDIHRARWTFVLRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARPGILGASVLGLDDIHRARWTFVLRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
Qy 781 QESTPLRDAVWLEQSSSLNEASSGLFDVFLRPMCHHVRIRKSVYQCOGIPQGSILSTL 840
Db 781 QESTPLRDAVWLEQSSSLNEASSGLFDVFLRPMCHHVRIRKSVYQCOGIPQGSILSTL 840
Qy 841 LCSLCYGDMEKFLAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVMNL 900
Db 841 LCSLCYGDMEKFLAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVMNL 900
Qy 901 RKTVMNPFVEDBALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSYSSYARTSIRASLTF 960
Db 901 RKTVMNPFVEDBALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSYSSYARTSIRASLTF 960
Qy 961 NRGFKAGNRMRKLGVLRLKCHSLFDLOVNSLQTVCTNIYKILLQAYRHACVQLQP 1020
Db 961 NRGFKAGNRMRKLGVLRLKCHSLFDLOVNSLQTVCTNIYKILLQAYRHACVQLQP 1020
Qy 1021 FHOQWKQNTFFLRVISTASLCYSLKAKNAGMSLGAKAAGPLPSEAVOMLCHQAFLL 1080
Db 1021 FHOQWKQNTFFLRVISTASLCYSLKAKNAGMSLGAKAAGPLPSEAVOMLCHQAFLL 1080
Qy 1081 KLTHRVTVVPLGLSLRTAQTLQSLRKLPGTTTILEAAANPALPSDFKTILD 1132
Db 1081 KLTHRVTVVPLGLSLRTAQTLQSLRKLPGTTTILEAAANPALPSDFKTILD 1132

RESULT 15
US-08-912-951-323
; Sequence 323, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/912,951

FILING DATE: 14-AUG-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002600US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 323:

SEQUENCE CHARACTERISTICS:

LENGTH: 1154 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-912-951-323

Query Match 100.0%; Score 5961; DB 4; Length 1154;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRRLGPGQWRLVQRGDPAAFRALVAQCLVCPW 60

Qy 61 DARPPPAAPSPFQVSCLELVARVLQRLCERGAKNVLAFFGALLDGGAGGPEAFTTSVR 120

Db 61 DARPPPAAPSPFQVSCLELVARVLQRLCERGAKNVLAFFGALLDGGAGGPEAFTTSVR 120

Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy 181 ATQARPPPHASGPRRLGCERAWNHSVREAGVPLGAPARRRRGGSASRSLPLPKRPRR 240

Db 181 ATQARPPPHASGPRRLGCERAWNHSVREAGVPLGAPARRRRGGSASRSLPLPKRPRR 240

Qy 241 GAAPEPERTVQGGSWAHPGTRGPDRCFCVVSAPAEATSLGALSGTRHSHPSVG 300

Db 241 GAAPEPERTVQGGSWAHPGTRGPDRCFCVVSAPAEATSLGALSGTRHSHPSVG 300

Qy 301 RQHAGPPESTRPRPMDTTPCPVVAETKHFYSSGDKQLRPSFLLSLRPSLTGARRL 360

Db 301 RQHAGPPESTRPRPMDTTPCPVVAETKHFYSSGDKQLRPSFLLSLRPSLTGARRL 360

Qy 361 VETIFLGSRRPWWPGTPRRLPRLPQRYQWMRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420

Db 361 VETIFLGSRRPWWPGTPRRLPRLPQRYQWMRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420

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QY 421 PAAGVCAREKPGQSVAAPEEDTDPRLVOLLROHSSPMQVYGVFRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEDTDPRLVOLLROHSSPMQVYGVFRACLRRLVPPGLWGS 480
QY 481 RHNERRFLNKKFTISLGHAKLSIQELTWKMSVRDCAWLRRSPQVGCVPAAEHLRLEEI 540
Db 481 RHNERRFLNKKFTISLGHAKLSIQELTWKMSVRDCAWLRRSPQVGCVPAAEHLRLEEI 540
QY 541 LAKFLHMLSVVVELLSRFPYVTTETTFQKNRLFFYRKSVMSKLSQSIGIRQHLKRVQRE 600
Db 541 LAKFLHMLSVVVELLSRFPYVTTETTFQKNRLFFYRKSVMSKLSQSIGIRQHLKRVQRE 600
QY 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMDDVVGARTFRKRAERLTSRVKA 660
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QY 661 LFSVLNVERARRPGLLGASVLGLDDIHRAMWTFVLRVRAQDPPPELYFVKVDVDTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRAMWTFVLRVRAQDPPPELYFVKVDVDTGAYDTI 720
QY 721 PODRLTEVIASIIKPNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSPRLDAVIEQSSSINEASSGLFDVFLRPMCHHVRIRGKSVQCGIPQGSILSTL 840
Db 781 QETSPRLDAVIEQSSSINEASSGLFDVFLRPMCHHVRIRGKSVQCGIPQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRDDGLLRLVDDFLVPLPHTHAKTFLRTLVRGVPYGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRDDGLLRLVDDFLVPLPHTHAKTFLRTLVRGVPYGCVVNL 900
QY 901 RKTVMNFPVEALGCTAFVQMPAHGLFPWCGLLDTRTLTVQSDYSSYARTSIRASLTF 960
Db 901 RKTVMNFPVEALGCTAFVQMPAHGLFPWCGLLDTRTLTVQSDYSSYARTSIRASLTF 960
QY 961 NRGFKAGNMRKLGVLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRHFACVLQLP 1020
Db 961 NRGFKAGNMRKLGVLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRHFACVLQLP 1020
QY 1021 FHQQWKNPTFFLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVOWLCHQAFLL 1080
Db 1021 FHQQWKNPTFFLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVOWLCHQAFLL 1080
QY 1081 KLTHRVTVYVPLLSLRTAQQLSRKLPQTTLTALAAANPALPSDFKTLTD 1132
Db 1081 KLTHRVTVYVPLLSLRTAQQLSRKLPQTTLTALAAANPALPSDFKTLTD 1132
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RESULT 16

US-09-402-181B-611

; Sequence 611, Application US/09402181B

; Patent No. 6610839

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin B.

; Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 633

; CORRESPONDENCE ADDRESS:

; ADDRESS: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/402.181B
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; FILING DATE: 29-Sep-1997
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```
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
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```
; APPLICATION NUMBER: US 08/724,643
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```
; FILING DATE: 01-OCT-1996
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```
; APPLICATION NUMBER: US 08/844,419
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; FILING DATE: 18-APR-1997
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; APPLICATION NUMBER: US 08/846,017
```

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; FILING DATE: 25-APR-1997
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; APPLICATION NUMBER: US 08/851,843
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; FILING DATE: 06-MAY-1997
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; APPLICATION NUMBER: US 08/854,050
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; FILING DATE: 09-MAY-1997
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; APPLICATION NUMBER: US 08/911,312
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; FILING DATE: 14-AUG-1997
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; APPLICATION NUMBER: US 08/912,951
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; FILING DATE: 14-AUG-1997
```

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; APPLICATION NUMBER: US 08/915,503
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; FILING DATE: 14-AUG-1997
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; APPLICATION NUMBER: WO PCT/US97/17885
```

```
; FILING DATE: 01-OCT-1997
```

```
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Ausenhus, Scott L.
```

```
; REGISTRATION NUMBER: 42,271
```

```
; REFERENCE/DOCKET NUMBER: 015389-002620US
```

```
; TELECOMMUNICATION INFORMATION:
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```
; TELEPHONE: (415) 576-0200
```

```
; TELEFAX: (415) 576-0300
```

```
; INFORMATION FOR SEQ ID NO: 611:
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```
; SEQUENCE CHARACTERISTICS:
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```
; LENGTH: 1154 amino acids
```

```
; TYPE: amino acid
```

```
; STRANDEDNESS: <Unknown>
```

```
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: protein
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; FEATURE:
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; NAME/KEY: Protein
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```
; LOCATION: 1..1154
```

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; OTHER INFORMATION: /note= "fusion protein composed of hTERT
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protein sequence, vector sequences, the
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```
Myc epitope and His6 tag"
```

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; SEQUENCE DESCRIPTION: SEQ ID NO: 611:
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US-09-402-181B-611
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Query Match 100.0%; Score 5961; DB 4; Length 1154;
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Best Local Similarity 100.0%; Pred. No. 0;
```

```
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLGPGQWRVLVQRGDPAAFRALVAQCLVCPWM 60
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QY 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGANVLAFGPALLDGGARGGPEAFTTSVR 120
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Db 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGANVLAFGPALLDGGARGGPEAFTTSVR 120
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Db 121 SYLPTNTVTDALRGSGAWGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQGA 180
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Db 361 VETIFLGSRPWPGTFRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
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Db 421 PAAGVCAREKPOGSAVAPEEDTDRRLVQLLRQHSPPQVYGVFRACLRRLVPPGLWGS 480
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Db 541 LAKFLHMLSVVVELLRFFVYTTTFOKNRFFYKRSVWSKLSIGIRQHLKRVQLE 600
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Db 601 LSEAEVRQHREARPAALLTSRLRPIPKPDGLRPIVMNDYVVGARTFRREKRAERLTSRVKA 660
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Db 661 LFSVLNVERARPPGLGASVLGDDIHRARWTFVLRAQDPPPELYFKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKQNTYCVRYAVVQKAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKQNTYCVRYAVVQKAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QTSPLRDAVITQSSSLNEASSGLFDVFLRFMCHHVAIRGKSVYQCGIPQGSILSTL 840
Db 781 QTSPLRDAVITQSSSLNEASSGLFDVFLRFMCHHVAIRGKSVYQCGIPQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRDDGLLLRLVDDFLVTHLTHAKTFLRLVRGVEYGCYNL 900
Db 841 LCSLCYGMENKLFAGIRDDGLLLRLVDDFLVTHLTHAKTFLRLVRGVEYGCYNL 900
QY 901 RKTIVNFPVEDBALGTAFOVMPAGLFPWCGLLDDTRTLEQSYSSVARTSIRASLTF 960
Db 901 RKTIVNFPVEDBALGTAFOVMPAGLFPWCGLLDDTRTLEQSYSSVARTSIRASLTF 960
QY 961 NRGFKAGNRMRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNRMRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
QY 1021 FHQQVKNKPTFLRVISDTASLCYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFIL 1080
Db 1021 FHQQVKNKPTFLRVISDTASLCYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFIL 1080
QY 1081 KLTRHRVTYVPLGLSLRTAQTLSRKLPGTTLTALAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLGLSLRTAQTLSRKLPGTTLTALAAANPALPSDFKTILD 1132

RESULT 17

US-09-721-456-611

Sequence 611, Application US/09721456

Patent No. 6617110

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 611:

SEQUENCE CHARACTERISTICS:

LENGTH: 1154 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..1154

OTHER INFORMATION: /note= "fusion protein composed of hTERT

protein sequence, vector sequences, the

Myc epitope and His6 tag"

SEQUENCE DESCRIPTION: SEQ ID NO: 611:

US-09-721-456-611

Query Match 100.0%; Score 5961; DB 4; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPCRAVPSLLRSHYREVLPATFVRRLGPGQWRVLRQGDPAAFRALVAQCLVCPWM 60
Db 1 MPRAPCRAVPSLLRSHYREVLPATFVRRLGPGQWRVLRQGDPAAFRALVAQCLVCPWM 60
QY 61 DARPPAAPSPQVSCSLKELVARVLQRLCERGAKNVLAFFGALLDCAAGGPEAFTTSVR 120
Db 61 DARPPAAPSPQVSCSLKELVARVLQRLCERGAKNVLAFFGALLDCAAGGPEAFTTSVR 120
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Db 121 SYLNTVTVDALRGSGAWGLLLRRVGDVVLVHLLARCALFVLVAPSCAVQVCGPPYQLGA 180
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Qy 301 RQHAGPSTSRPRPMDTPCPVYAEKTHFLYSKGDEQLRPSFLSSLSPLTGAARL 360
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Db 481 RHNERRFLRNTKFTSLGKHAKLSIQELTWKMSVRDCAWLRSPGVGCVPAEHLREEI 540
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Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRARTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720
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Db 721 PQDRLTEVIASIIIPQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPYMQFVAHL 780
Qy 781 QETSLRDAVTEQSSSINEASSGIFDVLRFPMCHHAVIRGKSVQCGIPQGSILSTL 840
Db 781 QETSLRDAVTEQSSSINEASSGIFDVLRFPMCHHAVIRGKSVQCGIPQGSILSTL 840
Qy 841 LCSLCYGMENKLFAGIRRDGILLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRRDGILLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
Qy 901 RKTVMVFEDEALGGTAFVOMPAGHLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
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Db 961 NRGKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRPHACVLQLP 1020
Qy 1021 FHQQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTHRVTVYVPLGLSLRTAQOLSRKLPGLTTLTALEAAANPALPSDFKTIILD 1132
Db 1081 KLTHRVTVYVPLGLSLRTAQOLSRKLPGLTTLTALEAAANPALPSDFKTIILD 1132

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RESULT 18

US-08-974-549A-613
; Sequence 613, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.

```

; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 0153899-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 613:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1189
; OTHER INFORMATION: /note= "fusion protein composed of
; OTHER INFORMATION: melittin signal sequence and full length

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OTHER INFORMATION: hTBT protein"
US-08-974-549A-613

Query Match	100.0%;	Score 5961;	DB 3;	Length 1189;
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Matches 1132;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLGPOGWRLVQ	RQDPAAFRALVAQCLVCPW 60
DB	58	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLGPOGWRLVQ	RQDPAAFRALVAQCLVCPW 117
QY	61	DARPPAPAFRQVSCLELVARVLQ	RLCERGAKNVLA	FGFALLDGARGGPPPEAFTTSVR 120
DB	118	DARPPAPAFRQVSCLELVARVLQ	RLCERGAKNVLA	FGFALLDGARGGPPPEAFTTSVR 177
QY	121	SVLPNTVTDALRGSGAWGLLLRR	VGGDDVLLVHLLARCALFVL	VAPSCAYQVCGPPLYQLGA 180
DB	178	SVLPNTVTDALRGSGAWGLLLRR	VGGDDVLLVHLLARCALFVL	VAPSCAYQVCGPPLYQLGA 237
QY	181	ATQARPPPHASGPRRLRCERAWN	HSVREAGVPLGLPAPGAR	RRGGSASRSLLPKRPRR 240
DB	238	ATQARPPPHASGPRRLRCERAWN	HSVREAGVPLGLPAPGAR	RRGGSASRSLLPKRPRR 297
QY	241	GAAPERTPVQGSWAHPGTRG	PSDRGFCVVS	PARPAEATSLLEGALSGTRHSPSVG 300
DB	298	GAAPERTPVQGSWAHPGTRG	PSDRGFCVVS	PARPAEATSLLEGALSGTRHSPSVG 357
QY	301	ROHAGPPSTSRPPRPMWDT	PCPVVATKHYFLSSG	KEQLRPSFLSSRLPSLTGARRL 360
DB	358	ROHAGPPSTSRPPRPMWDT	PCPVVATKHYFLSSG	KEQLRPSFLSSRLPSLTGARRL 417
QY	361	VETIFLGRPMWPGTPRRLPRL	PORYWQMRPLFLELLGN	HACQPYGVLLKTHCPLRAAVT 420
DB	418	VETIFLGRPMWPGTPRRLPRL	PORYWQMRPLFLELLGN	HACQPYGVLLKTHCPLRAAVT 477
QY	421	PAGVCAREKPGSVAAP	EEEDTPRRLVOLLRQH	SSPWQVYGFVRACLRRLVPPGLWGS 480
DB	478	PAGVCAREKPGSVAAP	EEEDTPRRLVOLLRQH	SSPWQVYGFVRACLRRLVPPGLWGS 537
QY	481	RHNERFLRNTKFLSLGKHAK	LSLOELTWKMSVRDCA	WLRRSPGVGCVPAAEHLRREI 540
DB	538	RHNERFLRNTKFLSLGKHAK	LSLOELTWKMSVRDCA	WLRRSPGVGCVPAAEHLRREI 597
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DB	598	LAKFLHLMSSVVVELLRS	FFYTTTQKNRLFFYRK	SVMSKLSQIGIRQHLKRVOLRE 657
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DB	658	LSEAEVRQHREARPALLTS	RLRFPKPDGLRPIVNM	DYVVGARTFRREKRAERLTSRVKA 717
QY	661	LFSVLNTERARRPGLLGAS	VLGLDDHRAWRTFVL	RVRAQDPPPELYFVKVDVTGAYDTI 720
DB	718	LFSVLNTERARRPGLLGAS	VLGLDDHRAWRTFVL	RVRAQDPPPELYFVKVDVTGAYDTI 777
QY	721	PODRLTEVIASIIKPNQ	TYCVRYAVVQKAAHGH	VRKAFKSHVSTLTDLQPYMRQFVAHL 780
DB	778	PODRLTEVIASIIKPNQ	TYCVRYAVVQKAAHGH	VRKAFKSHVSTLTDLQPYMRQFVAHL 837
QY	781	QETSPLRDAVVIQSSSL	NEASSGLFDVFLRPMCH	HAVIRGKSVYVQCGIPQGSILSTL 840
DB	838	QETSPLRDAVVIQSSSL	NEASSGLFDVFLRPMCH	HAVIRGKSVYVQCGIPQGSILSTL 897
QY	841	LCSLCYGD MENKLFAGIR	RRDGLLLRLVDDFL	LVTPHLTHAKTFLTLVRGVPYGCNNL 900
DB	898	LCSLCYGD MENKLFAGIR	RRDGLLLRLVDDFL	LVTPHLTHAKTFLTLVRGVPYGCNNL 957
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QY	961	NRGFKAGNMRRLKFGV	RLRKLCHSLFLDLQ	VNSLQVCTNIIYKILLQAYRPHACVQLP 1020

DB	1018	NRGFKAGNMR	KLFGVLR	LKCHSLFLDLQ	VNSLQVCTNIIYKILLQAYRPHACVQLP 1077
QY	1021	FHQQVWKNTF	FLRVIS	DTASICYSILKAK	NAGMSLGAKGAGPLPSEAVQWLCHOAFL 1080
DB	1078	FHQQVWKNTF	FLRVIS	DTASICYSILKAK	NAGMSLGAKGAGPLPSEAVQWLCHOAFL 1137
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DB	1138	KLTHRRVTY	VPVLLGSL	RTRTAQ	TSLSRKLPFGTTLTALEAAANPALPSDFKTILD 1189
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; Sequence 325, Application US/08912951					
; Patent No. 6475789					
; GENERAL INFORMATION:					
; APPLICANT: Cech, Thomas R.					
; APPLICANT: Lingner, Joachim					
; APPLICANT: Nakamura, Toru					
; APPLICANT: Chapman, Karen B.					
; APPLICANT: Morin, Gregg B.					
; APPLICANT: Harley, Calvin					
; APPLICANT: Andrews, William H.					
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND					
; NUMBER OF SEQUENCES: 335					
; CORRESPONDENCE ADDRESS:					
; ADDRESSEE: Townsend and Townsend and Crew LLP					
; STREET: Two Embarcadero Center, 8th Floor					
; CITY: San Francisco					
; STATE: California					
; COUNTRY: United States of America					
; ZIP: 94111					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: Patent In Release #1.0, Version #1.30					
; CURRENT APPLICATION DATA:					
; APPLICATION NUMBER: US/08/912,951					
; FILING DATE: 14-AUG-1997					
; CLASSIFICATION: 435					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: US 08/854,050					
; FILING DATE: 09-MAY-1997					
; CLASSIFICATION: 435					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: US 08/851,843					
; FILING DATE: 06-MAY-1997					
; CLASSIFICATION: 435					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: US 08/846,017					
; FILING DATE: 25-APR-1997					
; CLASSIFICATION: 435					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: US 08/844,419					
; FILING DATE: 18-APR-1997					
; CLASSIFICATION: 435					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: US 08/724,643					
; FILING DATE: 01-OCT-1996					
; CLASSIFICATION: 435					
; ATTORNEY/AGENT INFORMATION:					
; NAME: Apple, Randolph T.					
; REGISTRATION NUMBER: 36,429					
; REFERENCE/DOCKET NUMBER: 015389-002600US					
; TELECOMMUNICATION INFORMATION:					
; TELEPHONE: (415) 576-0200					
; TELEFAX: (415) 576-0300					
; INFORMATION FOR SEQ ID NO: 325:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 1189 amino acids					
; TYPE: amino acid					

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Qy	1021	PHQOVWKNPTFFLRLVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL	1080
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RESULT 20			
US-09-402-181B-613			
; Sequence 613, Application US/09402181B			
; Patent No. 6610839			
GENERAL INFORMATION:			
APPLICANT: Cech, Thomas R.			
Lingner, Joachim			
Nakamura, Toru			
Chapman, Karen B.			
Morin, Gregg B.			
Harley, Calvin B.			
Andrews, William H.			
TITLE OF INVENTION: Human Telomerase Catalytic Subunit			
NUMBER OF SEQUENCES: 633			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Townsend and Townsend and Crew LLP			
STREET: Two Embarcadero Center, Eighth Floor			
CITY: San Francisco			
STATE: California			
COUNTRY: USA			
ZIP: 94111-3834			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
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CLASSIFICATION: <Unknown>			
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FILING DATE: 25-APR-1997			
APPLICATION NUMBER: US 08/851,843			
FILING DATE: 06-MAY-1997			
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APPLICATION NUMBER: US 08/911,312			
FILING DATE: 14-AUG-1997			
APPLICATION NUMBER: US 08/912,951			
FILING DATE: 14-AUG-1997			
APPLICATION NUMBER: US 08/915,503			
FILING DATE: 14-AUG-1997			
APPLICATION NUMBER: WO PCT/US97/17885			
FILING DATE: 01-OCT-1997			
ATTORNEY/AGENT INFORMATION:			
NAME: Ausenhus, Scott L.			
REGISTRATION NUMBER: 42,271			
REFERENCE/DOCKET NUMBER: 015389-002620US			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (415) 576-0200			
TELEFAX: (415) 576-0300			
INFORMATION FOR SEQ ID NO: 613:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 1189 amino acids			
TYPE: amino acid			

STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: protein
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OTHER INFORMATION: /note= "fusion.protein composed of
melittin signal sequence and full length
hTERT protein"
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US-09-402-181B-613

Query Match 100.0%; Score 5961; DB 4; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 SYLNTVTDLRGSGAWGALLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPYQLGA 180
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DB 238 ATOARPPHAGSPRELCCERAWNSVREAGVPLGLPAPGARRRGSASRSILPLKRRR 297
QY 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSGTRHSPVSG 300
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QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLTLVRGVPYGCVVNL 900

DB 898 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLTLVRGVPYGCVVNL 957
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DB 958 RKTVVNPFVEDEALGGTAFOVMPAHGLFPWCGLLDTRTLEVOSSDYSSVARTSIRASLTF 1017
QY 961 NRGFKAGRNMRKLFVLRKCHSLFLDLQVNSLQTVCTNYYKILLQAYRPHACVQLP 1020
DB 1018 NRGFKAGRNMRKLFVLRKCHSLFLDLQVNSLQTVCTNYYKILLQAYRPHACVQLP 1077
QY 1021 FHOQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVOWLCHOAFLL 1080
DB 1078 FHOQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVOWLCHOAFLL 1137
QY 1081 KLTHRRVTVYVPLLGSLRTAQTLQSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
DB 1138 KLTHRRVTVYVPLLGSLRTAQTLQSRKLPGLTTLTALEAAANPALPSDFKTILD 1189
RESULT 21
US-09-721-456-613
; Sequence 613, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.
; ; Morin, Gregg B.
; ; Harley, Calvin B.
; ; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-Nov. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
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; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997

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1021	F	H	Q	O	W	K	N	T	F	F	L	R	V	I	S	D	T	A	S	I	C	Y	S	I	L	K	A	K	N	A	G	M	S	L	G	A	G	A	G	P	L	S	E	A	V	O	M	L	C	H	O	A	F	L	1080	
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1081	K	L	T	R	H	R	V	T	V	P	L	L	G	S	L	R	T	A	O	T	S	R	K	L	P	G	T	T	L	T	A	L	E	A	A	A	N	P	A	L	P	S	D	F	K</											

Qy	421	PAAGVCAREKPGQSVAAPEEEDTDPRLVLQLLRQHSWPQVYGFVACLRRLVPPGLWGS	481
Db	489	PAAGVCAREKPGQSVAAPEEEDTDPRLVLQLLRQHSWPQVYGFVACLRRLVPPGLWGS	548
Qy	481	RHNERRFLRNTKFIISLGKHAKLISOELTWKMSVRDCAWLRSPGVGCVPAAEHRLUREE	540
Db	549	RHNERRFLRNTKFIISLGKHAKLISOELTWKMSVRDCAWLRSPGVGCVPAAEHRLUREE	608
Qy	541	LAKFLHLMMSVYVVELLRSFPYVTTETTFQKNRLFYRKSVMSKLOSIGIROHLKRVLRE	600
Db	609	LAKFLHLMMSVYVVELLRSFPYVTTETTFQKNRLFYRKSVMSKLOSIGIROHLKRVLRE	668
Qy	601	LSEAEVQHREARPAALLTSRLRFPKPDGLRPIVMDYVVGARTFRREKRAEALRSRKA	660
Db	669	LSEAEVQHREARPAALLTSRLRFPKPDGLRPIVMDYVVGARTFRREKRAEALRSRKA	728
Qy	661	LFSVLNTERARRPGLLGASVLGLDDIHRAWTFLVLVRAQDPPPELYFVKVDVTGAYDTI	720
Db	729	LFSVLNTERARRPGLLGASVLGLDDIHRAWTFLVLVRAQDPPPELYFVKVDVTGAYDTI	788
Qy	721	PODLRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLOPYMRQFVAHL	780
Db	789	PODLRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLOPYMRQFVAHL	848
Qy	781	QETSPLRDVAVVEOSSLINEASSGLFDVFLRFMCHHVAIRIRKSVVQCGIPQGSILSTL	840
Db	849	QETSPLRDVAVVEOSSLINEASSGLFDVFLRFMCHHVAIRIRKSVVQCGIPQGSILSTL	908
Qy	841	LCSICYGDMENKLPAGIRRDGLLRLLVDDFLVLTPLHTHAKTFLTLVRGPEYGCNVNL	900
Db	909	LCSICYGDMENKLPAGIRRDGLLRLLVDDFLVLTPLHTHAKTFLTLVRGPEYGCNVNL	968
Qy	901	RKTVVPNFVEDEALGGTAFVQMPAHGLFPPWCGLLLDTRTLEVSQSYSSYARTSIRASLTF	960
Db	969	RKTVVPNFVEDEALGGTAFVQMPAHGLFPPWCGLLLDTRTLEVSQSYSSYARTSIRASLTF	102
Qy	961	NRGFKAGNRMRRLFGVLRLKCHSLFDLDQVNSLQTVCTNYYKILLLOAYRPHACVLQLP	102
Db	1029	NRGFKAGNRMRRLFGVLRLKCHSLFDLDQVNSLQTVCTNYYKILLLOAYRPHACVLQLP	108
Qy	1021	FHQOVKNPFTFFLRVISTASLCSYILKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL	108
Db	1089	FHQOVKNPFTFFLRVISTASLCSYILKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL	114
Qy	1081	KLTRHRYVYVPLGLSLRTAQTOLSRKLPCTGTLTALAAAAANPALPSDFKTLTD	1132
Db	1149	KLTRHRYVYVPLGLSLRTAQTOLSRKLPCTGTLTALAAAAANPALPSDFKTLTD	1200

RESULT 23
US-08-912-951-324
; Sequence 324, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/912,951
;; FILING DATE: 14-AUG-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002600US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 324:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1200 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-912-951-324

Query Match 100.0%; Score 5961; DB 4; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCVAVSLRLSHYREVLPATFVRRLLGPOGWRLLVQRGDPAAPRALVAQCLVCVPW 60
Db 69 MPAPRCVAVSLRLSHYREVLPATFVRRLLGPOGWRLLVQRGDPAAPRALVAQCLVCVPW 128

Qy 61 DARPPPAAPSPQVSCLELVARVLQRCERGAKNVLAQFALLDARGGPEAFTTSVR 120
Db 129 DARPPPAAPSPQVSCLELVARVLQRCERGAKNVLAQFALLDARGGPEAFTTSVR 188

Qy 121 SYLNTVNTDALRGSGAWGLLIRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPLYQLGA 180
Db 189 SYLNTVNTDALRGSGAWGLLIRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPLYQLGA 248

Qy 181 ATQARPPPHAGPRRRLLCERAWNHSVREAGVPLGLPAGPARRRGSGASRLPLPKRPRR 240
Db 249 ATQARPPPHAGPRRRLLCERAWNHSVREAGVPLGLPAGPARRRGSGASRLPLPKRPRR 308

Qy 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPAPAEATSLGALSCTRHSFSPVG 300
Db 309 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPAPAEATSLGALSCTRHSFSPVG 368

Qy 301 ROHAGPSTSRPRPMDTPCPVVAETKHFVLSGDKQLRPSFLSSLRPSLTGARRL 360
Db 369 ROHAGPSTSRPRPMDTPCPVVAETKHFVLSGDKQLRPSFLSSLRPSLTGARRL 428

Qy 361 VETIFLAGSRPMPGTPRRLLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 429 VETIFLAGSRPMPGTPRRLLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 488
Qy 421 PAAGVCAREKPOGSAVAPEEEDTDPRRLVQLLRHSSPQWYGVFVRACLRRLVPPGLWGS 480
Db 489 PAAGVCAREKPOGSAVAPEEEDTDPRRLVQLLRHSSPQWYGVFVRACLRRLVPPGLWGS 548
Qy 481 RHNERFLRNTKRFISLGKHAQLSLQBLTWKMSVRDCAWLRSPGCVCPAAEHLRBEI 540
Db 549 RHNERFLRNTKRFISLGKHAQLSLQBLTWKMSVRDCAWLRSPGCVCPAAEHLRBEI 608
Qy 541 LAKFLHMLMSVYVVELLSRFYVTTETFOKNRLLFFYRKSVMSKLSQSIGIROHLKRVOLRE 600
Db 609 LAKFLHMLMSVYVVELLSRFYVTTETFOKNRLLFFYRKSVMSKLSQSIGIROHLKRVOLRE 668
Qy 601 LSAEVRQHREARPAALTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
Db 669 LSAEVRQHREARPAALTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 728
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRANRTFVLRAQDPPPELFFVKVDVTGAYDTI 720
Db 729 LFSVLNYERARRPGLLGASVLGLDDIHRANRTFVLRAQDPPPELFFVKVDVTGAYDTI 788
Qy 721 PODRLTEVIASIIKPONTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLQPYMQFVAHL 780
Db 789 PODRLTEVIASIIKPONTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLQPYMQFVAHL 848
Qy 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYVQCGIPOGSIILSTL 840
Db 849 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYVQCGIPOGSIILSTL 908
Qy 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
Db 909 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 968
Qy 901 RKTVMNFPVDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDYSYARTSIRASLTF 960
Db 969 RKTVMNFPVDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDYSYARTSIRASLTF 1028
Qy 961 NRGFKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVQLP 1020
Db 1029 NRGFKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVQLP 1088
Qy 1021 FHOQVWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL 1080
Db 1089 FHOQVWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL 1148
Qy 1081 KLTRHRYVYVPLLGSLRTAQTLRSRKLPGTTLTALEAAANPALPSDFKTILD 1132
Db 1149 KLTRHRYVYVPLLGSLRTAQTLRSRKLPGTTLTALEAAANPALPSDFKTILD 1200

RESULT 24
US-09-402-181B-612
; Sequence 612, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 612:
SEQUENCE CHARACTERISTICS:
LENGTH: 1200 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1200
OTHER INFORMATION: /note= "fusion protein composed of His6 and Anti-Xpress tags, enterokinase cleavage site and full length hrRT protein"
SEQUENCE DESCRIPTION: SEQ ID NO: 612:
US-09-402-181B-612
Query Match 100.0%; Score 5961; DB 4; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAPRCRAVRLSHRYREVLPATFVRRLGPOGWRVQRGDPAAFRALVAQCLVCVPW 60
DB 69 MPAPRCRAVRLSHRYREVLPATFVRRLGPOGWRVQRGDPAAFRALVAQCLVCVPW 128
QY 61 DARPPPAAPSFQVSCLEKELVARVLQRCERGAKNVLAFGFALLDCAARGGPPPEAFTTSVR 120
DB 129 DARPPPAAPSFQVSCLEKELVARVLQRCERGAKNVLAFGFALLDCAARGGPPPEAFTTSVR 188
QY 121 SYLPTNTVDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
DB 189 SYLPTNTVDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 248
QY 181 ATQARPPPHASFRRLGCERAWNHVSREAGVPLGLPAPCARRRGGSASRSLPLKPRRR 240
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DB 309 GAAPPERTPVQGSWAHPGRTGRGFCVVSPPARPAEATSLGALSGRTRHSHPSVG 368
QY 301 ROHAGAPSTSRPPRPMDTPCPVYAEATKHFYSSGDEQELRPSFLLSLSPSLTGARRL 360
DB 369 ROHAGAPSTSRPPRPMDTPCPVYAEATKHFYSSGDEQELRPSFLLSLSPSLTGARRL 428
QY 361 VETIFLAGSRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
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QY 421 PAAGVCAREKPOGSAVAPEEEDTPRRLVQLLRHOSSPMQVYGVRACLRLVPPGLWGS 480
DB 489 PAAGVCAREKPOGSAVAPEEEDTPRRLVQLLRHOSSPMQVYGVRACLRLVPPGLWGS 548
QY 481 RHNERRFLRNTKFTISLGKHAKLISQELTWMSVRDCAWLRRSPGVGCVPAAEHRLREI 540
DB 549 RHNERRFLRNTKFTISLGKHAKLISQELTWMSVRDCAWLRRSPGVGCVPAAEHRLREI 608
QY 541 LAKFLHMLMSVYVVELLRSPFYVTTETTPQKRLFPYRKSVMSKLSQSIGIROLKRVQURE 600
DB 609 LAKFLHMLMSVYVVELLRSPFYVTTETTPQKRLFPYRKSVMSKLSQSIGIROLKRVQURE 668
QY 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRYKA 660
DB 669 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRYKA 728
QY 661 LFSVLNVERARRPGLIGASVLGLDDIHRAWRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
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QY 901 RKTVVNFEVEALGGTAFVQMPAHGLFPWCGLLDTLRTLEVQSDYSSYARTSIRASLTF 960
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QY 961 NRGFKAGNMRKLFVGLRLKCHSLFLDLQVNSLOTCTNIYKILLLOAYRPHACVQLP 1020
DB 1029 NRGFKAGNMRKLFVGLRLKCHSLFLDLQVNSLOTCTNIYKILLLOAYRPHACVQLP 1088
QY 1021 FHQQVKNPTFFLRVSDTASLCYSILKAKNAGSLGAGPLPSEAVOMLCHQAFLL 1080
DB 1089 FHQQVKNPTFFLRVSDTASLCYSILKAKNAGSLGAGPLPSEAVOMLCHQAFLL 1148
QY 1081 KLTHRVTVYVPLLSGLSRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
DB 1149 KLTHRVTVYVPLLSGLSRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1200
RESULT 25
US-09-721-456-612
; Sequence 612, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.
; ; Morin, Gregg B.
; ; Harley, Calvin B.
; ; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/721,456
;; FILING DATE: 22-NOV-2000
;; CLASSIFICATION: <Unknown>
;;
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US/08/974,549A
;; FILING DATE: 19-NOV-1997
;; APPLICATION NUMBER: US/08/724,643
;; FILING DATE: 01-OCT-1996
;; APPLICATION NUMBER: US/08/844,419
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US/08/846,017
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US/08/851,843
;; FILING DATE: 06-MAY-1997
;; APPLICATION NUMBER: US/08/854,050
;; FILING DATE: 09-MAY-1997
;; APPLICATION NUMBER: US/08/911,312
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US/08/912,951
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US/08/915,503
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: WO PCT/US97/17618
;; FILING DATE: 01-OCT-1997
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph Ted
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002610US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;;
;; INFORMATION FOR SEQ ID NO: 612:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1200 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..1200
;; OTHER INFORMATION: /note= "fusion protein composed of His6
;; and Anti-Xpress tags, enterokinase
;; cleavage site and full length hTERT
;; protein";;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 612:

US-09-721-456-612

Query Match 100.0%; Score 5961; DB 4; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRVLVQRGDPAAFPALVAQCCLVCPW 60
DB 69 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRVLVQRGDPAAFPALVAQCCLVCPW 128
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DB 129 DARPPPAAPSPFQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 188
QY 121 SYLENTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 189 SYLENTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 248
QY 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGGSASRSLPLPKRRR 240
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QY 241 GAAPERTPVGQSWAHGRTGRTGSPDRGFCVSPARPAAEATSLGALSTRISHPSVG 300
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DB 489 PAAGVCAREKPOGSAVAPEBEDTPRRLVOLLROHSSPWQVYGFVRACLRLRVPGLWGS 548
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DB 609 LAKEFLHLMMSVYVVELLRSFFYVTTTFOKNRLFYFKSVWSKLOSGIROIHLKRVQURE 668
QY 601 LSEAEVRQHREARPAALLTSRLRFTPKDGLRPIVNMDYVVGARTFRREKRAERLTSRKA 660
DB 669 LSEAEVRQHREARPAALLTSRLRFTPKDGLRPIVNMDYVVGARTFRREKRAERLTSRKA 728
QY 661 LFSVLNYERARRPGLLGASVLGDDIHRWRTFVLVRAQDPPPELYPVKVDVTGAYDTI 720
DB 729 LFSVLNYERARRPGLLGASVLGDDIHRWRTFVLVRAQDPPPELYPVKVDVTGAYDTI 788
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DB 789 PODRLTEVIASIIKPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLPYMQFVAHL 848
QY 781 QETSPLRDAVVEOSSSINEASSGLFDVFLRFMCHHAVRIRGKSVQCOGIPQGSILSTL 840
DB 849 QETSPLRDAVVEOSSSINEASSGLFDVFLRFMCHHAVRIRGKSVQCOGIPQGSILSTL 908
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DB 909 LCSLCYGDGMENKLPAGIRRDGLLRLVDDFLVLTPLHAKTFLRLTVRGVPEYGCVVNL 968
QY 901 RKTVNFPEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVQSDYSYARTSTRASLTF 960
DB 969 RKTVNFPEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVQSDYSYARTSTRASLTF 1028
QY 961 NRGFKAGRNMRRLFGVLRLLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
DB 1029 NRGFKAGRNMRRLFGVLRLLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1088
QY 1021 FHQQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
DB 1089 FHQQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1148
QY 1081 KLTRHRVTYVPLGLSLRTAQTOLSRKLPGLTTLTALEAANPALSDPKTILD 1132
DB 1149 KLTRHRVTYVPLGLSLRTAQTOLSRKLPGLTTLTALEAANPALSDPKTILD 1200

RESULT 26
US-08-974-549A-600

Sequence 600, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 600:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Protein
LOCATION: 1..1285
OTHER INFORMATION: /note= "fusion protein composed of
enterokinase cleavable, His tagged
OTHER INFORMATION: thioerodoxin moiety and full length hTRI"
US-08-974-549A-600
Query Match 100.0%; Score 5961; DB 3; Length 1285;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRRLGPGQWRLLVORCDPAAFRALVAQCLVCVPM 60
DB 154 MPRAPRCRAVRSLLRSHYREVLPATFVRRRLGPGQWRLLVORCDPAAFRALVAQCLVCVPM 213
QY 61 DARPPPAAPSFRQVSKLKLVARVLQRLCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120
DB 214 DARPPPAAPSFRQVSKLKLVARVLQRLCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 273
QY 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 274 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 333
QY 181 ATQARPPPHASGPRRRRLCERAWNHSVREAGVPLGLPAGARRRGGASRSRLPLKRRPR 240
DB 334 ATQARPPPHASGPRRRRLCERAWNHSVREAGVPLGLPAGARRRGGASRSRLPLKRRPR 393
QY 241 GAAPEPRTVPGQGSWAHPGRTGRGSDRGFCVSPARPAEATSLEGALSGRHSHPSVG 300
DB 394 GAAPEPRTVPGQGSWAHPGRTGRGSDRGFCVSPARPAEATSLEGALSGRHSHPSVG 453
QY 301 RQHAGAPSTSRPPRPMDTPCPVYAEATKHYLSGDKQELRSPFLSSLSRSLTGARRL 360
DB 454 RQHAGAPSTSRPPRPMDTPCPVYAEATKHYLSGDKQELRSPFLSSLSRSLTGARRL 513
QY 361 VETIFLGRPMWPGTPRRLPRLPQRYQWMDPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420
DB 514 VETIFLGRPMWPGTPRRLPRLPQRYQWMDPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 573
QY 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVOLLRQHSHPQVYGFVRACLRRLVPPGLMGS 480
DB 574 PAAGVCAREKPGQSVAAPEEDTDPRRLVOLLRQHSHPQVYGFVRACLRRLVPPGLMGS 633
QY 481 RHNERRFLRNTKKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGCVGCPAAEHLRREI 540
DB 634 RHNERRFLRNTKKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGCVGCPAAEHLRREI 693
QY 541 LAKFLHLMVSVYVELLSRPFYVTTTTPQKRLFPYRKSVMKLSQSIGIRQHLKRVQRE 600
DB 694 LAKFLHLMVSVYVELLSRPFYVTTTTPQKRLFPYRKSVMKLSQSIGIRQHLKRVQRE 753
QY 601 LSEAEVROHREARPAALLTSRLRFTPKDGLRPIVNMDDYVVGARTPRRKRERLTSRVKA 660
DB 754 LSEAEVROHREARPAALLTSRLRFTPKDGLRPIVNMDDYVVGARTPRRKRERLTSRVKA 813
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWTFVLVRQAQPPPPPLYFVKVDVTGAYDTI 720
DB 814 LFSVLNYERARRPGLLGASVLGLDDIHRAWTFVLVRQAQPPPPPLYFVKVDVTGAYDTI 873
QY 721 PDRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTLDQPYMRFVAHL 780
DB 874 PDRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTLDQPYMRFVAHL 933
QY 781 QETSPLRDAVVEQSSSLNEASSGLFDVFLPFCMHAVIRKKSVMQCGIPQGSILSTL 840
DB 934 QETSPLRDAVVEQSSSLNEASSGLFDVFLPFCMHAVIRKKSVMQCGIPQGSILSTL 993
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYECVNL 900
DB 994 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYECVNL 1053
QY 901 RKTVVNFFVEDEALGGTAFVQMPAGLFPWCGLLDTRTLEVQSDYSYSSARTSIRASLTF 960

Db 1054 RKTUVNPFVEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQDSYARTSIRASLTP 1113
Qy 961 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAVRFHACVQLP 1020
Db 1114 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAVRFHACVQLP 1173
Qy 1021 FHQQWKNPTFLRVIDSTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAPLL 1080
Db 1174 FHQQWKNPTFLRVIDSTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAPLL 1233
Qy 1081 KLTRHRTVTVPLGLSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
Db 1234 KLTRHRTVTVPLGLSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1285

RESULT 27

US-08-912-951-314
; Sequence 314, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 314:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1285 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-912-951-314

Query Match 100.0%; Score 5961; DB 4; Length 1285;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPPLATFVRRLGPGCWRLVQRGDPAAPALVAQCLVCVPW 60
Db 154 MPRAPRCRAVRSLLRSHYREVLPPLATFVRRLGPGCWRLVQRGDPAAPALVAQCLVCVPW 213
Qy 61 DARPPPAAPSFQVSCUKELVARVLQRLCERGAKNVLAFGFALLDARGGGPEAFTTSVR 120
Db 214 DARPPPAAPSFQVSCUKELVARVLQRLCERGAKNVLAFGFALLDARGGGPEAFTTSVR 273
Qy 121 SYLPTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 274 SYLPTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 333
Qy 181 ATQARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAPGARRRGGSASRSPLPKRPRR 240
Db 334 ATQARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAPGARRRGGSASRSPLPKRPRR 393
Qy 241 GAAPERTPVGGSWAHGRTGCPSDRGFCVVSPPARPEATSEALSGALSTRSHSPSVG 300
Db 394 GAAPERTPVGGSWAHGRTGCPSDRGFCVVSPPARPEATSEALSGALSTRSHSPSVG 453
Qy 301 ROHHAGPPSTSRPPRWDTPCPVVAETKHFLYSSGDKQLRPSFLSSLPSTGARRL 360
Db 454 ROHHAGPPSTSRPPRWDTPCPVVAETKHFLYSSGDKQLRPSFLSSLPSTGARRL 513
Qy 361 VETIFLGSRPWMPGTPRRLPRLPORYWQMRPLFLELLGNHACQYGVLLKTHCPLRAAVT 420
Db 514 VETIFLGSRPWMPGTPRRLPRLPORYWQMRPLFLELLGNHACQYGVLLKTHCPLRAAVT 573
Qy 421 PAAGVCAREKPOGSVAAPBEEDTPRRLVOLLROHSSPQWVYGFVRACLRLVPGLWGS 480
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Qy 481 RHNERFLRNTKCFISLGKHAQLSLOBLTWKMSVRDCAWLRSPGVCPAAEHRLREBI 540
Db 634 RHNERFLRNTKCFISLGKHAQLSLOBLTWKMSVRDCAWLRSPGVCPAAEHRLREBI 693
Qy 541 LAKELHWMVYVVELLRSFYVTTTFOKNRLFYKSVWSKLOSIGIROHLKRVOLRE 600
Db 694 LAKELHWMVYVVELLRSFYVTTTFOKNRLFYKSVWSKLOSIGIROHLKRVOLRE 753
Qy 601 LSEAEVQHRREARPAALLTSRLRFIPKDPGLRPIVNMDYVVGARTFRREKRAERLTSRYKA 660
Db 754 LSEAEVQHRREARPAALLTSRLRFIPKDPGLRPIVNMDYVVGARTFRREKRAERLTSRYKA 813
Qy 661 LFSVLNTERARRPGLLGASVLGDDIHRWRTFVLVRAQDPPPELVFKVDVTGAYDTI 720
Db 814 LFSVLNTERARRPGLLGASVLGDDIHRWRTFVLVRAQDPPPELVFKVDVTGAYDTI 873
Qy 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMQFVAHL 780
Db 874 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMQFVAHL 933
Qy 781 QETSPDRDAVVIEOSSINEASSGLFDVFLRFMCHAVIRKGSYVVOCGIPQGSILSTL 840
Db 934 QETSPDRDAVVIEOSSINEASSGLFDVFLRFMCHAVIRKGSYVVOCGIPQGSILSTL 993
Qy 841 LCSLCYGD MENKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVNIL 900
Db 994 LCSLCYGD MENKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVNIL 1053

Db 934 QETSLRDVIEQSSSNEASSGLFVFLPFCMHAVIRKSVQCGIPQSGIISTL 993
Qy 841 LCSLCYGMENKLFAGIRRDGLLLRLVDFFLLVTPHLTHAKTFLRTLVRGVPYXGCVNVL 900
Db 994 LCSLCYGMENKLFAGIRRDGLLLRLVDFFLLVTPHLTHAKTFLRTLVRGVPYXGCVNVL 1053
Qy 901 RKTVVNFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLTF 960
Db 1054 RKTVVNFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLTF 1113
Qy 961 NRGFKAGNRMRKLFGLVRLKCHSLFDLQVNSLQVCTNLYKILLQAVRHFACVLQLP 1020
Db 1114 NRGFKAGNRMRKLFGLVRLKCHSLFDLQVNSLQVCTNLYKILLQAVRHFACVLQLP 1173
Qy 1021 FHQQWKNPFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Db 1174 FHQQWKNPFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1233
Qy 1081 KLTHRVTVYVPLGLSLRTAQOLSKLPGTTLTALBAANPALPSDFKTILD 1132
Db 1234 KLTHRVTVYVPLGLSLRTAQOLSKLPGTTLTALBAANPALPSDFKTILD 1285

RESULT 29

US-09-721-456-600
; Sequence 600, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-NOV. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 600:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1285 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1285
; OTHER INFORMATION: /note= "fusion protein composed of
; enterokinase cleavable, His tagged
; thioredoxin moiety and full length hTERT"
; ; SEQUENCE DESCRIPTION: SEQ ID NO: 600:
; US-09-721-456-600

Query Match 100.0%; Score 5961; DB 4; Length 1285;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCRAVRSLLRSHYREVLPPLATFVRLPGPQWRLVQRGDPAAFRALVAQCLVCVPW 60
Db 154 MPAPRCRAVRSLLRSHYREVLPPLATFVRLPGPQWRLVQRGDPAAFRALVAQCLVCVPW 213
Qy 61 DARPPAPSPFQVSCUKELVARVLQRLCERGAQKLVAFGALLDARGGPEAFTTSVR 120
Db 214 DARPPAPSPFQVSCUKELVARVLQRLCERGAQKLVAFGALLDARGGPEAFTTSVR 273
Qy 121 SYLPTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 274 SYLPTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 333
Qy 181 ATQARPPPHASGPRRLRGCBANMHSVRBAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
Db 334 ATQARPPPHASGPRRLRGCBANMHSVRBAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 393
Qy 241 GAAPERTPVGGGSAHPGRTGSDRGFCVSPARPAEATSLGALSGTRHSHPSVG 300
Db 394 GAAPERTPVGGGSAHPGRTGSDRGFCVSPARPAEATSLGALSGTRHSHPSVG 453
Qy 301 RQHAGPSTSRPDPWDTPCPVYATKHFYLSGGDKQLRPSFLLSSRLPSLTGARRL 360
Db 454 RQHAGPSTSRPDPWDTPCPVYATKHFYLSGGDKQLRPSFLLSSRLPSLTGARRL 513
Qy 361 VETIFGSRPMPGTPRRRLPRLPQRYQMRPLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
Db 514 VETIFGSRPMPGTPRRRLPRLPQRYQMRPLFLELGNHAQCPYGVLLKTHCPLRAAVT 573
Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRLVOLLROHSSPQVYGVFRACLRELVPGLMGS 480
Db 574 PAAGVCAREKPGQSVAAPEEDTDPRLVOLLROHSSPQVYGVFRACLRELVPGLMGS 633
Qy 481 RHNERRFLRNTKTFISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCPVAAEHLREI 540
Db 634 RHNERRFLRNTKTFISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCPVAAEHLREI 693
Qy 541 LAKEFLHLMMSVYVVELLSRPFYVTTETTFQKNRLFFYKSVWSKLOSIGIROHLKRVQURE 600
Db 694 LAKEFLHLMMSVYVVELLSRPFYVTTETTFQKNRLFFYKSVWSKLOSIGIROHLKRVQURE 753
Qy 601 LSEAEVQREARPAALLTSRLRFTPKDGLRPIVNMVYVVGARTPRRKRERLTSRVKA 660

Db 754 LSEAEVQRHREARBPALLTSRLRPIPKPDGLRPIVMNDYVVGARTPRREKRAERLRSVKA 813
QY 661 LFSVLNRYEARPGLGASVLGLDDIHRARWTFVLVRADQDPPPELYFVKVDVTGAYDTI 720
Db 814 LFSVLNRYEARPGLGASVLGLDDIHRARWTFVLVRADQDPPPELYFVKVDVTGAYDTI 873
QY 721 PODRLTEVIASIIKQNTYCVRYAVVQAAHGHVRKAPKSHVSTLTDLQPTMROFVAHL 780
Db 874 PODRLTEVIASIIKQNTYCVRYAVVQAAHGHVRKAPKSHVSTLTDLQPTMROFVAHL 933
QY 781 QETSLRDAVTEQSSSLEASSGLFDVFLRPMCHHAVIRKSVYVQCGIPQGSILSTL 840
Db 934 QETSLRDAVTEQSSSLEASSGLFDVFLRPMCHHAVIRKSVYVQCGIPQGSILSTL 993
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRLVRGVPYGCYVNL 900
Db 994 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRLVRGVPYGCYVNL 1053
QY 901 RKTVMFPVEDALGCTAFVQMPAHLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLTF 960
Db 1054 RKTVMFPVEDALGCTAFVQMPAHLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLTF 1113
QY 961 NRGPKAGNRMRKLGVLRLKCHSLFLDLQVNSLOTVCNTIYKILLQAYRPHACVLOLP 1020
Db 1114 NRGPKAGNRMRKLGVLRLKCHSLFLDLQVNSLOTVCNTIYKILLQAYRPHACVLOLP 1173
QY 1021 FHQQWKNPFTFLRVISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1174 FHQQWKNPFTFLRVISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1233
QY 1081 KLTHRVTVYVPLGLSLRTAQTSKLPGLTTLTALBAANPALPSDFKTILD 1132
Db 1234 KLTHRVTVYVPLGLSLRTAQTSKLPGLTTLTALBAANPALPSDFKTILD 1285

RESULT 30

US-08-974-549A-344
; Sequence 344, Application US/08974549A
; Patent No. 6166178

GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997

CLASSIFICATION:

; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Red
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 344:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-549A-344

Query Match 99.8%; Score 5952; DB 3; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLPGQWRVLRQGDPAAFRALVAQCLVCPWM 60
Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLPGQWRVLRQGDPAAFRALVAQCLVCPWM 60
QY 61 DARPPAPSPROVSKLKLAVRLQRLCERAKNVLAFGALLDARGGPEAFTTSVR 120
Db 61 DARPPAPSPROVSKLKLAVRLQRLCERAKNVLAFGALLDARGGPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGAWGLLLRRVDDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVDALRGSGAWGLLLRRVDDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRRRLGECERAWNHSVREAGVPLGAPAGARRRGGSSASRLPLPKRRR 240
Db 181 ATQARPPPHASGPRRRRLGECERAWNHSVREAGVPLGAPAGARRRGGSSASRLPLPKRRR 240
QY 241 GAAPEPRTVPGQSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRHSHPVG 300
Db 241 GAAPEPRTVPGQSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRHSHPVG 300
QY 301 RQHHAGPPSTSRPPRPMDTPCPVVAETKHFYSSGDKQLRPSFLLSSRLPSLTGARRL 360
Db 301 RQHHAGPPSTSRPPRPMDTPCPVVAETKHFYSSGDKQLRPSFLLSSRLPSLTGARRL 360
QY 361 VETIFLGSRRPMPGTPRRLPRLPQRYWMRFLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRLPRLPQRYWMRFLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGQSWAAPAEEDTDPRLVQLLRQHSHPWQYVGFVRACLRRLVPPGLWS 480
Db 421 PAAGVCAREKPGQSWAAPAEEDTDPRLVQLLRQHSHPWQYVGFVRACLRRLVPPGLWS 480

QY 481 RHNRERFLRNTKFKTISLGHAKHLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
DB 481 RHNRERFLRNTKFKTISLGHAKHLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
QY 541 LAKFLHLMWSVYVVELLSFFVYVTTTFQKNRLFYRKSVMKLSQSIGIRQHLKRVQVRE 600
DB 541 LAKFLHLMWSVYVVELLSFFVYVTTTFQKNRLFYRKSVMKLSQSIGIRQHLKRVQVRE 600
QY 601 LSEAEVROHREARPAALLSRIRFPKPDGLRPINVMQYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVROHREARPAALLSRIRFPKPDGLRPINVMQYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRARTEFLVRQAQPPPELYFVKVDVTCAYDTI 720
DB 661 LFSVLNYERARRPGLLGASVLGLDDIHRARTEFLVRQAQPPPELYFVKVDVTCAYDTI 720
QY 721 PQDRLETVIASIIKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
DB 721 PQDRLETVIASIIKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
QY 781 QETSPIRDVAVIEQSSSINEASSGLFDVFLRPMCHAVIRKGSYVQCQIPQGSII STL 840
DB 781 QETSPIRDVAVIEQSSSINEASSGLFDVFLRPMCHAVIRKGSYVQCQIPQGSII STL 840
QY 841 LCSLCYGDMENKLFAGIRRDGLLRLVDDELLVTPHLTHAKTFLRTLRVGPVCCVNL 900
DB 841 LCSLCYGDMENKLFAGIRRDGLLRLVDDELLVTPHLTHAKTFLRTLRVGPVCCVNL 900
QY 901 RKTVMNFFVEDEALGTAFAVQMPAHGLFPWCGLLDDTRTLEVSQSYSSYARTSIRASLTF 960
DB 901 RKTVMNFFVEDEALGTAFAVQMPAHGLFPWCGLLDDTRTLEVSQSYSSYARTSIRASLTF 960
QY 961 NRGFKAGNRMRKLGVLRLKCHSLFLOVNSLQTVCTNIYKILLOAYRFHACVLQLP 1020
DB 961 NRGFKAGNRMRKLGVLRLKCHSLFLOVNSLQTVCTNIYKILLOAYRFHACVLQLP 1020
QY 1021 FHQQVWKNTFFLRVISTASI-CYSILKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL 1080
DB 1021 FHQQVWKNTFFLRVISTASI-CYSILKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL 1080
QY 1081 KLTHRVTYVPLGLSLRTAQTLRSKLPCTTITALEAANPALPSDFKTIILD 1132
DB 1081 KLTHRVTYVPLGLSLRTAQTLRSKLPCTTITALEAANPALPSDFKTIILD 1132

RESULT 31

US-09-402-181B-344
Sequence 344, Application US/09402181B
Patent No. 6610839

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181B

FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 344:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 344:
US-09-402-181B-344

Query Match 99.8%; Score 5952; DB 4; Length 1132;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLGPGQWRLVQRGDDPAAPRALVAQCILVCVPW 60
DB 1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLGPGQWRLVQRGDDPAAPRALVAQCILVCVPW 60
QY 61 DAREPPAAPSPFRQVSCLELVARVLQRLCERGAKNVLAFCGFALLDARGGPEAFTTSVR 120
DB 61 DAREPPAAPSPFRQVSCLELVARVLQRLCERGAKNVLAFCGFALLDARGGPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGANGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPTNTVDALRGSGANGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATOARPPPHASGPRRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSSASRSLPLPKRRR 240
DB 181 ATOARPPPHASGPRRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSSASRSLPLPKRRR 240
QY 241 GAAPERTPVQGSWAHPGRTGRGFCVSPARPAPAEATSLGALSCTRHSHPVG 300
DB 241 GAAPERTPVQGSWAHPGRTGRGFCVSPARPAPAEATSLGALSCTRHSHPVG 300
QY 301 RQHHAGPPSTSRPPRPMWDTCPVYAEKTHLYSSGDKQLRPSFLSSLRPSLTGARRL 360
DB 301 RQHHAGPPSTSRPPRPMWDTCPVYAEKTHLYSSGDKQLRPSFLSSLRPSLTGARRL 360
QY 361 VETIFLGSRRPMPGTPRRLPRLPORYQWMRPLFLELLCNHQAQCPVGVLLKTHCPRAAVT 420
DB 361 VETIFLGSRRPMPGTPRRLPRLPORYQWMRPLFLELLCNHQAQCPVGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSHPQVYGVFVACLRRLRVLPPGLWGS 480
DB 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSHPQVYGVFVACLRRLRVLPPGLWGS 480

QY 481 RHNRFRFNTKKTSLGKHAKLSQELTWKMSVDRDCAWLRSPGVCVPAAEHRLREI 540
DB RHNRFRFNTKKTSLGKHAKLSQELTWKMSVDRDCAWLRSPGVCVPAAEHRLREI 540
QY 541 LAKFLHLMMSVVVVELLSFFVVTETTKQKRLFFYRKSVMSKLSQIGIROLKKEVQRE 600
DB LAKFLHLMMSVVVVELLSFFVVTETTKQKRLFFYRKSVMSKLSQIGIROLKKEVQRE 600
QY 601 LSEAEVROHREARPALLTSRLRFIPKPDGLRPIVNMDDVVGARTFRREKRAERLTSRVKA 660
DB LSEAEVROHREARPALLTSRLRFIPKPDGLRPIVNMDDVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNREARRPGLLGASVLGLDDIHRARTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
DB LFSVLNREARRPGLLGASVLGLDDIHRARTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PODRUTEVIASIIKQNTYCVRRYAVVQAAHGHVKAFKSHVSTLTLDOPVMOFVAHL 780
DB PODRUTEVIASIIKQNTYCVRRYAVVQAAHGHVKAFKSHVSTLTLDOPVMOFVAHL 780
QY 781 QETSLRDAVIEQSSSNEASSGLFDVFLRFMCHHVAVRIGKSVYQCGIPOGSIILSTL 840
DB QETSLRDAVIEQSSSNEASSGLFDVFLRFMCHHVAVRIGKSVYQCGIPOGSIILSTL 840
QY 841 LSCSLCYGMENKLFAGIRRDGLLLRLVDLFTPLHPLTHAKTFLTLVRGVPEYGCNNL 900
DB LSCSLCYGMENKLFAGIRRDGLLLRLVDLFTPLHPLTHAKTFLTLVRGVPEYGCNNL 900
QY 901 RKTWNFVEDEALGGTAVQMPAHGLFPWCGLLDITLTVQSDYSYARTSIRASLTFF 960
DB RKTWNFVEDEALGGTAVQMPAHGLFPWCGLLDITLTVQSDYSYARTSIRASLTFF 960
QY 961 NRGKAGNMRRKLFGLVRLKCHSLFDLQVNSLQTVCTNIIKILLQAYRFHACVLQLP 1020
DB NRGKAGNMRRKLFGLVRLKCHSLFDLQVNSLQTVCTNIIKILLQAYRFHACVLQLP 1020
QY 1021 FHQQWKNTFFLRVISVTSASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHOAFIL 1080
DB FHQQWKNTFFLRVISVTSASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHOAFIL 1080
QY 1081 KLTHRVTVPLGLSLRTAQTLKSLPGTTLTALEAAANPALPSDFKTILD 1132
DB KLTHRVTVPLGLSLRTAQTLKSLPGTTLTALEAAANPALPSDFKTILD 1132

RESULT 32

US-09-721-456-344
; Sequence 344, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456

FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 344:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 344:
US-09-721-456-344

Query Match 99.8%; Score 5952; DB 4; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPCRVRSLRSHYREVLPATFVRRLGPOGWRVLVQRGDPAAFRALVAQCLVCPW 60
DB 1 MPRAPCRVRSLRSHYREVLPATFVRRLGPOGWRVLVQRGDPAAFRALVAQCLVCPW 60
QY 61 DARPPPAAPSPROVSKLKLVARVLQRLCERGAKNVLAFFGALLDARGGPPPEAFTTSVR 120
DB 61 DARPPPAAPSPROVSKLKLVARVLQRLCERGAKNVLAFFGALLDARGGPPPEAFTTSVR 120
QY 121 SYLPTNTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
DB 121 SYLPTNTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
QY 181 ATOARPPPHASGPPRRRLGCEBWNHVSREAGVPLGLPAGARRGGSSASRSLPLPKRRR 240
DB 181 ATOARPPPHASGPPRRRLGCEBWNHVSREAGVPLGLPAGARRGGSSASRSLPLPKRRR 240
QY 241 GAAPEPERTVQGSWAHPGTRGPDGRCFCVSPARPAAEATSLGALSCTRSHSPSVG 300
DB 241 GAAPEPERTVQGSWAHPGTRGPDGRCFCVSPARPAAEATSLGALSCTRSHSPSVG 300
QY 301 ROHHAGPSTSRPPRPMDTTCPPVYAEKTHFLYSSGDKQLRPSFLSSLPSTGARRL 360
DB 301 ROHHAGPSTSRPPRPMDTTCPPVYAEKTHFLYSSGDKQLRPSFLSSLPSTGARRL 360
QY 361 VETIFLGSRRPMPGTPRLPRLPQRYWOMRPLFLELLGNHACQPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRRPMPGTPRLPRLPQRYWOMRPLFLELLGNHACQPYGVLLKTHCPLRAAVT 420

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QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRVLVOLLROHSSPMQVYGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRVLVOLLROHSSPMQVYGFVRACLRRLVPPGLWGS 480
QY 481 RHNERFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
QY 541 LAKFLHMLMSVVVELLSFFVTTETTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVQJRE 600
Db 541 LAKFLHMLMSVVVELLSFFVTTETTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVQJRE 600
QY 601 LSEAEVROHREARPAALTSLRFPKPDGLRPIVNMDDYVVCARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVROHREARPAALTSLRFPKPDGLRPIVNMDDYVVCARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNVERARRPGLLGASVLGLDDIHRAMWTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRAMWTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PQDRLTEVIASIIKPONTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLPYMQFVAHL 780
Db 721 PQDRLTEVIASIIKPONTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLPYMQFVAHL 780
QY 781 QETSLRDAVIEOSSSINEASSGLFDVFLRFMCHHVRIRGKSVQCGIPQGSILSTL 840
Db 781 QETSLRDAVIEOSSSINEASSGLFDVFLRFMCHHVRIRGKSVQCGIPQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
QY 901 RKTVMNPFVEALGGTAFVQMPAHGLFPWCGLLDDTLTLVQSDYSYARTSIRASLTF 960
Db 901 RKTVMNPFVEALGGTAFVQMPAHGLFPWCGLLDDTLTLVQSDYSYARTSIRASLTF 960
QY 961 NRGFKAGNMRKLGVLRLKCHSLFDLQVNSLQVCTNYKILLQAYRFAHCVLQLP 1020
Db 961 NRGFKAGNMRKLGVLRLKCHSLFDLQVNSLQVCTNYKILLQAYRFAHCVLQLP 1020
QY 1021 FHQQWKNTFFLRVISDTASLCYSILKAKNAGMSLGAAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQQWKNTFFLRVISDTASLCYSILKAKNAGMSLGAAGPLPSEAVQWLCHQAFLL 1080
QY 1081 KLTHRVTVYVPLLSLRTAQTLQRKLPGLTTLTALAAANPALPSDFKTLILD 1132
Db 1081 KLTHRVTVYVPLLSLRTAQTLQRKLPGLTTLTALAAANPALPSDFKTLILD 1132
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RESULT 33

US-08-974-549A-628
Sequence 628, Application US/08974549A
Patent No. 6166178

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A

FILING DATE: 19-NOV-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 628:

SEQUENCE CHARACTERISTICS:

LENGTH: 1407 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..1407

OTHER INFORMATION: /note= "fusion protein composed of

enhanced green fluorescent protein

OTHER INFORMATION:

OTHER INFORMATION: 5' untranslated region of hTERT mRNA and

OTHER INFORMATION: hTERT protein sequence"

US-08-974-549A-628

Query Match 99.8%; Score 5952; DB 3; Length 1407;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRLGPGQWRLVQKGDPAAFRALVAQCILVCVPW 60

Db 276 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRLGPGQWRLVQKGDPAAFRALVAQCILVCVPW 335

QY 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGPALLDARGGPPFAFTTSVR 120

Db 336 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGPALLDARGGPPFAFTTSVR 395

QY 121 SYLPNTVTDALRGSGAWGLLRLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180

Db 396 SYLPNTVTDALRSGAWGLLRRVGDVVLHLLARCALFVLVAPSCAYQVCGPPLYQLCA 455
Qy 181 ATOARPPPHASPRRLGGERAWNSVREAGVPLGLPAGARRRGSSASRSLPLPKRPR 240
Db 456 ATOARPPPHASPRRLGGERAWNSVREAGVPLGLPAGARRRGSSASRSLPLPKRPR 515
Qy 241 GAAPPERTPVQGSWAHPGRTGRPSDRGFCVVSAPAEAEATSEALSGTRHSHPSVG 300
Db 516 GAAPPERTPVQGSWAHPGRTGRPSDRGFCVVSAPAEAEATSEALSGTRHSHPSVG 575
Qy 301 ROHAGPSTSRPPRPDTPCPVVAETHKFLYSSGDKQLRPSFLLSLRSLTGARRL 360
Db 576 ROHAGPSTSRPPRPDTPCPVVAETHKFLYSSGDKQLRPSFLLSLRSLTGARRL 635
Qy 361 VETIFLGRPMWPGTFRRLPLRPLQRYWQMRPLFLELLGNHACQPYGVLLKTHCPRAAVT 420
Db 636 VETIFLGRPMWPGTFRRLPLRPLQRYWQMRPLFLELLGNHACQPYGVLLKTHCPRAAVT 695
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSSPMQVYGFVRACLRLRVPFGLMGS 480
Db 696 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSSPMQVYGFVRACLRLRVPFGLMGS 755
Qy 481 RHNERFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLRBEI 540
Db 756 RHNERFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLRBEI 815
Qy 541 LAKFLHMLSVVVBLLRSFFVVTETTFQKNLFFVRKSVMSKLSIGIRQHLKRVOLRE 600
Db 816 LAKFLHMLSVVVBLLRSFFVVTETTFQKNLFFVRKSVMSKLSIGIRQHLKRVOLRE 875
Qy 601 LSEAEVRQHREARPAALLSRFLFKPKDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
Db 876 LSEAEVRQHREARPAALLSRFLFKPKDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 935
Qy 661 LFSVLNVRARRPGLLGASVLGLDIDHRAWRFTVLVRADQPPPELYFKVDVDTGAYDTI 720
Db 936 LFSVLNVRARRPGLLGASVLGLDIDHRAWRFTVLVRADQPPPELYFKVDVDTGAYDTI 995
Qy 721 PODRLTEVIASIIKPNQTYCVBRYAVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
Db 996 PODRLTEVIASIIKPNQTYCVBRYAVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 1055
Qy 781 QETSPLRDAVLEQSSSINEASGLFDVFLRPMCHAVRIRKSVVQCGIPQGSILSTL 840
Db 1056 QETSPLRDAVLEQSSSINEASGLFDVFLRPMCHAVRIRKSVVQCGIPQGSILSTL 1115
Qy 841 LCSLCYGMENKLPAGIRRDGILLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYCCVNL 900
Db 1116 LCSLCYGMENKLPAGIRRDGILLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYCCVNL 1175
Qy 901 RKTWNFFVEDEALGCTAFVQMPAHGLFPWCGLLLDTRTLEQSDYSYARTSIRASLTF 960
Db 1176 RKTWNFFVEDEALGCTAFVQMPAHGLFPWCGLLLDTRTLEQSDYSYARTSIRASLTF 1235
Qy 961 NRGFKAGNMRKLFVGLKCHSLFDLDQVNSLOTVCNTIYKILLQAYRPHACVLOLP 1020
Db 1236 NRGFKAGNMRKLFVGLKCHSLFDLDQVNSLOTVCNTIYKILLQAYRPHACVLOLP 1295
Qy 1021 FHOQWKNPFTFLRVIDSTASICYILKAKNAGMSLGAKGAGPLPSEAVOMLCHQAFLL 1080
Db 1296 FHOQWKNPFTFLRVIDSTASICYILKAKNAGMSLGAKGAGPLPSEAVOMLCHQAFLL 1355
Qy 1081 KLTRHRVTVPLLSRLTAQTLQSLKLPQTTLTALAAANPALPSDFKTLTD 1132
Db 1356 KLTRHRVTVPLLSRLTAQTLQSLKLPQTTLTALAAANPALPSDFKTLTD 1407

RESULT 34

US-08-912-951-334

; Sequence 334, Application US/08912951

; Patent No. 6475789

; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 334:
SEQUENCE CHARACTERISTICS:
LENGTH: 1407 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-951-334

Query Match 99.8%; Score 5952; DB 4; Length 1407;
Best Local Similarity 99.8%; Fred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPAPRCRAVRSLLRSHYREVLPPLATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCPVW 60
Db 276 MPAPRCRAVRSLLRSHYREVLPPLATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCPVW 335
Qy 61 DARPPPAAPSPQVSCSKLKVRLQRLCERGAKNVLAFFGALLDARGGPPPEAFTTSVR 120
Db 336 DARPPPAAPSPQVSCSKLKVRLQRLCERGAKNVLAFFGALLDARGGPPPEAFTTSVR 395

Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		
QY	1	MPAPRCRAVRSLLRSHREVLPATFVRLRGQGWRLVQRGDPAARALVAQCLVCPW 60
Db	276	MPAPRCRAVRSLLRSHREVLPATFVRLRGQGWRLVQRGDPAARALVAQCLVCPW 335
QY	61	DARPPAAPSFRQVSCLEKELVARVQLRCERGAQKVLAFGPFALLDGGARGGPPPEATTTSVR 120
Db	336	DARPPAAPSFRQVSCLEKELVARVQLRCERGAQKVLAFGPFALLDGGARGGPPPEATTTSVR 395
QY	121	SYLPNTVTDALRGSGAWGLLRVGDVLLHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
Db	396	SYLPNTVTDALRGSGAWGLLRVGDVLLHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 455
QY	181	ATOARPPPHASGPRRLGCERAMNHSVREAGVPLGLPAPGARRRGSSASRSLPLKPRRR 240
Db	456	ATOARPPPHASGPRRLGCERAMNHSVREAGVPLGLPAPGARRRGSSASRSLPLKPRRR 515
QY	241	GAAPERTPVQCGSWAHFGRTRGSDRGFCVVSAPPAEATSLGALSGTRHSHPSVG 300
Db	516	GAAPERTPVQCGSWAHFGRTRGSDRGFCVVSAPPAEATSLGALSGTRHSHPSVG 575
QY	301	ROHAGAPSTSPRPMDTPCPVVAETHKFLYSSGDKQLRPSFLLSRLSLTGARRL 360
Db	576	ROHAGAPSTSPRPMDTPCPVVAETHKFLYSSGDKQLRPSFLLSRLSLTGARRL 635
QY	361	VETIFLGRPMWPGTFRRLPRLPQRYQWMLPFLLELGNHAQCPYGVLLKTHCPLRAAVT 420
Db	636	VETIFLGRPMWPGTFRRLPRLPQRYQWMLPFLLELGNHAQCPYGVLLKTHCPLRAAVT 695
QY	421	PAAGVCAEKPGQSWAABEEDTPRRLVQLLRHSSPWQVYGFVRACLRRLVPPGLMGS 480
Db	696	PAAGVCAEKPGQSWAABEEDTPRRLVQLLRHSSPWQVYGFVRACLRRLVPPGLMGS 755
QY	481	RINERFLRNTKFFLSLGHAKLSQELTKWMSVRDCAWLRSFGVCPVPAEHLRREI 540
Db	756	RINERFLRNTKFFLSLGHAKLSQELTKWMSVRDCAWLRSFGVCPVPAEHLRREI 815
QY	541	LAKFLHLMSSVYVVELLSFFVYTTTQKNRLFYFRKSVMSKLSQIGIRQLKRVQRE 600
Db	816	LAKFLHLMSSVYVVELLSFFVYTTTQKNRLFYFRKSVMSKLSQIGIRQLKRVQRE 875
QY	601	LSEAVROHREARPAALLSRFLPKPGLRLPIVMDYVVGARTPRRKRABRLTSRVKA 660
Db	876	LSEAVROHREARPAALLSRFLPKPGLRLPIVMDYVVGARTPRRKRABRLTSRVKA 935
QY	661	LFSVLNVERARPGLLGASVGLDDIHRARWTFVLVRAQDPPPELYFKVDVTGAYDTI 720
Db	936	LFSVLNVERARPGLLGASVGLDDIHRARWTFVLVRAQDPPPELYFKVDVTGAYDTI 995
QY	721	PODRLTEVTIASIKPQNTYCVRRYAVQKAAGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
Db	996	PODRLTEVTIASIKPQNTYCVRRYAVQKAAGHVRKAFKSHVSTLTDLQPMRQFVAHL 1055
QY	781	QTSPLRDAVVIQSSSLNEASSGLFVPLRPMCHHAVIRGKSVYVQCGIPQGSILSTL 840
Db	1056	QTSPLRDAVVIQSSSLNEASSGLFVPLRPMCHHAVIRGKSVYVQCGIPQGSILSTL 1115
QY	841	LCSLCYGMENKLPAGIRDDGLLLRLVDDFLVTHPLTHAKTFLRLVRGPEYCCVNL 900
Db	1116	LCSLCYGMENKLPAGIRDDGLLLRLVDDFLVTHPLTHAKTFLRLVRGPEYCCVNL 1175
QY	901	RKTVNVFVDEALGATFVQMPAGLPPWCGLLDTRTLEVSQSYSSVARTSIRASLTF 960
Db	1176	RKTVNVFVDEALGATFVQMPAGLPPWCGLLDTRTLEVSQSYSSVARTSIRASLTF 1235
QY	961	NRGFKAGRMNRRLFGVRLKCHSLFLLDQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
Db	1236	NRGFKAGRMNRRLFGVRLKCHSLFLLDQVNSLQTVCTNIYKILLQAYRFHACVQLP 1295
QY	1021	FHQQVWKNPFTFLRVIDSTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db	1296	FHQQVWKNPFTFLRVIDSTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1355

QY 1081 KLTRHRTVTVPLGLSRLTAQTSKRLPGTTLTLEAAANPALPSDFKTILD 1132
 Db 1356 KLTRHRTVTVPLGLSRLTAQTSKRLPGTTLTLEAAANPALPSDFKTILD 1407

RESULT 36

US-09-721-456-628
 ; Sequence 628, Application US/09721456
 ; Patent No. 6617110

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456

FILING DATE: 22-NOV-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 628:

SEQUENCE CHARACTERISTICS:

LENGTH: 1407 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

```
;
;
; NAME/KEY: Protein
; LOCATION: 1..1407
; OTHER INFORMATION: /note= "fusion protein composed of
; enhanced green fluorescent protein
; (EGFP) residues, residues encoded by the
; 5' untranslated region of hTERT mRNA and
; hTERT protein sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 628:
US-09-721-456-628

Query Match          99.8%; Score 5952; DB 4; Length 1407;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPOGWRLLVQRGDPAAFRALVAQCLVCVPW 60
Db MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPOGWRLLVQRGDPAAFRALVAQCLVCVPW 335

Qy 61 DARPPPAAPSPROVSCLELVARVQLRCERGAKNVLAFGFALLDGARGGPEAFTTSVR 120
Db DARPPPAAPSPROVSCLELVARVQLRCERGAKNVLAFGFALLDGARGGPEAFTTSVR 395

Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 455

Qy 181 ATQARPPPHASGRRRLGRCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLLPKRPRR 240
Db ATQARPPPHASGRRRLGRCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLLPKRPRR 515

Qy 241 GAAPEPERTVPGQSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 300
Db GAAPEPERTVPGQSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 575

Qy 301 ROHHAGPSTSRPRPMDTPCPVVAETKHFYSSGDKQLRPSFLSSLPSTTGARRL 360
Db ROHHAGPSTSRPRPMDTPCPVVAETKHFYSSGDKQLRPSFLSSLPSTTGARRL 635

Qy 361 VETIFLGSRRPMPGTPRRLPRLPQRYQMWRPLFLELLGNHAQCPYGVLLKTHCFLRAAVT 420
Db VETIFLGSRRPMPGTPRRLPRLPQRYQMWRPLFLELLGNHAQCPYGVLLKTHCFLRAAVT 695

Qy 421 PAAGVCAREKQGSVAAPAEEDTDPRLLVQLLRHSSSPWQYVGFVRACLRRLVPPGLWGS 480
Db PAAGVCAREKQGSVAAPAEEDTDPRLLVQLLRHSSSPWQYVGFVRACLRRLVPPGLWGS 755

Qy 481 RHNERRFLRNTKFTISLGKHAKLISLQELTWKMSVRDCAWLRSSPGVCPVAAEHLRREEI 540
Db RHNERRFLRNTKFTISLGKHAKLISLQELTWKMSVRDCAWLRSSPGVCPVAAEHLRREEI 815

Qy 541 LAKFLHLMMSVYVVELLRSPFYVTETTFQKNRLFYFRKSVMSKLSQSIGIRHLKRVQRE 600
Db LAKFLHLMMSVYVVELLRSPFYVTETTFQKNRLFYFRKSVMSKLSQSIGIRHLKRVQRE 875

Qy 601 LSEAEVQCHREARALLTSRLRFTPKDGLRPIVNMVYVVGARTFREKRAERLTSRVKA 660
Db LSEAEVQCHREARALLTSRLRFTPKDGLRPIVNMVYVVGARTFREKRAERLTSRVKA 935

Qy 661 LFSVLNTERARRPGLIGASVLGLDDIHRAWTFVLVRAQDPPPELYFVKVDVTVGAYDTI 720
Db LFSVLNTERARRPGLIGASVLGLDDIHRAWTFVLVRAQDPPPELYFVKVDVTVGAYDTI 995

Qy 721 PQDLRLTEVIASIIKPQNTYCVRRYAVVQKAAHGVKAFKSHVSTLTDLPYMQFVAHL 780
Db PQDLRLTEVIASIIKPQNTYCVRRYAVVQKAAHGVKAFKSHVSTLTDLPYMQFVAHL 1055

Qy 781 QETSPLRDVAVIEOSSSINEASSGLFVFLRFMCHHVRIRGKSVYOCQIGPQSSILSTL 840
Db QETSPLRDVAVIEOSSSINEASSGLFVFLRFMCHHVRIRGKSVYOCQIGPQSSILSTL 1115

Qy 841 LCSLCYGDGMENKLPAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEPYGCVVNL 900
Db LCSLCYGDGMENKLPAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEPYGCVVNL 1175

1116 LCSLCYGDGMENKLPAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEPYGCVVNL 1175
901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRASLTF 960
1176 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRASVTF 1235
961 NRGFKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIIYKILLQAVRFHACVLQLP 1020
1236 NRGFKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIIYKILLQAVRFHACVLQLP 1295
1021 FHOQVWKNPTFFLRVISDTASLCYSILKAKNAGSLGAKGAAGPLPGEAVOMLCHQAPLL 1080
1296 FHOQVWKNPTFFLRVISDTASLCYSILKAKNAGSLGAKGAAGPLPGEAVOMLCHQAPLL 1355
1081 KLTRHRTVYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTIILD 1132
1356 KLTRHRTVYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTIILD 1407

RESULT 37
US-09-949-016-11712
; Sequence 11712, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11712
; LENGTH: 1193
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11712

Query Match          97.4%; Score 5807; DB 4; Length 1193;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 1105; Conservative 3; Mismatches 15; Indels 10; Gaps 1;

Qy 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPOGWRLLVQRGDPAAFRALVAQCLVCVPW 60
Db MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPOGWRLLVQRGDPAAFRALVAQCLVCVPW 78

Qy 61 DARPPPAAPSPROVSCLELVARVQLRCERGAKNVLAFGFALLDGARGGPEAFTTSVR 120
Db DARPPPAAPSPROVSCLELVARVQLRCERGAKNVLAFGFALLDGARGGPEAFTTSVR 138

Qy 79 DARPPPAAPSPROVSCLELVARVQLRCERGAKNVLAFGFALLDGARGGPEAFTTSVR 138
Db DARPPPAAPSPROVSCLELVARVQLRCERGAKNVLAFGFALLDGARGGPEAFTTSVR 180

Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 198

Qy 181 ATQARPPPHASGRRRLGRCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLLPKRPRR 240
Db ATQARPPPHASGRRRLGRCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLLPKRPRR 258

Qy 241 GAAPEPERTVPGQSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 300
Db GAAPEPERTVPGQSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 318

Qy 259 GAAPEPERTVPGQSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 318
Db GAAPEPERTVPGQSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 360

Qy 301 ROHHAGPSTSRPRPMDTPCPVVAETKHFYSSGDKQLRPSFLSSLPSTTGARRL 360
Db ROHHAGPSTSRPRPMDTPCPVVAETKHFYSSGDKQLRPSFLSSLPSTTGARRL 378

Qy 319 ROHHAGPSTSRPRPMDTPCPVVAETKHFYSSGDKQLRPSFLSSLPSTTGARRL 378
Db VETIFLGSRRPMPGTPRRLPRLPQRYQMWRPLFLELLGNHAQCPYGVLLKTHCFLRAAVT 420
```

Db 379 VETIFLGRPMWPGTFRRLRLPQRYWQWPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 438
Qy 421 PAAGVCAREKPGSGVAAPDEEDTDPRRLVOLLROHSSPMOVYGFVRACLRRLVPPGLMGS 480
Db 439 PAAGVCAREKPGSGVAAPDEEDTDPRRLVOLLROHSSPMOVYGFVRACLRRLVPPGLMGS 498
Qy 481 RHNERFLRNTKFFISLGHAKLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHLRBEI 540
Db 499 RHNERFLRNTKFFISLGHAKLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHLRBEI 558
Qy 541 LAKFLHLMVSVVVELLSFFVTYTTTQKNLFFYRKSVMSKLSQSIGIRQHLKRVQURE 600
Db 559 LAKFLHLMVSVVVELLSFFVTYTTTQKNLFFYRKSVMSKLSQSIGIRQHLKRVQURE 618
Qy 601 LSEAEVROHREARPAALLTSRLRFIPKPGDLRPIVNMDDYVVGARTFRKRAERLTSRYKA 660
Db 619 LSEAEVROHREARPAALLTSRLRFIPKPGDLRPIVNMDDYVVGARTFRKRAERLTSRYKA 678
Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFKVDVTGAYDTI 720
Db 679 LFSVLNTERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFKVDVTGAYDTI 738
Qy 721 PODRLTEVIASIIKQNTYCVRRYAVQKAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
Db 739 PODRLTEVIASIIKQNTYCVRRYAVQKAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 798
Qy 781 QETSLRDAVTEQSSNEASSGLPDVFLRPMCHHVRIRGKSVVCOGIPQGSILSTL 840
Db 799 QETSLRDAVTEQSSNEASSGLPDVFLRPMCHHVRIRGKSVVCOGIPQGSILSTL 858
Qy 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGPEYGCVVNL 900
Db 859 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGPEYGCVVNL 918
Qy 901 RKTVPNPFVEBALGGTAFVQMPAHLFPWCGLLDTRTLEVSQDYSSYARTSIRASLTF 960
Db 919 RKTVPNPFVEBALGGTAFVQMPAHLFPWCGLLDTRTLEVSQDYSSYARTSIRASLTF 978
Qy 961 NRGFKAGNMRKLPGLVRLKCHSLFDLQVNSLQVCTNIIKILLQAYRPHACVLOLP 1020
Db 979 NRGFKAGNMRKLPGLVRLKCHSLFDLQVNSLQVCTNIIKILLQAYRPHACVLOLP 1038
Qy 1021 FHOQVWKNPTFLRIVISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1039 FHOQVWKNPTFLRIVISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1098
Qy 1081 KLTRHRTVYVPLGLSLRTAQTLQSLKLPFTTL-----TALEAAANPAL 1123
Db 1099 KLTRHRTVYVPLGLSLRTGKYAAESEAFQDDADCPGGRSQPGTALRLQDHPLG 1151

RESULT 38

US-08-974-549A-5

; Sequence 5, Application US/08974549A

; Patent No. 6166178

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin B.

; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

; CORRESPONDENCE ADDRESS:

; ADDRESS: Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-974-549A-5

Query Match 68.0%; Score 4052; DB 3; Length 807;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRIGPQGWRLVQRGDPAAFRALVAQCLVCPW 60

Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRIGPQGWRLVQRGDPAAFRALVAQCLVCPW 60

Qy 61 DAREPPAAPSPROVSCIKELVARVLQRLCERCAKNVLAFGALLDARGGPEAFTTSVR 120

Db 61 DAREPPAAPSPROVSCIKELVARVLQRLCERCAKNVLAFGALLDARGGPEAFTTSVR 120

Qy 121 SYLPTVNTDALRGSGAWGLLRRVDDVLLHLLARCALFVLVAPSCAYQVCGPPLYLGA 180

Db 121 SYLPTVNTDALRGSGAWGLLRRVDDVLLHLLARCALFVLVAPSCAYQVCGPPLYLGA 180

Qy 181 ATQARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAGARRRGGSASRLPLPKRPR 240

Db 181 ATQARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAGARRRGGSASRLPLPKRPR 240

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QY 241 GAAPEPRTVQGQSWAHPGTRGSDRGFCVSPARPAEBEATSLEGALSCTRSHSPSVG 300
Db 241 GAAPEPRTVQGQSWAHPGTRGSDRGFCVSPARPAEBEATSLEGALSCTRSHSPSVG 300
QY 301 ROHAGPSTSRPPRPWDTPCPVVAETKHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
Db 301 ROHAGPSTSRPPRPWDTPCPVVAETKHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
QY 361 VETIFLGSRPWMPGTPRRLPRLPQRYQWMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPWMPGTPRRLPRLPQRYQWMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSWAAPPEEDTPRRLVQLLRQHSSPWQYGVFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSWAAPPEEDTPRRLVQLLRQHSSPWQYGVFVRACLRRLVPPGLWGS 480
QY 481 RHNERFLRNTKKFISLGKHAKLISQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERFLRNTKKFISLGKHAKLISQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
QY 541 LAKFLHLMWSVYVVELLSFFVYTTTQKNRLFYRKSVMSKLSQSIGIRQHLKRVQLRE 600
Db 541 LAKFLHLMWSVYVVELLSFFVYTTTQKNRLFYRKSVMSKLSQSIGIRQHLKRVQLRE 600
QY 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWETVLRVBAQDPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWETVLRVBAQDPPELYFVKVDVTGAYDTI 720
QY 721 PQDRLETVIASIIRKQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763
Db 721 PQDRLETVIASIIRKQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763

RESULT 39
US-08-912-951-5
; Sequence 5, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-912-951-5

Query Match 68.0%; Score 4052; DB 4; Length 807;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPPLATEFVRLPGQWELVORGDDPAAFRALVAQCLVCVPM 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPPLATEFVRLPGQWELVORGDDPAAFRALVAQCLVCVPM 60
QY 61 DARPPPAAPSFROVSCICKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
Db 61 DARPPPAAPSFROVSCICKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
QY 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLRGCCERAMNHSVREAGVPLGLPAPGARRRGGSASRLPLPKRPRR 240
Db 181 ATQARPPPHASGPRRLRGCCERAMNHSVREAGVPLGLPAPGARRRGGSASRLPLPKRPRR 240
QY 241 GAAPEPRTVQGQSWAHPGTRGSDRGFCVSPARPAEBEATSLEGALSCTRSHSPSVG 300
Db 241 GAAPEPRTVQGQSWAHPGTRGSDRGFCVSPARPAEBEATSLEGALSCTRSHSPSVG 300
QY 301 ROHAGPSTSRPPRPWDTPCPVVAETKHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
Db 301 ROHAGPSTSRPPRPWDTPCPVVAETKHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
QY 361 VETIFLGSRPWMPGTPRRLPRLPQRYQWMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPWMPGTPRRLPRLPQRYQWMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSWAAPPEEDTPRRLVQLLRQHSSPWQYGVFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSWAAPPEEDTPRRLVQLLRQHSSPWQYGVFVRACLRRLVPPGLWGS 480
QY 481 RHNERFLRNTKKFISLGKHAKLISQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERFLRNTKKFISLGKHAKLISQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
QY 541 LAKFLHLMWSVYVVELLSFFVYTTTQKNRLFYRKSVMSKLSQSIGIRQHLKRVQLRE 600
Db 541 LAKFLHLMWSVYVVELLSFFVYTTTQKNRLFYRKSVMSKLSQSIGIRQHLKRVQLRE 600
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Db 541 LAKFLHLMSSVVVVELLSFFVVTETTFQKNRLFYRKSVWSKLSQSIGIRHKLKRVQLRE 600
QY 601 LSEAEVRQHREARPAALLSRLEFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQHREARPAALLSRLEFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHV 763
Db 721 PDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHV 763

RESULT 40
US-09-402-181B-5
; Sequence 5, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.
; ; Morin, Gregg B.
; ; Harley, Calvin B.
; ; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-00262005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

LENGTH: 807 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-402-181B-5
Query Match 68.0%; Score 4052; DB 4; Length 807;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAPRCRAVRSLLRSHYREVLPPLATFVRRLLGPGQWRLVQRGDDPAAFALVAQCILVCVPM 60
Db 1 MPAPRCRAVRSLLRSHYREVLPPLATFVRRLLGPGQWRLVQRGDDPAAFALVAQCILVCVPM 60
QY 61 DARPPPAAPSROVSCLELVARVLCRCERGAKNVLAFFGALLDARGGGPEAFTTSVR 120
Db 61 DARPPPAAPSROVSCLELVARVLCRCERGAKNVLAFFGALLDARGGGPEAFTTSVR 120
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Db 121 SYLPTNTVDALRGSGAMGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
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Db 181 ATQARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAPGARRRGGSASRLPLPKRPRR 240
QY 241 GAAPERTPVQGSWAHPGTRGPGSCVFCVSPARPAEATSLGALSCTRSHSPSVG 300
Db 241 GAAPERTPVQGSWAHPGTRGPGSCVFCVSPARPAEATSLGALSCTRSHSPSVG 300
QY 301 RQHHAGPSTSRPPRMDTPCPVYAEYTKHFLYSYGKQELRPSFLSSLPSTGARRL 360
Db 301 RQHHAGPSTSRPPRMDTPCPVYAEYTKHFLYSYGKQELRPSFLSSLPSTGARRL 360
QY 361 VETIFLGSRPMPGTPRRLLPRLPORYQWMPRLFLELLGNHACQPYGVLLKTHCPLEAAVT 420
Db 361 VETIFLGSRPMPGTPRRLLPRLPORYQWMPRLFLELLGNHACQPYGVLLKTHCPLEAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYVGFVACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYVGFVACLRRLVPPGLWGS 480
QY 481 RHNERRFLRNTKFTISLGKHAKLISQELTWKMSVRDCAWLRSPGVCVPAAEHLRBEI 540
Db 481 RHNERRFLRNTKFTISLGKHAKLISQELTWKMSVRDCAWLRSPGVCVPAAEHLRBEI 540
QY 541 LAKFLHLMSSVVVVELLSFFVVTETTFQKNRLFYRKSVWSKLSQSIGIRHKLKRVQLRE 600
Db 541 LAKFLHLMSSVVVVELLSFFVVTETTFQKNRLFYRKSVWSKLSQSIGIRHKLKRVQLRE 600
QY 601 LSEAEVRQHREARPAALLSRLEFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQHREARPAALLSRLEFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHV 763
Db 721 PDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHV 763

RESULT 41
US-09-721-456-5
; Sequence 5, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.

;; Morin, Gregg B.
;; Harley, Calvin B.
;; Andrews, William H.
;; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
;; NUMBER OF SEQUENCES: 727
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; STATE: California
;; CITY: San Francisco
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/721,456
;; FILING DATE: 22-Nov-2000
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/974,549A
;; FILING DATE: 19-NOV-1997
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; APPLICATION NUMBER: US 08/911,312
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/912,951
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; APPLICATION NUMBER: WO PCT/US97/17618
;; FILING DATE: 01-OCT-1997
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph Ted
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002610US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 807 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-721-456-5
Query Match 68.0%; Score 4052; DB 4; Length 807;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPCRAVRLSLRSHRYEVLPLATFVRRLLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
Db 1 MPRAPCRAVRLSLRSHRYEVLPLATFVRRLLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
Qy 61 DARPPAAPSPROVSLCKELVARVLQRLCEGAKNVLAFGALLDARGGPPPEAFTTSVR 120
Db 61 DARPPAAPSPROVSLCKELVARVLQRLCEGAKNVLAFGALLDARGGPPPEAFTTSVR 120
Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGRRRLGRCERAWNHSVREAGVPLGLPAPGARRRRGSSASRLPLPKPRR 240
Db 181 ATQARPPPHASGRRRLGRCERAWNHSVREAGVPLGLPAPGARRRRGSSASRLPLPKPRR 240
Qy 241 GAAPPERTPVGGSWAHPGTRGSPDRGFCVVSPPARPAEATSLGALSSTRHSHPSVG 300
Db 241 GAAPPERTPVGGSWAHPGTRGSPDRGFCVVSPPARPAEATSLGALSSTRHSHPSVG 300
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Db 301 ROHHAGPPSTSRPRPMDTTPCPVYAEKTHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRRPMPCTPRRLPRLPQRYWQMRPLFLELLGNHAQCYPYVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPCTPRRLPRLPQRYWQMRPLFLELLGNHAQCYPYVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVOLLRHQSSPWQYGVFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVOLLRHQSSPWQYGVFVRACLRLVPPGLWGS 480
Qy 481 RHNERRELNTKXIFISLGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Db 481 RHNERRELNTKXIFISLGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Qy 541 LAKFLHWMLSVYVVELLRSFFYVTTETTFQKNRFFYFKSVMSKLSQSIGIRQHLKRVQLRE 600
Db 541 LAKFLHWMLSVYVVELLRSFFYVTTETTFQKNRFFYFKSVMSKLSQSIGIRQHLKRVQLRE 600
Qy 601 LSEAEVRQHREARPAALTSRLRPIPKDGLRPIVNMVYVVGARTFREKKAERLTSRVKA 660
Db 601 LSEAEVRQHREARPAALTSRLRPIPKDGLRPIVNMVYVVGARTFREKKAERLTSRVKA 660
Qy 661 LFSVLNYERARRPCLLGASVLGLDDIHRAWRTFVLVRADODPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPCLLGASVLGLDDIHRAWRTFVLVRADODPPPELYFVKVDVTGAYDTI 720
Qy 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763
Db 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763
RESULT 42
US-08-851-843A-217
; Sequence 217, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997

Qy	732	IIPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLOPYMRQFVAHLQXNSPLRDVV	791
Db	603	IIPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLOPYMRQFVAHLQXNSPLRDVV	662
Qy	792	IEOSSSNEASSGLFDVFLRFMCHAVRIRGKSVVOCQIPQSGIISLTLCSLCYGD MEN	851
Db	663	IEOSSSNEASSGLFDVFLRFMCHAVRIRGKSVVOCQIPQSGIISLTLCSLCYGD MEN	722
Qy	852	KLFPAGIRRDGLLRLLVDDFLVLPPLTHAKTFLRTLVRGVPEYGCVVNLKTKTVNFPVED	911
Db	723	KLFPAGIRRDGLLRLLVDDFLVLPPLTHAKTFLRTLVRGVPEYGCVVNLKTKTVNFPVED	782
Qy	912	EALGGTAFVOMPAGHLFPWCGLLDTRTLEVDQSDYSYARTSTRASLTFNRGFKAGNMR	971
Db	783	EALGGTAFVOMPAGHLFPWCGLLDTRTLEVDQSDYSYARTSTRASLTFNRGFKAGNMR	842
Qy	972	RKLFVGLRLKCHSLFDLDQVNSLQTVCTNLYKILLQAVRFHACVLQLPFHQQVWKNPTF	1031
Db	843	RKLFVGLRLKCHSLFDLDQVNSLQTVCTNLYKILLQAVRFHACVLQLPFHQQVWKNPTF	902
Qy	1032	FLRVIDSTASLCSYILKAKNAGSLGAKGAAGPLPSEAVOMLCHQAFLLKLTJHRVTYVP	1091
Db	903	FLRVIDSTASLCSYILKAKNAGSLGAKGAAGPLPSEAVOMLCHQAFLLKLTJHRVTYVP	962
Qy	1092	LLGSLRTAQTLRSKLPGGTTLTALEAAANPALPSDFKTILD	1132
Db	963	LLGSLRTAQTLRSKLPGGTTLTALEAAANPALPSDFKTILD	1003
RESULT 43			
US-08-974-549A-336			
; Sequence 336, Application US/08974549A			
; Patent No. 6166178			
; GENERAL INFORMATION:			
; APPLICANT: Cech, Thomas R.			
; APPLICANT: Lingner, Joachim			
; APPLICANT: Nakamura, Toru			
; APPLICANT: Chapman, Karen B.			
; APPLICANT: Morin, Gregg B.			
; APPLICANT: Harley, Calvin B.			
; APPLICANT: Andrews, William H.			
; TITLE OF INVENTION: Human telomerase Catalytic Subunit			
; NUMBER OF SEQUENCES: 727			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Townsend and Townsend and Crew LLP			
; STREET: Two Embarcadero Center, Eighth Floor			
; CITY: San Francisco			
; STATE: California			
; COUNTRY: USA			
; ZIP: 94111-3834			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/974,549A			
; FILING DATE: 19-NOV-1997			
; CLASSIFICATION: 536			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/724,643			
; FILING DATE: 01-OCT-1996			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/844,419			
; FILING DATE: 18-APR-1997			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/846,017			
; FILING DATE: 25-APR-1997			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/851,843			
; FILING DATE: 06-MAY-1997			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/854,050			

Db	543	RPGLLGASVGLGDDIHRWRTFVLRVRAQPPPELYFVKVDVTGAYDTIPQDRLTEVIAS	602
QY	732	IKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMQFVAHLOETSPLRDAVV	791
Db	603	IKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMQFVAHLOXNSPLRDAVV	662
QY	792	IEOSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOGSIILSTLCSLCYGD MEN	851
Db	663	IEOSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOGSIILSTLCSLCYGD MEN	722
QY	852	KLPAGTRRGLLRVLVDDELVTTPHITHAKTFRTLVRGVPSEVGVNLRKTVNFPFVED	911
Db	723	KLPAGTRRGLLRVLVDDELVTTPHITHAKTFRTLVRGVPSEVGVNLRKTVNFPFVED	782
QY	912	EALGGTAFVQMPAHGLFPMCGILLDTRTLEVOQSDYSSYARTSIRASLTFNRGFKAGNMR	971
Db	783	EALGGTAFVQMPAHGLFPMCGILLDTRTLEVOQSDYSSYARTSIRASLTFNRGFKAGNMR	842
QY	972	RKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLPFHQQVWKNPTF	1031
Db	843	RKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLPFHQQVWKNPTF	902
QY	1032	FLRVISDTASLCSYILKAKNAGSLGAKAAGPLPSEAVQWLCHQAFLLKLTTRHRTVYP	1091
Db	903	FLRVISDTASLCSYILKAKNAGSLGAKAAGPLPSEAVQWLCHQAFLLKLTTRHRTVYP	962
QY	1092	LLGSLRTAQTOLSRKPLPGTTLTALEAAANPALPSDFKTILD	1132
Db	963	LLGSLRTAQTOLSRKPLPGTTLTALEAAANPALPSDFKTILD	1003

RESULT 44

US-08-854-050-217
; Sequence 217, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997

Qy	852	KL	FAGIRRDGLLLRLVDDFLVTPH	THAKTFTLTVRGVPEYGCVVNLAKTVVNF	PVED	911
Db	723	KL	FAGIRRDGLLLRLVDDFLVTPH	THAKTFTLTVRGVPEYGCVVNLAKTVVNF	PVED	782
Qy	912	EALGGTAFVQMPAHGLFPWCGL	LLDTRTLEVOQSDYSSYARTSIRASLT	FNRGFKAGNMR	971	
Db	783	EALGGTAFVQMPAHGLFPWCGL	LLDTRTLEVOQSDYSSYARTSIRASLT	FNRGFKAGNMR	842	
Qy	972	RKLFVGLRLKCHSLFLDLQVNS	LQTVCTNYIKILLQAVRPHACVQLP	PHQQVWKNPTF	1031	
Db	843	RKLFVGLRLKCHSLFLDLQVNS	LQTVCTNYIKILLQAVRPHACVQLP	PHQQVWKNPTF	902	
Qy	1032	FLRIVSDTASLCYSILKAKNAG	SLGAKGAGPLPSEAVOMLCHQAFLL	KLTRHRTVYP	1091	
Db	903	FLRIVSDTASLCYSILKAKNAG	SLGAKGAGPLPSEAVOMLCHQAFLL	KLTRHRTVYP	962	
Qy	1092	LLGSLRTAQTLGRKPLPGTTLT	ALEAAANPALPSDFKTILD	1132		
Db	963	LLGSLRTAQTLGRKPLPGTTLT	ALEAAANPALPSDFKTILD	1003		
RESULT 45						
US-09-430-323-217						
: Sequence 217, Application US/09430323						
: Patent No. 6309867						
GENERAL INFORMATION:						
APPLICANT: Cech, Thomas R.						
Lingner, Joachim						
Nakamura, Toru						
Chapman, Karen B.						
Morin, Gregg B.						
Harley, Calvin						
Andrews, William H.						
TITLE OF INVENTION: No. 6309867el Telomerase						
NUMBER OF SEQUENCES: 225						
CORRESPONDENCE ADDRESS:						
ADDRESSEE: Townsend and Townsend and Crew LLP						
STREET: Two Embarcadero Center, 8th Floor						
CITY: San Francisco						
STATE: California						
COUNTRY: United States of America						
ZIP: 94111						
COMPUTER READABLE FORM:						
MEDIUM TYPE: Floppy disk						
COMPUTER: IBM PC Compatible						
OPERATING SYSTEM: PC-DOS/MS-DOS						
SOFTWARE: PatentIn Release #1.0, Version #1.30						
CURRENT APPLICATION DATA:						
APPLICATION NUMBER: US/09/430,323						
FILING DATE: 29-Oct-1999						
CLASSIFICATION: <Unknown>						
PRIOR APPLICATION DATA:						
APPLICATION NUMBER: US 08/854,050						
FILING DATE: 09-MAY-1997						
APPLICATION NUMBER: US 08/851,843						
FILING DATE: 06-MAY-1997						
APPLICATION NUMBER: US 08/846,017						
FILING DATE: 25-APR-1997						
APPLICATION NUMBER: US 08/844,419						
FILING DATE: 18-APR-1997						
APPLICATION NUMBER: US 08/724,643						
FILING DATE: 01-OCT-1996						
ATTORNEY/AGENT INFORMATION:						
NAME: Apple, Randolph T.						
REGISTRATION NUMBER: 36,429						
REFERENCE/DOCKET NUMBER: 015389-002930US						
TELECOMMUNICATION INFORMATION:						
TELEPHONE: (415) 576-0200						
TELEFAX: (415) 576-0300						
INFORMATION FOR SEQ ID NO: 217:						
SEQUENCE CHARACTERISTICS:						
LENGTH: 1003 amino acids						
TYPE: amino acid						

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;
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 217:
US-09-430-323-217

Query Match          64.1%; Score 3819.5; DB 3; Length 1003;
Best Local Similarity 78.7%; Pred. No. 0;
Matches 788; Conservative 23; Mismatches 123; Indels 67; Gaps 18;

Qy 163 APS-CAYOVCPPLYQLGAATQARPPPHASQPRRL-----GGERAMNHSVRBAGVPLG 215
Db 39 APTXCAGRC-----TSSALXLR-----GPRHTLDPXASGIQRAWNHSVRBAGVPLG 87

Qy 216 LPAGARRRGASAKSLPLPKRPR-RGAAPPERT--PVGGSWAHPGRTT-RGPSDRGFC 271
Db 88 CQ--PRVRGAGAVPAEVCRCRPGVALPLSRGRLGRG----PGPTRAGRLDR-VT 139

Qy 272 VVS-----PARP-----AEEATSLGALSGTSHSPSVCRQ--HHAGPSTSRP 313
Db 140 VVSVMCHLPDPKPKPLMRVRSARATPHMAASTTTRAPHPHRGHHVGLHALSPGVRR- 198

Qy 314 PRPMDTCPVVAETKHFYSSGQKEQLRPSFLSSRLSPSTGARRLVETIFLGSRPMP 373
Db 199 ----DQALPLLLRQXHC-----XPPSYSI-YLRPSLTGYREVGRDXLSGRPMP 244

Qy 374 GTPRLRLPLQRYWQMRPLFLELGNHAQCYPGVLLK--THCPLRAAVTPAAGVCAREKP 431
Db 245 GFPAGCAPCPXKTCGCFWSCGLTTRASPTGCCSSRRRTARCELRSPOQPV--VPGRSP 302

Qy 432 QGSVAAPPEEEDTDPRLVOLLAROHSSPMONVGVFRACLRRLVPPCLGSRNRRERLNT 491
Db 303 RALWRPERRRNDPRLVOLLAROHSSPMONVGVFRACLRRLVPPCLGSRNRRERLNT 362

Qy 492 KKFISLGHAKLSLOELTWKMSVRDCAMLRSPGVCVPAAEHRLREILAKFLHLMVSV 551
Db 363 KKFISLGHAKLSLOELTWKMSVRDCAMLRSPGVCVPAAEHRLREILAKFLHLMVSV 422

Qy 552 YVVELLRFFVYTTTFOKNRLFFVRKSVMSKLSIGIRQHLKRVQLRELSAEVQHRE 611
Db 423 YVVELLRFFVYTTTFOKNRLFFVRKSVMSKLSIGIRQHLKRVQLRELSAEVQHRE 482

Qy 612 ARPALLTSRLRFIPKPDGLRPIVNMVYVVGARTFRERKGAERLSRVKALFSLVNYERAR 671
Db 483 ARPALLTSRLRFIPKPDGLRPIVNMVYVVGARTFRERKGAERLSRVKALFSLVNYERAR 542

Qy 672 RPLGLGASVLGLDDIHRARWTFVLVRADQPPPELYFVKVDVTGAYDTIPQDRLTEVIAS 731
Db 543 RPLGLGASVLGLDDIHRARWTFVLVRADQPPPELYFVKVDVTGAYDTIPQDRLTEVIAS 602

Qy 732 IIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPMRFVAFHQLQTSPLRDAV 791
Db 603 IIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPMRFVAFHQLQTSPLRDAV 662

Qy 792 IEQSSSLNEASGLPDVFLRFMCHHAVIRKGSVYOCQGIPOGSIITSLTLLCSLCYGDWEN 851
Db 663 IEQSSSLNEASGLPDVFLRFMCHHAVIRKGSVYOCQGIPOGSIITSLTLLCSLCYGDWEN 722

Qy 852 KLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCVMNLRTVNVFPVED 911
Db 723 KLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCVMNLRTVNVFPVED 782

Qy 912 BALGCTAFVQMPAHGLFPWCGLLDTRTLLEVQSDYSSYARTSIRASLTFNFRGFKAGRNM 971
Db 783 BALGCTAFVQMPAHGLFPWCGLLDTRTLLEVQSDYSSYARTSIRASLTFNFRGFKAGRNM 842

Qy 972 RKLFGVRLKCHSLFLDIQVNSLQVCTNIYKILLQAYRHACVLQLPFHQQVWKQPTF 1031
Db 843 RKLFGVRLKCHSLFLDIQVNSLQVCTNIYKILLQAYRHACVLQLPFHQQVWKQPTF 902

Qy 1032 FLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLLKLTRHRTVYVP 1091
Db 903 FLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLLKLTRHRTVYVP 962

Qy 1092 LGLSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
Db 963 LGLSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1003

RESULT 46
US-09-402-181B-336
; Sequence 336, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402.181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Aussenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-00262005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 336:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1003 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 336:
US-09-402-181B-336

Query Match          64.1%; Score 3819.5; DB 4; Length 1003;
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[illegible]

RESULT 47

Query Match	64.1%	Score 3819.5;	DB 4;	Length 1003;
Best Local Similarity	78.7%	Pred. No. 0;		
Matches 788; Conservative	23;	Mismatches 123;	Indels 67;	

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US-09-721-456-336
; Sequence 336, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-No. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 336:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1003 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 336:
US-09-721-456-336

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TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-042-460-2

Query Match 58.8%; Score 3505; DB 4; Length 1122;
Best Local Similarity 62.4%; Pred. No. 6.7e-314; Mismatches 260; Indels 52; Gaps 13;
Matches 719; Conservative 122;
QY 1 MPAPRCRAVRSLRSHRYEVLPLATFVRRRLGPGQWRRLVQRGDPAAFRALVAQCCLVCPW 60
DB 1 MTRAPRCPAVRSLRSHRYEVLPLATFVRRRLGPGQWRRLVQRGDPAAFRALVAQCCLVCPW 60
QY 61 DARPPAPDSFQVSCLEKELVARVORLCERCAKAVLARGPALLDARGCPPEATTTSVR 120
DB 61 GSQPPADLSFRQVSLKELVARVORLCERCAKAVLARGPALLDARGCPPEATTTSVR 120
QY 121 SYLPTNTVDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYOVCCPPLVQLCA 180
DB 121 SYLPTNTVIELTRVSGAWMLLRLSRVGDVLLVHLLARCALFVLVAPSCAYOVCCPPLVQLCA 180
QY 181 ATQARPPPHAS-GPRRLRG-----CERAMNHSVREAGVPLGLPAPGARRRGGSASRS 231
DB 181 TTDIWPVSASVPRTPGVGNTNLRFLQOIKSSRQEAQPLALPSRGTGKHLSTSTS 240
QY 232 LPLPKRPRGAAPERTPVGGGWAHPGRTGSPDRGFCVVSAPAR-----PABEATSL 286
DB 241 VPSAKKARCPVPRVEEGP-----HRQVLTPSGKSW-VPSPARSPVPPTAEDLSK 292
QY 287 GALSCTRSHSPVGHQHHAGPSTSRPPRPWDTCPVVAETKHFYSSGD-KEQLRPSF 345
DB 293 GKVSLSUS-GVCCCKHPSSTLSLPPKQNAFQLRP-PIETRHFLYSGRQDQERLNPSF 350
QY 346 LLSLRPSLTGARRIVETIFLGRSPWMPGTTPRLPQRYWQMPPLFLELGNHAQCPY 405
DB 351 LLSLNQPNLTGARRIVEIFLGRSPRTSGPLCRTHLSRYWQMPPLFQOLLVNHACQY 410
QY 406 GVLLKTHCPDRAA-----VTPAAGVCAREKPGGSAAPAEEDTDPRLVOLLRQHSFPQY 462
DB 411 VLLRSHCRFRNTAQVTDAL-----NTSPHMLDLLRLHSPFWQY 452
QY 463 GPRACLRRLVPPGLWGRSHNERFLNTKKISLGKAKLSLOBLTWKMSVRDCAWLR 522
DB 453 GFLRACLCVKSASLWGTTHNERRFFKNLKKFISLGKYKLSQBLMMKMYEDCHWLS 512
QY 523 SPGVGCVPAAEHRLREELILAKLHLMMSVYVVELLSRFFYVTTTFQKRLFFYKSVMS 582
DB 513 SPKDRVPAAEHRLREELILATFLWMDTYVYVQLLSRFFYITESTFQKRLFFYKSVMS 572
QY 583 KLSIGIRQHLKRVOLRELSEAEVQHRREARPAALLTSRLRFTPKDGLRPIVNM DYVGA 642
DB 573 KLSIGVRQHLKRVOLRELSEAEVQHRHODTWLAMPICRLRFTPKNGLRPIVNM SYSMTG 632
QY 643 RTFREKRAERLTSVKALFSLVNLNERARRPGLLGASVLGLDDIHRMRTFVLVRAQDP 702
DB 633 RALGRKQQAQHTFQRLKTLFSLMNTERTKPHLMGSSVLGMNDIYRTWRFAVLVRLDQ 692
QY 703 PPFLYFVVDVTGAYDTIPQDRLTEVIASIIK-PONTYCVRRYAVVOKAAHGHVRKAFKS 761
DB 693 TPRTMFVKADVTGADALPQGLKEVEVAMNIRHSESTICIRYAVRRDSQQVHKSFRR 752
QY 762 HVSITLTDLPYMRQFVAHLQET--SPLRDVAVIEQSSSINEASSGLFDVFLRFMCHAVR 819
DB 753 QVTTLSDLQPYMGQFLKHLQDSASALRNSVIEQSSISNNESSSISLFDFFLHFLRHSVK 812
QY 820 IRGKSYVQCQIPQSSISLTLCSLCYGDMEKLFAGIRRDGLLRLVDDFLVTPHLLTH 879
DB 813 IGDRCYTOCQIPQSSISLTLCSLCFGDMENKLFQVQDGLLRLVDDFLVTPHLLDQ 872
QY 880 AKTFLRTLVRGPEYGCYVNLKTVNPPVEALGGTAFVQMPAHGLFPWCGLLDTRT 939
DB 873 AKTFLSTLVHGPEYGCYVNLKTVNPPVEFGTLGGAPYQLPAHCLFPWCGLLDTQT 932
QY 940 LEVQSDYSSYARTSIRASLTNRGFKAGRNMRKLFGLVRLKCHSLFLDLQVNSLQTCT 999

RESULT 49

US-09-582-924B-12
; Sequence 12, Application US/09582924B
; Patent No. 6608188
; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIVAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: No. 6608188el Gene Having Reverse Transcriptase Motif
; FILE REFERENCE: 46124-5034-US
; CURRENT APPLICATION NUMBER: US/09/582,924B
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: JP 10/13232
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: JP 10/33584
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: JP 10/139177
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: PCT/JP99/00039
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 12
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-582-924B-12
Query Match 52.6%; Score 3134; DB 4; Length 622;
Best Local Similarity 97.9%; Pred. No. 4.5e-280;
Matches 610; Conservative 3; Mismatches 6; Indels 4; Gaps 1;
QY 510 WKMSVRDCAWLRSPGVGCVPAAEHRLREELILAKLHLMMSVYVVELLSRFFYVTTTFQ 569
DB 4 WRLTRAVILAR---VGCVPAAEHRLREELILAKLHLMMSVYVVELLSRFFYVTTTFQ 59
QY 570 KNLRFYFKSVMSKLSIGIRQHLKRVOLRELSEAEVQHRREARPAALLTSRLRFTPKDPG 629
DB 60 KNLRFYFKSVMSKLSIGIRQHLKRVOLRELSEAEVQHRREARPAALLTSRLRFTPKDPG 119
QY 630 LRPIVNM DYVVGARTFREKRAERLTSVKALFSLVNLNERARRPGLLGASVLGLDDIHR 689
DB 120 LRPIVNM DYVVGARTFREKRAERLTSVKALFSLVNLNERARRPGLLGASVLGLDDIHR 179
QY 690 WRTFVLVRAQDPPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PONTYCVRRYAVVOK 749
DB 180 WRTFVLVRAQDPPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PONTYCVRRYAVVOK 239
QY 750 AAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQETSPLRDVAVIEQSSSINEASSGLFDV 809
DB 240 AAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQETSPLRDVAVIEQSSSINEASSGLFDV 299
QY 810 LRFMCHAVIRGKSYVQCQIPQSSISLTLCSLCYGDMEKLFAGIRRDGLLRLVDD 869
DB 300 LRFMCHAVIRGKSYVQCQIPQSSISLTLCSLCYGDMEKLFAGIRRDGLLRLVDD 359
QY 870 FLLVTPHLLTHAKTFLRTLVRGPEYGCYVNLKTVNPPVEALGGTAFVQMPAHGLFP 929

Db 360 FLVTPHLTHAKTFLRTLVRGVPVGVNLRKTVNPPVVEDEALGGTAFVQMPAHGLFP 419
Qy 930 WCGLLDTRTLEVSQSDYSYARTSIRASLTNNRGFKAGNNRRKLFVGLRLKCHSLFIDL 989
Db 420 WCGLLDTRTLEVSQSDYSYARTSIRASLTNNRGFKAGNNRRKLFVGLRLKCHSLFIDL 479
Qy 990 QVNSIQVCTNYYKILLQAVRFHACVQLQLPFHQQVWKNPTFFLRVSDTASLCYSILKA 1049
Db 480 QVNSIQVCTNYYKILLQAVRFHACVQLQLPFHQQVWKNPTFFLRVSDTASLCYSILKA 539
Qy 1050 KNAGMSLGAKGAGPLPSEAVQWLCHQAFLLKLTFRHRYVYVPLLGSLRTAQTLSRKLPG 1109
Db 540 KNAGMSLGAKGAGPLPSEAVQWLCHQAFLLKLTFRHRYVYVPLLGSLRTAQTLSRKLPG 599
Qy 1110 TTLEAAANPALPSDPKTTILD 1132
Db 600 TTLEAAANPALPSDPKTTILD 622

RESULT 50

US-09-582-924B-10
; Sequence 10, Application US/09582924B
; Patent No. 6608188
; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: No. 6608188el Gene Having Reverse Transcriptase Motif
; FILE REFERENCE: 46124-5034-US
; CURRENT APPLICATION NUMBER: US/09/582,924B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: JP 10/13232
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: JP 10/33584
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: JP 10/139177
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: PCT/JP99/00039
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 10
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-582-924B-10

Query Match 36.6%; Score 2184; DB 4; Length 438;
Best Local Similarity 97.0%; Pred. No. 1.2e-192;
Matches 425; Conservative 3; Mismatches 6; Indels 4; Gaps 1;
Qy 510 WMSVRDCAWLRRSPGCVGCPAAEHRLREEILAKFLHLMVYVVELLSRPFYVTTTFQ 569
Db 4 WRLTRRAVILAR---VGCVPAAEHRLREEILAKFLHLMVYVVELLSRPFYVTTTFQ 59
Qy 570 KNRLFFYKSVWSKLQSIGIQHLKRVOLRELSAEVQHEAREAPALLTSRLRTPKPDG 629
Db 60 KNRLFFYKSVWSKLQSIGIQHLKRVOLRELSAEVQHEAREAPALLTSRLRTPKPDG 119
Qy 630 LRPIVNDYVVGARTFRREKRAERLTSRVKALFVNLNYERARRPGLLGASVIGLDDIHRA 689
Db 120 LRPIVNDYVVGARTFRREKRAERLTSRVKALFVNLNYERARRPGLLGASVIGLDDIHRA 179
Qy 690 WRTFVLVRADQPPPELVFKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQK 749
Db 180 WRTFVLVRADQPPPELVFKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQK 239
Qy 750 AAHGHRKAFKSHVSTLTDLPYMEQFVAHLQETSPLRDQVIEQSSSINEASSGLFDVF 809
Db 240 AAHGHRKAFKSHVSTLTDLPYMEQFVAHLQETSPLRDQVIEQSSSINEASSGLFDVF 299
Qy 810 LRFMCHHAVIRGKSVYVQCGIPQGSILSTLLCSLCYGDMMENKLPAGIRRDGLLRVDD 869
Db 300 LRFMCHHAVIRGKSVYVQCGIPQGSILSTLLCSLCYGDMMENKLPAGIRRDGLLRVDD 359

Qy 870 FLVTPHLTHAKTFLRTLVRGVPVGVNLRKTVNPPVVEDEALGGTAFVQMPAHGLFP 929
Db 360 FLVTPHLTHAKTFLRTLVRGVPVGVNLRKTVNPPVVEDEALGGTAFVQMPAHGLFP 419
Qy 930 WCGLLDTRTLEVSQSDYS 947
Db 420 WCGLLDTRTLEVSQSDYS 437

Search completed: August 5, 2005, 14:22:37
Job time : 66 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 5, 2005, 14:04:32 ; Search time 175 Seconds
(without alignments)
2501.787 Million cell updates/sec

Title: US-10-053-758-225
Perfect score: 5961
Sequence: 1 MPRAPRCNVRSLRLSHYRE.....TALSAANPALPSPDKTILD 1132

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003s:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5961	100.0	1132	2 AAW46957	Aaw46957 Human tel
2	5961	100.0	1132	2 AAW90251	Aaw90251 Human cat
3	5961	100.0	1132	2 AAY28881	Aay28881 Human tel
4	5961	100.0	1132	2 AAY32090	Aay32090 Human tel
5	5961	100.0	1132	2 AAY43621	Aay43621 A human t
6	5961	100.0	1132	2 AAY25680	Aay25680 Human tel
7	5961	100.0	1132	4 AAG64859	Aag64859 Heart mus
8	5961	100.0	1132	4 AAG64329	Aag64329 Human pro
9	5961	100.0	1132	4 AAB99930	Aab99930 Human tel
10	5961	100.0	1132	4 AAB82765	Aab82765 Human tel
11	5961	100.0	1132	5 AAE29226	Aae29226 Human tel
12	5961	100.0	1132	5 AAU72735	Aau72735 Human tel
13	5961	100.0	1132	6 ABR42384	Abr42384 Human tel
14	5961	100.0	1132	6 ABR42063	Abr42063 Human tel
15	5961	100.0	1132	6 ABP56676	Abp56676 Human tel
16	5961	100.0	1132	6 ABR58045	Abt58045 Human tel
17	5961	100.0	1132	7 ADD21420	Add21420 Human TER
18	5961	100.0	1132	7 ADH72743	Adh72743 Human pro
19	5961	100.0	1132	8 ADG70114	Adg70114 hTERT pro
20	5961	100.0	1132	8 ADG90599	Adg90599 Human TER
21	5961	100.0	1132	8 ADI82172	Adi82172 Human tel
22	5961	100.0	1132	8 ADR70482	Adr70482 Human tel
23	5961	100.0	1132	2 AAW61350	Aaw61350 Human tel
24	5961	100.0	1189	2 AAW47008	Aaw47008 Glutathio
25	5955	99.9	1285	2 AAW47000	Aaw47000 HIS tagge

ALIGNMENTS

RESULT 1

AAW46957
ID AAW46957 standard; protein; 1132 AA.

AC AAW46957;

DT 13-AUG-1998 (first entry)

DE Human telomerase reverse transcriptase.

KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein.

OS Homo sapiens.

PN GB2317891-A.

PD 08-APR-1998.

PF 01-OCT-1997; 97GB-00020890.

PR 01-OCT-1996; 96US-00724643.

PR 18-APR-1997; 97US-00844419.

PR 25-APR-1997; 97US-00846017.

PR 06-MAY-1997; 97US-00851843.

PR 09-MAY-1997; 97US-00854050.

PR 14-AUG-1997; 97US-00911312.

PR 14-AUG-1997; 97US-00912951.

PR 14-AUG-1997; 97US-00915503.

(GERO-) GERON CORP.

(UYTE-) UNIV TECHNOLOGY CORP.

Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;

Andrews WH;

WPI; 1998-171633/16.

N-PSDB; AAW22379.

Pure and recombinant human Telomerase Reverse Transcriptase and its

variants - are useful in the diagnosis, prognosis and treatment of cell

proliferation conditions especially cancer and ageing.

Claim 3; Fig 17; 387pp; English.

AAW71376 Human tel
Aay00627 Human tel
Aay00638 Truncated
Aay28401 Human EST
Aay96566 hEST2, a
Aac47061 Human TER
Ade40482 Human tel
Aaw56113 Human tel
Aay00647 Telomeras
Aaw56101 Enhanced
Aaw47007 Glutathio
Aay00641 Telomeras
Aay00650 Telomeras
Aay47006 Glutathio
Aay00640 Altered C
Aay00649 Altered C
Aay00652 Altered C
Aay00643 Altered C
Aay00639 N-termina
Aay00648 Truncated

CC is a modulator of hTERT, by detecting the change in hTERT recombinant
CC protein or polynucleotide, on administration of the compound; (B)
CC preparation of recombinant telomerase by contacting a protein preparation
CC of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or
CC protein in a sample by binding a relevant probe to the sample and
CC detecting the complex formed or in the case of RNA detection, amplifying
CC the product and correlating the presence of complex or amplification
CC product with presence of hTERT in the sample; and (D) increasing the
CC proliferation of a vertebrate cell by increasing hTERT expression; and (E)
CC the use of an agent that causes an increase in cell vertebrate cell
CC proliferation to create a medicament that inhibits ageing. A protein
CC preparation of hTERT and the polynucleotide encoding hTERT can be used in
CC the manufacture of medicaments for inhibiting the effect of ageing or
CC cancer. Inhibitors of telomerase activity can be used to treat conditions
CC that are associated with high telomerase activity. A protein preparation
CC of hTERT can also be used in the new methods

XX SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRLSHRYEVLPLATFVRRLLGPGQWRVLVQRGDPAAPEALVAQCGLVCVPW 60
DB 1 MPAPRCRAVRLSHRYEVLPLATFVRRLLGPGQWRVLVQRGDPAAPEALVAQCGLVCVPW 60

QY 61 DARPPPAAPSPROVSKLXELVARVLQRLCERGAKNVLAFGFALLDGGAGGPEAFTTSVR 120
DB 61 DARPPPAAPSPROVSKLXELVARVLQRLCERGAKNVLAFGFALLDGGAGGPEAFTTSVR 120

QY 121 SYLNTVTDALRGSGANGLLRRVGDVVLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVTDALRGSGANGLLRRVGDVVLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASPRRLCERANVHSVREAGVPLGLPAGARRRGGASRLPLPKPRR 240
DB 181 ATQARPPPHASPRRLCERANVHSVREAGVPLGLPAGARRRGGASRLPLPKPRR 240

QY 241 GAAPEPERTVPGQGSWAHPGRTGFSDRGFCVSPARPAEATSLGALSCTRHSHPVSG 300
DB 241 GAAPEPERTVPGQGSWAHPGRTGFSDRGFCVSPARPAEATSLGALSCTRHSHPVSG 300

QY 301 RQHAGPPSTSRPRPMDTPCPVYAEYTKHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
DB 301 RQHAGPPSTSRPRPMDTPCPVYAEYTKHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360

QY 361 VETIFLGSRPWMPGTFRPLPRLPORYWOMRPLELLELGNHAQCPYGVLLKTHCPLRAVT 420
DB 361 VETIFLGSRPWMPGTFRPLPRLPORYWOMRPLELLELGNHAQCPYGVLLKTHCPLRAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEDTPRRLVQLLRQHSPPQVYGFVRACLRRLVPPGLWGS 480
DB 421 PAAGVCAREKPGQSVAAPEEDTPRRLVQLLRQHSPPQVYGFVRACLRRLVPPGLWGS 480

QY 481 RHNERFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
DB 481 RHNERFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540

QY 541 LAKFLHLMWSVYVVELLSRFFVTETTFQKRLFPYKSVMSKLQSIGIROHLKRVQLE 600
DB 541 LAKFLHLMWSVYVVELLSRFFVTETTFQKRLFPYKSVMSKLQSIGIROHLKRVQLE 600

QY 601 LSEAFVQRHREARPALTSRLRIFPKPDGLRPIVMNDYVVGARTFRREKRAERLTSRYKA 660
DB 601 LSEAFVQRHREARPALTSRLRIFPKPDGLRPIVMNDYVVGARTFRREKRAERLTSRYKA 660

QY 661 LFSVLNHERARRPGLLGASVLGLDDIHRAWTFVLVRQAQPPPELYFKVDVTGAYDTI 720
DB 661 LFSVLNHERARRPGLLGASVLGLDDIHRAWTFVLVRQAQPPPELYFKVDVTGAYDTI 720

QY 721 PQDLRTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMQFVAHL 780

DB 721 PQDLRTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMQFVAHL 780

QY 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHVRIRGKSVYQCQGIPOGSII STL 840

DB 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHVRIRGKSVYQCQGIPOGSII STL 840

QY 841 LCSLCYGDGMENKLPAGIRRRDGLLLRLVDDFLVTPHLLTHAKTFLRTRVGRPEYGCVVNL 900

DB 841 LCSLCYGDGMENKLPAGIRRRDGLLLRLVDDFLVTPHLLTHAKTFLRTRVGRPEYGCVVNL 900

QY 901 RKTWNPFVDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSRASLTF 960

DB 901 RKTWNPFVDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSRASLTF 960

QY 961 NRGFAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRHFACVLQLP 1020

DB 961 NRGFAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRHFACVLQLP 1020

QY 1021 FHQOVWKNPTFFLRVISDTSATSLCYSLIKAKNAGSLGAKNAGPLPSEAVQWLCHQAFLL 1080

DB 1021 FHQOVWKNPTFFLRVISDTSATSLCYSLIKAKNAGSLGAKNAGPLPSEAVQWLCHQAFLL 1080

QY 1081 KLTRHRVTYVYVPLLGSLRTAQTLRSKLPGTTLTALEAAANPALPSDFKTILD 1132

DB 1081 KLTRHRVTYVYVPLLGSLRTAQTLRSKLPGTTLTALEAAANPALPSDFKTILD 1132

RESULT 2

AAW90251

ID AAW90251 standard; protein; 1132 AA.

XX AC AAW90251;

XX DT 24-MAY-1999 (first entry)

XX DE Human catalytic telomerase sub-unit protein.

XX KW Human; catalytic telomerase subunit; therapy; diagnosis; hTC; assay; modulator; treatment; inhibit; cellular disorder; death; defect; cancer; ageing; antisense; neoplastic cell; telomerase-related condition; tumour cell.

XX OS Homo sapiens.

XX FN WO9859040-A2.

XX PD 30-DEC-1998.

XX PF 09-JUN-1998; 98WO-EP003468.

XX PR 20-JUN-1997; 97DE-01026329.

XX PR 26-MAR-1998; 98DE-01013274.

XX PR 14-APR-1998; 98DE-01016496.

XX PA (FARB) BAYER AG.

XX PI Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;

XX PS WPI; 1999-081276/07.

XX PT N-PSDB; AAV72117.

XX PT New catalytically active subunit of human telomerase - used in the modulation of telomerase activity, particularly for treating cancer and ageing.

XX PS Claim 2; Fig 2; 76pp; German.

XX CC This sequence represents a novel human catalytic telomerase sub-unit (hTC). This protein can be used in screening assays to identify modulators of telomerase and to treat or inhibit cellular disorders, death, defects and/or other pathological processes involving telomerase, particularly cancer and ageing (also suitable for this are agents that stimulate, inhibit or mimic the activity of the subunit). Antisense

CC nucleic acids inhibit telomerase action (by binding to specific mRNA),
CC particularly in neoplastic cells and may be expressed in vivo. Antibodies
CC and fragments of the protein, used as probes or primers, are used to
CC diagnose telomerase-related conditions (especially neoplasia) by (i)
CC detecting abnormal levels of the subunit protein in body fluids or
CC tissues or (ii) by measuring the amount of the encoding nucleic acid.
CC Expression of the nucleic acid encoding the subunit mRNA is confined to
CC tumour cells, in contrast to the ubiquitous expression of the telomerase
CC RNA subunit
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVSLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAPALVAQCVCVPW 60
DB 1 MPAPRCRAVSLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAPALVAQCVCVPW 60

QY 61 DARPPPAAPSPROVSKLVARVLQRLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120
DB 61 DARPPPAAPSPROVSKLVARVLQRLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120

QY 121 SYLNTVTDALRGSGAWGLLRVDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVTDALRGSGAWGLLRVDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATOARPPHAGSPRRRLCERAWNSVREAGVPLGLPARGARRGGSASRLPLPKRRR 240
DB 181 ATOARPPHAGSPRRRLCERAWNSVREAGVPLGLPARGARRGGSASRLPLPKRRR 240

QY 241 GAAPPERTPVQGSWAHPGRTGRPSDRGFCVSPARPAEATSLGALSGTRSHPSVG 300
DB 241 GAAPPERTPVQGSWAHPGRTGRPSDRGFCVSPARPAEATSLGALSGTRSHPSVG 300

QY 301 RQHAGPSTGRPPRWDTPCPVYATKHFYLSGDKQLRPSFLLSRLSPSLTGARRL 360
DB 301 RQHAGPSTGRPPRWDTPCPVYATKHFYLSGDKQLRPSFLLSRLSPSLTGARRL 360

QY 361 VETIFLGRPMWPGTFRPLRLPQRYQWMLPFLLELGNHAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGRPMWPGTFRPLRLPQRYQWMLPFLLELGNHAQCPYGVLLKTHCPLRAAVT 420

QY 421 PAAGVCAREKPGSVAAPEEDTDPRRLVQLLRQHSPPQVYGFVACLRRLVPPGLWGS 480
DB 421 PAAGVCAREKPGSVAAPEEDTDPRRLVQLLRQHSPPQVYGFVACLRRLVPPGLWGS 480

QY 481 RHNERFLRNTKFTISLGHAKLSLQELTWKMSVRDCAWLRRSPGVCVPAAEHLRBEI 540
DB 481 RHNERFLRNTKFTISLGHAKLSLQELTWKMSVRDCAWLRRSPGVCVPAAEHLRBEI 540

QY 541 LAKFLHMLSVVVBELLSPFYVTTTFOKNRLPFYKRSVNSKLSQIGIRHLKRVQLRE 600
DB 541 LAKFLHMLSVVVBELLSPFYVTTTFOKNRLPFYKRSVNSKLSQIGIRHLKRVQLRE 600

QY 601 LSEAEVROHREARPAALLTSRLPFIKPGCLRPINVMYVVGARTFRKRAERLTSRYKA 660
DB 601 LSEAEVROHREARPAALLTSRLPFIKPGCLRPINVMYVVGARTFRKRAERLTSRYKA 660

QY 661 LFSVLNYEARPPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNYEARPPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720

QY 721 PQDLTEVIASIIKQNTYCVRRYAVVQAAHGHVKAFKSHVSTLTDLQPMRFVAHL 780
DB 721 PQDLTEVIASIIKQNTYCVRRYAVVQAAHGHVKAFKSHVSTLTDLQPMRFVAHL 780

QY 781 QSTPLRAVVIQSSSLNEASSGLFDVFLRPMCHAVIRKGSYVQCGIPQGSILSTL 840
DB 781 QSTPLRAVVIQSSSLNEASSGLFDVFLRPMCHAVIRKGSYVQCGIPQGSILSTL 840

QY 841 LCSLCYGDMEKNLPAFIRRDGLLRLVDDFLVTPHLLTHAKTFLTLVRGVPYGCVVNL 900

DB 841 LCSLCYGDMEKNLPAFIRRDGLLRLVDDFLVTPHLLTHAKTFLTLVRGVPYGCVVNL 900

QY 901 RKTVVNPVEALGGTAFAVQMPAHGLPPWCGLLDTRTLEVSQSYSSYARTSTRASLTF 960

DB 901 RKTVVNPVEALGGTAFAVQMPAHGLPPWCGLLDTRTLEVSQSYSSYARTSTRASLTF 960

QY 961 NRGFAGRNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020

DB 961 NRGFAGRNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020

QY 1021 FHOQWKNKPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOWLCHOAFLL 1080

DB 1021 FHOQWKNKPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOWLCHOAFLL 1080

QY 1081 KLTRHRYTVYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTIID 1132

DB 1081 KLTRHRYTVYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTIID 1132

RESULT 3
AAY28881
ID AAY28881 standard; protein; 1132 AA.
XX
AC AAY28881;
XX
DT 17-JAN-2000 (first entry)
XX
DE Human telomerase reverse transcriptase protein.
XX
KW Human telomerase reverse transcriptase protein; hTERT; telomerase; hEST2;
KW catalytic protein component; cell proliferative capacity; DNA primer;
KW telomerase substrate; telomeric DNA synthesis; cell immortality;
KW neoplastic phenotype; diagnostic application; prognostic application;
KW telomerase related condition; cancer; therapeutic agent;
KW telomerase expression; telomerase activity.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 608 /note= "Corresponds to cac codon"
FT
XX
PN WO9950279-A1.
XX
PD 07-OCT-1999.
XX
PF 31-MAR-1999; 99WO-US007160.
XX
PR 31-MAR-1998; 98US-00052919.
XX
PA (GERO-) GERON CORP.
XX
PI (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
XX Andrews WH;
XX
DR WPI; 1999-610834/52.
DR N-PSDB; AAZ08150.
XX
XX Antisense polynucleotides for human telomerase reverse transcriptase used
XX for diagnosing or treating cancer.
XX
PS Claim 2; Fig 2; 31pp; English.
XX
CC The present sequence is human telomerase reverse transcriptase protein.
CC This is the catalytic protein component of telomerase and is also
CC referred to as hEST2. hTERT has the ability to extend a DNA primer that
CC functions as a telomerase substrate for telomeric DNA synthesis. This
CC correlates with cell proliferative capacity, cell immortality, and the
CC development of a neoplastic phenotype. Human TERT antisense
CC oligonucleotides are useful for diagnostic or prognostic applications to
CC telomerase related conditions, including cancer. They are also useful as

CC	therapeutic agents, for inhibition of telomerase expression and activity									
XX										
SQ	Sequence 1132 AA;									
	Query Match	100.0%;	Score 5961;	DB 2;	Length 1132;					
	Best Local Similarity	100.0%;	Pred. No. 0;							
	Matches 1132;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
Qy	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLGPGQWRVLVQ	RGDPAAFRALVAQCLVCVPW	60					
Db	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLGPGQWRVLVQ	RGDPAAFRALVAQCLVCVPW	60					
Qy	61	DARPPAAPSPROVSCLELVARVL	ORLCERGAKNVLAFFALD	GAAGGPEAFTTSVR	120					
Db	61	DARPPAAPSPROVSCLELVARVL	ORLCERGAKNVLAFFALD	GAAGGPEAFTTSVR	120					
Qy	121	SYLPTNTVDALRGSGAWGLLRV	GDVLLVHLARCALFVLVAP	SCAYQVCGPPLYLGA	180					
Db	121	SYLPTNTVDALRGSGAWGLLRV	GDVLLVHLARCALFVLVAP	SCAYQVCGPPLYLGA	180					
Qy	181	ATOARPPPHASGPRRLRCERAM	NHVSREAGVPLGLPAPGAR	RRGGASRSRLPKRPRR	240					
Db	181	ATOARPPPHASGPRRLRCERAM	NHVSREAGVPLGLPAPGAR	RRGGASRSRLPKRPRR	240					
Qy	241	GAAPEPERTVQGSWAHPGRTG	PSDRGFCVSPARPAEATS	LEGALSCTRSHPSVG	300					
Db	241	GAAPEPERTVQGSWAHPGRTG	PSDRGFCVSPARPAEATS	LEGALSCTRSHPSVG	300					
Qy	301	RQHAGPPSTRPPRPMDTPCP	PPVVAETKFLYSSGDKQLR	PSFLSSRLPSLTGARRL	360					
Db	301	RQHAGPPSTRPPRPMDTPCP	PPVVAETKFLYSSGDKQLR	PSFLSSRLPSLTGARRL	360					
Qy	361	VETIFLGRPMWGTPRRLPLR	QRYWQMRPLFLELLGNHA	QCPYGVLLKTHCPLRAAVT	420					
Db	361	VETIFLGRPMWGTPRRLPLR	QRYWQMRPLFLELLGNHA	QCPYGVLLKTHCPLRAAVT	420					
Qy	421	PAAGVCAREKPGQSVAAPEE	BDTPRRVLVOLLRQHSSP	WQVYGFVRACLRLVPPGLWS	480					
Db	421	PAAGVCAREKPGQSVAAPEE	BDTPRRVLVOLLRQHSSP	WQVYGFVRACLRLVPPGLWS	480					
Qy	481	RHNERRFLRNTKKFISLKG	HAKLSLOELTWKMSVRD	CAWLRRSPGVCVPAAEHLREEI	540					
Db	481	RHNERRFLRNTKKFISLKG	HAKLSLOELTWKMSVRD	CAWLRRSPGVCVPAAEHLREEI	540					
Qy	541	LAKFLHLMVSVVVELLSR	FFVTETTPQKNRLFYRK	SVMSKLQSGIGIRQHLKRVQ	600					
Db	541	LAKFLHLMVSVVVELLSR	FFVTETTPQKNRLFYRK	SVMSKLQSGIGIRQHLKRVQ	600					
Qy	601	LSEAEVROHREARPA	LLTSRLRFPKPDGLRPI	VNMVVGARTFRREKRAERLTSRVKA	660					
Db	601	LSEAEVROHREARPA	LLTSRLRFPKPDGLRPI	VNMVVGARTFRREKRAERLTSRVKA	660					
Qy	661	LFSVLNTERARRPGL	LGGASVLGLDDI	IHWARTFVLVRAQDPPPELVFKVDVTGAYDTI	720					
Db	661	LFSVLNTERARRPGL	LGGASVLGLDDI	IHWARTFVLVRAQDPPPELVFKVDVTGAYDTI	720					
Qy	721	PDRLTEVIASIIKPQNTY	CVRRYAVQKAHGHVRK	AFKSHVSTLTDLPYMQFVAHL	780					
Db	721	PDRLTEVIASIIKPQNTY	CVRRYAVQKAHGHVRK	AFKSHVSTLTDLPYMQFVAHL	780					
Qy	781	QETSLRDAVVEQSSS	LINEASSGLFDVFLRF	MCCHAVIRKGSVVOCGIPQGSILSTL	840					
Db	781	QETSLRDAVVEQSSS	LINEASSGLFDVFLRF	MCCHAVIRKGSVVOCGIPQGSILSTL	840					
Qy	841	LCSLCYGDMENKLF	AGIRDDGLLRLLVDD	FLVTPHLLTHAKTFLRLTVRGVPEYGCVVNL	900					
Db	841	LCSLCYGDMENKLF	AGIRDDGLLRLLVDD	FLVTPHLLTHAKTFLRLTVRGVPEYGCVVNL	900					
Qy	901	RKTWNPFVEBALG	GTGTFVQMPAHGLP	PPWCGLLLDTRTLEVSQDYSYARTSTRASLTF	960					
Db	901	RKTWNPFVEBALG	GTGTFVQMPAHGLP	PPWCGLLLDTRTLEVSQDYSYARTSTRASLTF	960					
Qy	961	NRGFKAGRNMRK	LFGVLRKCHSLFLD	LQVNSLQTVCTNIYKILLQAYRFHACVLQLP	1020					

Db	961	NRGFKAGRNMRK	LFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP	1020	
Qy	1021	FHQQVWKNPTFFLR	IVISDTASLCYSTLKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL	1080	
Db	1021	FHQQVWKNPTFFLR	IVISDTASLCYSTLKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL	1080	
Qy	1081	KLTRHRVTYVPL	LGSLRTAQTQLSRKLP	PGTTLTALEAAANPALPSDFKLTLD	1132
Db	1081	KLTRHRVTYVPL	LGSLRTAQTQLSRKLP	PGTTLTALEAAANPALPSDFKLTLD	1132
RESULT 4					
AAV32090					
ID	AAV32090 standard; protein; 1132 AA.				
XX	AC	AAV32090;			
XX	DT	17-JAN-2000 (first entry)			
XX	DE	Human telomerase reverse transcriptase (hTERT).			
XX	DE				
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Db 1 MPAPRCRAVRSLLRSYREVLPPLATFVRRLGPOGRLVQRGDPAAFALVAQCILVCPW 60
QY 61 DARPPAAPSPFQVSLKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
Db 61 DARPPAAPSPFQVSLKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGANGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVDALRGSGANGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATOARPPPHASGPRRLCERAWNSHREAGVPLGLPAGARRRGSASRSILPKRRR 240
Db 181 ATOARPPPHASGPRRLCERAWNSHREAGVPLGLPAGARRRGSASRSILPKRRR 240
QY 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSGRTRHSPVSG 300
Db 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSGRTRHSPVSG 300
QY 301 ROHAGPSTGRPPRMDTPCPVVAETKHFLYSSGDKQLRPSFLLSRLPSLTGARRL 360
Db 301 ROHAGPSTGRPPRMDTPCPVVAETKHFLYSSGDKQLRPSFLLSRLPSLTGARRL 360
QY 361 VETIFLSRPPWPGTPRRLPRLPQRYQWOMRPLFELLGHNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLSRPPWPGTPRRLPRLPQRYQWOMRPLFELLGHNHAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGSVAAPPEEDTPRRLVOLLROHSSPWQVYGFVRACLRILVPPGLWGS 480
Db 421 PAAGVCAREKPGSVAAPPEEDTPRRLVOLLROHSSPWQVYGFVRACLRILVPPGLWGS 480
QY 481 RHNERFLRNTKFTSLGKHAKLSIQELTWMKSVRDCAWLRSPGVCVPAAEHLRREEI 540
Db 481 RHNERFLRNTKFTSLGKHAKLSIQELTWMKSVRDCAWLRSPGVCVPAAEHLRREEI 540
QY 541 LAKFLHMLSVVVELLSFFVVTETTFQKNRLLPFRKSVMSKLSQIGIRQHLKRVQLRE 600
Db 541 LAKFLHMLSVVVELLSFFVVTETTFQKNRLLPFRKSVMSKLSQIGIRQHLKRVQLRE 600
QY 601 LSEAEVROHREARPAALLSRFLFKPDKGLRPIVNDVVGARTPRRKRERLTSRYKA 660
Db 601 LSEAEVROHREARPAALLSRFLFKPDKGLRPIVNDVVGARTPRRKRERLTSRYKA 660
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRQAQPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRQAQPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSLRDAVWIEQSSSINEASSGLFDVFLRPMCHAVRIRCKSVYQCGIPOQSILSTL 840
Db 781 QETSLRDAVWIEQSSSINEASSGLFDVFLRPMCHAVRIRCKSVYQCGIPOQSILSTL 840
QY 841 LCSLCYGMENKLFAGIRDDGLLLRDLVDFLLVTHLTHAKTFLRTLVRGPEYCCVNL 900
Db 841 LCSLCYGMENKLFAGIRDDGLLLRDLVDFLLVTHLTHAKTFLRTLVRGPEYCCVNL 900
QY 901 RKTVNVFPVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVQSDYSYARTSIRASLTF 960
Db 901 RKTVNVFPVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVQSDYSYARTSIRASLTF 960
QY 961 NRGFKAGNRMRKLFVRLKCHSLFLDLQVNSLQTVCTNIYKILLLOAQRHACVQLP 1020
Db 961 NRGFKAGNRMRKLFVRLKCHSLFLDLQVNSLQTVCTNIYKILLLOAQRHACVQLP 1020
QY 1021 FHOQVWKPTFFLRVISTASICYSLKAKNAGMSLGAKGAGPLPSEAVQMLCHOAFL 1080
Db 1021 FHOQVWKPTFFLRVISTASICYSLKAKNAGMSLGAKGAGPLPSEAVQMLCHOAFL 1080
QY 1081 KLTRHRVTYVPLGSLRTAQTLRSKLPGLTTLTALAAAAANPALPSDFKTILD 1132

Db 1081 KLTRHRVTYVPLGSLRTAQTLRSKLPGLTTLTALAAAAANPALPSDFKTILD 1132
RESULT 5
AAY43621
ID AAY43621 standard; protein; 1132 AA.
XX AAY43621;
DT 26-JAN-2000 (first entry)
XX A human telomerase reverse transcriptase (TERT) polypeptide.
DE Human; telomerase reverse transcriptase; TERT; T lymphocyte activation;
KW dendritic cell; telomerase activity; cancer cell; proliferating cell;
KW immunological destruction; telomerase; cancer; proliferation disease.
XX Homo sapiens.
XX WO9950392-A1.
XX 07-OCT-1999.
XX 30-MAR-1999; 99WO-US006898.
XX 31-MAR-1998; 98US-0112006P.
XX (GERO-) GERON CORP.
XX Gaeta FCA;
XX WPI; 1999-610845/52.
XX N-PSDB; AAZ30154.
PT Eliciting an in vivo immune response for prevention and treatment of
PT cancers.
XX Claim 3; Fig 1; 26pp; English.
CC The present sequence represents a human telomerase reverse transcriptase
CC (TERT) polypeptide. The protein is used in the method of the invention.
CC The specification describes a method for activating a T lymphocyte,
CC comprising contacting the T lymphocyte with a dendritic cell that
CC expresses a TERT peptide in the context of a MHC class I or MHC class II
CC molecule. The protein causes induction of an in vivo immunological
CC response to telomerase activity. Cancer cells are characterized by
CC expression of endogenous TERT gene and the presence of detectable
CC telomerase activity. Therefore, by eliciting a specific immune response
CC to TERT or to TERT-expressing cells, it is possible to selectively target
CC proliferating cells for immunological destruction. The method is used for
CC eliciting an in vivo immune response to telomerase by activating a T
CC lymphocyte, and is useful for prevention and treatment of cancers and
CC other proliferation diseases/conditions
SQ Sequence 1132 AA;
Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAPRCRAVRSLLRSYREVLPPLATFVRRLGPOGRLVQRGDPAAFALVAQCILVCPW 60
Db 1 MPAPRCRAVRSLLRSYREVLPPLATFVRRLGPOGRLVQRGDPAAFALVAQCILVCPW 60
QY 61 DARPPAAPSPFQVSLKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
Db 61 DARPPAAPSPFQVSLKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGANGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVDALRGSGANGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATOARPPPHASGPRRLCERAWNSHREAGVPLGLPAGARRRGSASRSILPKRRR 240
Db 181 ATOARPPPHASGPRRLCERAWNSHREAGVPLGLPAGARRRGSASRSILPKRRR 240

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Db 181 ATQARPPHAGSPRRRLGCRANWHSVREAGVPLGLPAPGARRGGASRSRLPLPKPRR 240
Qy 241 GAAPERTPVGQSWAHGTRGSDRGFCVSPARPAEBATSLEGALSCTRSHPSVG 300
Db 241 GAAPERTPVGQSWAHGTRGSDRGFCVSPARPAEBATSLEGALSCTRSHPSVG 300
Qy 301 RQHAGPSTSRPRPMDTPCPVYAEYKHFYSSGDKQLRPSFLSSLPSTGARRL 360
Db 301 RQHAGPSTSRPRPMDTPCPVYAEYKHFYSSGDKQLRPSFLSSLPSTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMRPLFLELGNHQAQCPVGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMRPLFLELGNHQAQCPVGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSWAAPAEEDTPRRLVQLLRQHSSEPMQVYGFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSWAAPAEEDTPRRLVQLLRQHSSEPMQVYGFVRACLRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Db 481 RHNERRFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Qy 541 LAKFLHLWMSVYVVELLRSFFVYVTTETTFQKNRLLFFYKSVMSKLSQSGIRQHLKRVQLE 600
Db 541 LAKFLHLWMSVYVVELLRSFFVYVTTETTFQKNRLLFFYKSVMSKLSQSGIRQHLKRVQLE 600
Qy 601 LSEAEVROHREARPAALLTSRLRPIPKPDGLRPIVMNDYVVGARTFRREKRAERLTSRYKA 660
Db 601 LSEAEVROHREARPAALLTSRLRPIPKPDGLRPIVMNDYVVGARTFRREKRAERLTSRYKA 660
Qy 720 LFSVLNYERARRPGLLGASVIGLDIHRAWTFVLVRQAQPPPELFPVKVDVTGAYDTI 720
Db 720 LFSVLNYERARRPGLLGASVIGLDIHRAWTFVLVRQAQPPPELFPVKVDVTGAYDTI 720
Qy 780 PQDRLTEVIASIIKPNQYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMYQFVAHL 780
Db 780 PQDRLTEVIASIIKPNQYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMYQFVAHL 780
Qy 840 QETSPLRDAVVEQSSSLEASSGLFVFLRPMCHHAVIRKGSYVQCQGIPOGSILSTL 840
Db 840 QETSPLRDAVVEQSSSLEASSGLFVFLRPMCHHAVIRKGSYVQCQGIPOGSILSTL 840
Qy 900 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCYNL 900
Db 900 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCYNL 900
Qy 960 RKTVMNPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSDYSYARTSIRASLTF 960
Db 960 RKTVMNPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSDYSYARTSIRASLTF 960
Qy 1020 NRGFKAGNMRRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVILQLP 1020
Db 1020 NRGFKAGNMRRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVILQLP 1020
Qy 1080 FHQQWKNPTFFLRVISTASLCYSILKAKNAGMSLGKGAAGPLPSEAVOWLCHOAFLL 1080
Db 1080 FHQQWKNPTFFLRVISTASLCYSILKAKNAGMSLGKGAAGPLPSEAVOWLCHOAFLL 1080
Qy 1081 KLTRHRVTYVPLGLSLRFAQTQLSRKLPGLTTLTALEAAANPALPSDFKTIID 1132
Db 1081 KLTRHRVTYVPLGLSLRFAQTQLSRKLPGLTTLTALEAAANPALPSDFKTIID 1132
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RESULT 6

AAV26580

ID AAV26580 standard; protein; 1132 AA.

XX AC AAV26580;

XX DT 13-SEP-1999 (first entry)

XX DE Human telomerase reverse transcriptase (hTERT) enzyme.

```
XX KW Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
KW immunogen; enzyme; telomerase-mediated DNA replication; human.
OS Homo sapiens.
PN WO9927113-A1.
PD 03-JUN-1999.
PF 25-NOV-1998; 98WO-US025211.
PR 26-NOV-1997; 97US-00979742.
PR 16-MAR-1998; 98US-00042460.
XX (GERO-) GERON CORP.
PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
XX Morin GB, Allsopp R, Depinho R, Greenberg R;
XX WPI; 1999-347722/29.
XX Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
XX nucleic acids.
XX Disclosure; Fig 3; 135pp; English.
XX The invention relates to a mouse telomerase reverse transcriptase (mTERT)
XX enzyme. Compositions containing mTERT can be used in telomere length
XX assays. Isolated mTERT is useful as an immunogen for the production of
XX monoclonal or polyclonal antibodies. The method is useful for assessing
XX the degree of purification and identification of new mTERT species, such
XX as an mTERT allele, homolog or isoform, or to screen for modulators
XX (antagonists and agonists) of telomerase-mediated DNA replication.
XX Antagonists and agonists of mTERT can be used to modify the activity of
XX other telomerase enzymes such as human TERT (hTERT). The present sequence
XX represents a human TERT enzyme
XX Sequence 1132 AA;
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Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLGPGWRLVORGDPAAFRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLGPGWRLVORGDPAAFRALVAQCLVCVPW 60
Qy 61 DARPPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFGALLDARGGPEAFTTSVR 120
Db 61 DARPPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFGALLDARGGPEAFTTSVR 120
Qy 121 SYLPNTVTDALRSGAWGLLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPNTVTDALRSGAWGLLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPRRRRLGCRANWHSVREAGVPLGLPAPGARRGGASRSRLPLPKPRR 240
Db 181 ATQARPPPHASGPRRRRLGCRANWHSVREAGVPLGLPAPGARRGGASRSRLPLPKPRR 240
Qy 241 GAAPERTPVGQSWAHGTRGSDRGFCVSPARPAEBATSLEGALSCTRSHPSVG 300
Db 241 GAAPERTPVGQSWAHGTRGSDRGFCVSPARPAEBATSLEGALSCTRSHPSVG 300
Qy 301 RQHAGPSTSRPRPMDTPCPVYAEYKHFYSSGDKQLRPSFLSSLPSTGARRL 360
Db 301 RQHAGPSTSRPRPMDTPCPVYAEYKHFYSSGDKQLRPSFLSSLPSTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMRPLFLELGNHQAQCPVGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMRPLFLELGNHQAQCPVGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSWAAPAEEDTPRRLVQLLRQHSSEPMQVYGFVRACLRLVPPGLWGS 480
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Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYGFVFRACLRRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKFFISLGKHAQLSLQELTWKMSVDRDCAWLRRSPGVCPVAAEHLRREEI 540
Db 481 RHNERRFLRNTKFFISLGKHAQLSLQELTWKMSVDRDCAWLRRSPGVCPVAAEHLRREEI 540
Qy 541 LAKFLHLMMSVYVVELLSRFFVYVTTTQKNRLLFFYKRSVMSKLSQSGIRQHLKRVQRE 600
Db 541 LAKFLHLMMSVYVVELLSRFFVYVTTTQKNRLLFFYKRSVMSKLSQSGIRQHLKRVQRE 600
Qy 601 LSEAEVRQHRREARPAALLTSRLRFLPKDPGLRPIVNMDSYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQHRREARPAALLTSRLRFLPKDPGLRPIVNMDSYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWTFVLVRQAQPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWTFVLVRQAQPPPELYFVKVDVTGAYDTI 720
Qy 721 PQDLRLTEVIASIIKPONTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
Db 721 PQDLRLTEVIASIIKPONTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
Qy 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHAVRIRKSYVQCGIPQGSILSTL 840
Db 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHAVRIRKSYVQCGIPQGSILSTL 840
Qy 841 LCSLCYGMENKLFAGIRDRGLLRLVDDFLVTPHLTHAKTFLTLVRGPEYGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRDRGLLRLVDDFLVTPHLTHAKTFLTLVRGPEYGCVVNL 900
Qy 901 RKTVMNPFVEDEALGCTAFVQMPAHGLFPWCGLLDTLRTLEVQSDYSYARTSIRASLTF 960
Db 901 RKTVMNPFVEDEALGCTAFVQMPAHGLFPWCGLLDTLRTLEVQSDYSYARTSIRASLTF 960
Qy 961 NRGFKAGRMRRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGRMRRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Qy 1021 FHOQWKNTFFELRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHOQWKNTFFELRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTHRVTVYVPLGLSLRTAQQLSRKLPGLTTLTALAAANPALSDPKTILD 1132
Db 1081 KLTHRVTVYVPLGLSLRTAQQLSRKLPGLTTLTALAAANPALSDPKTILD 1132

RESULT 7

AAG64859

ID AAG64859 standard; protein; 1132 AA.

XX AC AAG64859;
XX

DT 21-SEP-2001 (first entry)

DE Heart muscle cell differentiation related protein SEQ ID NO: 31.

KW Heart muscle cell; human; cell differentiation; heart disease.

XX OS Homo sapiens.

XX PN WO200148151-A1.

XX PD 05-JUL-2001.

XX PF 27-DEC-2000; 2000WO-JP009323.

XX PR 28-DEC-1999; 95JP-00372826.

XX PR 28-FEB-2000; 2000WO-JP001148.

XX PR 02-NOV-2000; 2000WO-JP007741.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
PI Yamada Y;
XX WPI; 2001-425656/45.
DR N-PSDB; AAH48235.
XX Cells capable of differentiating into cardiomyocytes and originating in
PT bone marrow or umbilical blood cells for study of cardiomyocyte
PT differentiation and treatment of heart disease.
XX Claim 87; Page 143-147; 183pp; Japanese.
PS The present invention provides cells originating in the human bone marrow
XX or umbilical blood cells which are capable of differentiating into
CC cardiomyocytes. These cells are useful in the treatment of diseases
CC involving heart muscle degeneration, such as myocardial infarction, and
CC the study of cardiomyocyte differentiation. The present sequence is a
CC protein described in the exemplification of the invention
XX SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLPGQWRLVORGDPAAFRALVAQCLVCVPM 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLPGQWRLVORGDPAAFRALVAQCLVCVPM 60
Qy 61 DARPPAAPFRQVSCLELVARVLQRCERAGNNVLAFAFGALLDGGAGPPEAFTTSVR 120
Db 61 DARPPAAPFRQVSCLELVARVLQRCERAGNNVLAFAFGALLDGGAGPPEAFTTSVR 120
Qy 121 SYLNTVTDALRGSGANGLLRRVGGDVLVHLLARCALFVLVAPSCAYVQCGPLYLGA 180
Db 121 SYLNTVTDALRGSGANGLLRRVGGDVLVHLLARCALFVLVAPSCAYVQCGPLYLGA 180
Qy 181 ATOARPPHAGPRRRLGGERAWNHSVREAGVPLGPAPGARRRGGASRSLLPKRPRR 240
Db 181 ATOARPPHAGPRRRLGGERAWNHSVREAGVPLGPAPGARRRGGASRSLLPKRPRR 240
Qy 241 GAAPEPRTVPGQSWAHPCGTRGSDRGFCVSPARPAEATSLGALSCTRSHPSVG 300
Db 241 GAAPEPRTVPGQSWAHPCGTRGSDRGFCVSPARPAEATSLGALSCTRSHPSVG 300
Qy 301 RQHAGPSTSRPPRPMWDTPCPPVYAEKHPFLYSSGDKQLRPSFLSSLPSTGARRL 360
Db 301 RQHAGPSTSRPPRPMWDTPCPPVYAEKHPFLYSSGDKQLRPSFLSSLPSTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYGFVFRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYGFVFRACLRRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKFFISLGKHAQLSLQELTWKMSVDRDCAWLRRSPGVCPVAAEHLRREEI 540
Db 481 RHNERRFLRNTKFFISLGKHAQLSLQELTWKMSVDRDCAWLRRSPGVCPVAAEHLRREEI 540
Qy 541 LAKFLHLMMSVYVVELLSRFFVYVTTTQKNRLLFFYKRSVMSKLSQSGIRQHLKRVQRE 600
Db 541 LAKFLHLMMSVYVVELLSRFFVYVTTTQKNRLLFFYKRSVMSKLSQSGIRQHLKRVQRE 600
Qy 601 LSEAEVRQHRREARPAALLTSRLRFLPKDPGLRPIVNMDSYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQHRREARPAALLTSRLRFLPKDPGLRPIVNMDSYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWTFVLVRQAQPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWTFVLVRQAQPPPELYFVKVDVTGAYDTI 720

QY 721 PQDLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
Db 721 PQDLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
QY 781 QETSPLRDAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSVVOCQGIPOGSIILSTL 840
Db 781 QETSPLRDAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSVVOCQGIPOGSIILSTL 840
QY 841 LCSLCYGDMEKNLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
Db 841 LCSLCYGDMEKNLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
QY 901 RKTUVNPFVEALGGTAFVQMPAHGLPPWCGLLDTRTLEVSQSDYSYARTSTRASLTF 960
Db 901 RKTUVNPFVEALGGTAFVQMPAHGLPPWCGLLDTRTLEVSQSDYSYARTSTRASLTF 960
QY 961 NRGFKAGNMRRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNMRRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
QY 1021 FHQQWKNPTFPLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQMLCHQAFLL 1080
Db 1021 FHQQWKNPTFPLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQMLCHQAFLL 1080
QY 1081 KLTHRVTVYVPLLSLRTAQTLQRKLPDGTTLTALAAANPALPSDFKTILD 1132
Db 1081 KLTHRVTVYVPLLSLRTAQTLQRKLPDGTTLTALAAANPALPSDFKTILD 1132

RESULT 8

AAG64329 ID AAG64329 standard; protein; 1132 AA.
XX AC AAG64329;
XX DT 24-SEP-2001 (first entry)
XX DE Human protein #2.
XX KW Angiogenesis; cardiast; cell differentiating agent; bone marrow;
XX KW heart muscle cell; heart disease; human.
XX OS Homo sapiens.
XX FN WO200148149-A1.
XX PD 05-JUL-2001.
XX PF 28-FEB-2000; 2000WO-JP001148.
XX PR 28-DEC-1999; 99JP-00372826.
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX PI Umazawa A, Hata J, Fukuda K, Ogawa S, Sakurada K;
XX WPI; 2001-418252/44.
XX DR N-PSDB; AAH49601.
XX PT New adult bone marrow-originated cells capable of differentiating into
XX PT heart muscle cells, applicable as remedies for various heart diseases
XX PT particularly with damaged heart muscle accompanying degeneration.
XX PS Disclosure; Page 128-134; 158pp; Japanese.
XX CC The present invention relates to cells isolated from bone marrow, which
XX CC are capable of at least differentiating into heart muscle cells. The
XX CC cells are applicable as remedies for various heart diseases particularly
XX CC with damaged heart muscle accompanying degeneration. The present sequence
XX CC was used to illustrate the present invention
XX Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSLLRSHYREVLPATVRLPGOGWELVQRGDPAARFALVAOCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATVRLPGOGWELVQRGDPAARFALVAOCLVCVPW 60
QY 61 DARPPPAAPSFROVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPEAFTTSVR 120
Db 61 DARPPPAAPSFROVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPEAFTTSVR 120
QY 121 SYLPTNTVTDALRGSGAWGLLLRRVGGDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVTDALRGSGAWGLLLRRVGGDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGRRRLGGERANWHSVREAGVPLGLPAGARRGGGSASRLPKRPRR 240
Db 181 ATQARPPPHASGRRRLGGERANWHSVREAGVPLGLPAGARRGGGSASRLPKRPRR 240
QY 241 GAAPEPERTVGGQSWAHPGRTGRGSDRGFCVVSPPARPAEATSLGALSCTRHSHPVG 300
Db 241 GAAPEPERTVGGQSWAHPGRTGRGSDRGFCVVSPPARPAEATSLGALSCTRHSHPVG 300
QY 301 RQHHAGPPSTSRPPRWDTPCPVYAEKTHFLYSSGDKQELRPSFLLSRPSLTGARRL 360
Db 301 RQHHAGPPSTSRPPRWDTPCPVYAEKTHFLYSSGDKQELRPSFLLSRPSLTGARRL 360
QY 361 VETIFLGSRPMPGCTPRRLPRLPQRYWQMPLELLELGNHACQPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRPMPGCTPRRLPRLPQRYWQMPLELLELGNHACQPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPOGSVAAPPEEDTPRLVOLLRHSSPWQVYGFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPOGSVAAPPEEDTPRLVOLLRHSSPWQVYGFVRACLRLVPPGLWGS 480
QY 481 RHNERPLRNTKKFISLGKHAJLSLOELTWKMSVRDCAWLRRSGVGCVAAPAEHRLREEI 540
Db 481 RHNERPLRNTKKFISLGKHAJLSLOELTWKMSVRDCAWLRRSGVGCVAAPAEHRLREEI 540
QY 541 LAKFLHLMVSVYVVELLSRPFYVTTETFOKNRPFYKSVWSKLOSTGIRHLLKRVOLRE 600
Db 541 LAKFLHLMVSVYVVELLSRPFYVTTETFOKNRPFYKSVWSKLOSTGIRHLLKRVOLRE 600
QY 601 LSEAEVRQHREARPALTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVA 660
Db 601 LSEAEVRQHREARPALTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVA 660
QY 661 LFSVLNYERARRPGLLGASVGLDDIHRWRTFVLVRADPPPELTVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVGLDDIHRWRTFVLVRADPPPELTVKVDVTGAYDTI 720
QY 721 PQDLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
Db 721 PQDLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
QY 781 QETSPLRDAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSVVOCQGIPOGSIILSTL 840
Db 781 QETSPLRDAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSVVOCQGIPOGSIILSTL 840
QY 841 LCSLCYGDMEKNLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
Db 841 LCSLCYGDMEKNLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
QY 901 RKTUVNPFVEALGGTAFVQMPAHGLPPWCGLLDTRTLEVSQSDYSYARTSTRASLTF 960
Db 901 RKTUVNPFVEALGGTAFVQMPAHGLPPWCGLLDTRTLEVSQSDYSYARTSTRASLTF 960
QY 961 NRGFKAGNMRRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNMRRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020

Qy 1021 PHQVWKNPTFLRIVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
 Db 1021 PHQVWKNPTFLRIVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
 Qy 1081 KLTRHRTVTVPLGLSLRPAQQLSRKLPGLTTLTALEAAANPALSDPKTILD 1132
 Db 1081 KLTRHRTVTVPLGLSLRPAQQLSRKLPGLTTLTALEAAANPALSDPKTILD 1132

RESULT 9

AAB99930
 ID AAB99930 standard; protein; 1132 AA.
 XX
 AC AAB99930;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Human telomerase protein sequence SEQ ID NO:31.
 XX
 KW Differentiation; heart muscle cell; cytokine; transcription factor;
 KW proliferation; surface antigen; heart disease; cardiomyocyte;
 KW bone marrow; umbilical blood cell; heart muscle degeneration;
 KW myocardial infarction.
 XX
 OS Homo sapiens.
 XX
 PN WO200148150-A1.
 XX
 PD 05-JUL-2001.
 XX
 PF 02-NOV-2000; 2000WO-JP007741.
 XX
 PR 28-DEC-1999; 99JP-00372826.
 PR 28-FEB-2000; 2000WO-JP001148.
 XX
 PA (KTOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
 PI Yamada Y;
 XX
 DR WPI; 2001-425655/45.
 DR N-PSDB; AAH44366.
 XX
 PT Cells capable of differentiating into cardiomyocytes and originating in
 PT bone marrow or umbilical blood cells for study of cardiomyocyte
 PT differentiation and treatment of heart disease.
 XX
 PS Claim 146; Page 137-141; 187pp; Japanese.
 XX
 CC The present invention describes cells originating in bone marrow or
 CC umbilical blood cells which are capable of differentiating into
 CC cardiomyocytes. Also described are: (1) cardiomyocytes produced by the
 CC differentiation of the cells; (2) a method for carrying out the
 CC differentiation into cardiomyocytes, regulated by a promotonal and/or
 CC inhibitory factor; (3) a method for the differentiation of the cells into
 CC cell types other than cardiomyocytes; (4) drug compositions promoting the
 CC formation of heart muscle and regeneration of heart tissue which contain
 CC the cells; (5) a method for the production of antibodies which recognise
 CC the cells, especially antibodies which recognise a surface antigen on the
 CC cells; (6) a method for screening factors which promote the proliferation
 CC of the cells; (7) a method for immortalising the cells by expressing
 CC telomerase in them; (8) drug compositions for the treatment of heart
 CC disease which contain the immortalised cells; and (9) cell-free
 CC supernatant from the culture of the cells and its use in promoting their
 CC differentiation into cardiomyocytes. The cells are used in the treatment
 CC of diseases involving heart muscle degeneration, such as myocardial
 CC infarction and in the study of cardiomyocyte differentiation. AAH44351 to
 CC AAH44409 and AAB99915 to AAB99935 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 1132 AA;
 Query Match 100.0%; Score 5961; DB 4; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MPRAPCRAVRSLLRSHYREVLPVPLATFVRLPGOGWRLVORGDDPAAAFALVAQCCLVCVPM 60
 Db 1 MPRAPCRAVRSLLRSHYREVLPVPLATFVRLPGOGWRLVORGDDPAAAFALVAQCCLVCVPM 60
 Qy 61 DAREPPAAPSFQVSCIKELVARVLQRLCERGANVLAFGFALLDGGARGGPEAFTTSVR 120
 Db 61 DAREPPAAPSFQVSCIKELVARVLQRLCERGANVLAFGFALLDGGARGGPEAFTTSVR 120
 Qy 121 SYLNTVTDALRGSGAWGLLLRRVGGDDVLVHLARCALFVLVAPSCAYQVCGPPLYLQGA 180
 Db 121 SYLNTVTDALRGSGAWGLLLRRVGGDDVLVHLARCALFVLVAPSCAYQVCGPPLYLQGA 180
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 Db 181 ATQARPPPHASGPRRRIGCERAMNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRPRR 240
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 Db 481 RHNERRFLRNTKXPIGLGHAKLSLOBLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
 Qy 541 LAKFLHLWMSVYVVELLSRSPFYVTETTFQKRLFFYKRSVMSKLOSTGIRQHLKRVQLE 600
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 Db 601 LSAEAVRQHREARPAALLTSRLRFPKDPGLRPIVNMVYVVGARTFREKKAERLTSRKA 660
 Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELYFVKVDVTGAVDTI 720
 Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELYFVKVDVTGAVDTI 720
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 Db 721 PDRLTEVIASIIKPNQTYCVRRYAVVOKAAHGHVKAFKSHVSTLTDLPYMQFVAHL 780
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Qy      1081 KLTRHRYTVVPLLSRLTAQTLGRKLPSTTLTALAAANPALPSDFKTIILD 1132
Db      1081 KLTRHRYTVVPLLSRLTAQTLGRKLPSTTLTALAAANPALPSDFKTIILD 1132

RESULT 10
AAB82765
ID      AAB82765 standard; protein; 1132 AA.
XX
AC      AAB82765;
XX
DT      29-OCT-2001 (first entry)
XX
DE      Human telomerase reverse transcriptase.
XX
KW      Telomerase reverse transcriptase; hTERT; human; cancer; tumour;
KW      cytotoxic T lymphocyte; major histocompatibility complex;
KW      human leucocyte antigen; HLA-A2.1; vaccine.
XX
OS      Homo sapiens.
XX
FH      Key
FH      Peptide
FT      13..21 Location/Qualifiers
FT      /note= "HLA-A2.1 binding motif"
FT      23..31
FT      /note= "HLA-A2.1 binding motif"
FT      76..84
FT      /note= "HLA-A2.1 binding motif"
FT      96..104
FT      /note= "HLA-A2.1 binding motif"
FT      140..148
FT      /note= "HLA-A2.1 binding motif"
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1122..1130
/note= "HLA-A2.1 binding motif"
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PN      WO200160391-A1.
XX
XX      23-AUG-2001.
XX
PD      15-FEB-2001; 2001WO-US005143.
XX
PF      15-FEB-2000; 2000US-0182685P.
PR      15-FEB-2001; 2001US-00182685.
XX
PA      (RBGC ) UNIV CALIFORNIA.
XX
PI      Zanetti M;
XX
DR      WPI; 2001-536552/59.
XX
PT      Vaccine for initiating and enhancing a cytotoxic T lymphocyte response,
PT      for treating cancers or tumors or for inducing immune response against
PT      tumors, comprises a telomerase reverse transcriptase peptide.
XX
PS      Disclosure; Fig 5; 52pp; English.
XX
CC      The present sequence is that of human telomerase reverse transcriptase
CC      (hTERT). The sequence was analysed for 9-mer peptide sequences containing
CC      known binding motifs for the human leukocyte antigen HLA-A2.1 molecule.
CC      From an initial panel of about 30 candidate peptides, 2 sequences,
CC      denoted p540 (see AAB82772) and p865 (see AAB82773), were examined. The
CC      majority of healthy individuals as well as patients with prostate cancer
CC      immunised in vitro against these 2 HLA-A2.1 restricted peptides developed
CC      hTERT-specific cytotoxic T lymphocytes (CTL). The cancer patients' CTL
CC      specifically lysed a variety of HLA-A2+ cancer cell lines such as
CC      prostate, breast, colon, lung and melanoma, demonstrating immunological
CC      recognition of endogenously-processed hTERT peptides. In vivo immunisation
CC      of HLA-A2.1 transgenic mice generated a specific CTL response against
CC      both hTERT peptides. The induction of CTL responses in vitro and in vivo,
CC      and the susceptibility to lysis of tumour cells of various origins by
CC      hTERT CTL suggest that hTERT could serve as a universal cancer vaccine for
CC      humans. Thus, a claimed universal vaccine for treating tumours of any
CC      origin comprises at least 1 hTERT peptide in an amount effective for
CC      initiating and enhancing a CTL response against cancer cells. The peptide
CC      is 7-15 amino acid residues in length and may be modified to enhance
CC      binding to the major histocompatibility complex. Also claimed is a method
CC      for inducing and enhancing a CTL response against cancer cells, involving
CC      harvesting blood leucocytes, pulsing with hTERT, and contacting cancer
CC      cells with the pulsed leucocytes. A method for targeting CTL to tumour
CC      cells is also claimed, and involves administering a hTERT peptide to a
CC      mammal, especially a cancer patient
XX
SQ      Sequence 1132 AA;

Query Match      100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVQRGDPAAFRALVAQCILVCVPM 60
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DB 61 DARPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFFGALLDARGGPPPEAFTTSVR 120
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DB 121 SYLNTVNTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
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DB 181 ATQARPPPHASGPRRLCERAWNHSVREAGVPLGLPAPGARRRGGASRSILPKRPRR 240
QY 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVVSAPAEAEATSLGALSGRHSHPSVG 300
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DB 301 RQHAGPSTSRPPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLLSLRPSLTGARRL 360
QY 361 VETIFLGSRPWPGTRPLRLPQRYQWMPPLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRPWPGTRPLRLPQRYQWMPPLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAEKPOGSAVAEEDDTPRRLVOLLROHSSPMQVYGFVRACLRRLVPPGLWS 480
DB 421 PAAGVCAEKPOGSAVAEEDDTPRRLVOLLROHSSPMQVYGFVRACLRRLVPPGLWS 480
QY 481 RHNERFLRNTKFFISLKGHAKLSIQELTWKMSVRDCAWLRSPGVGCVPAEHLRBEI 540
DB 481 RHNERFLRNTKFFISLKGHAKLSIQELTWKMSVRDCAWLRSPGVGCVPAEHLRBEI 540
QY 541 LAKFLHMLSVTVVLLRSFFVTETTFQKNRLLFPYRKSVWSKLSQIGIRHQLKRVQRE 600
DB 541 LAKFLHMLSVTVVLLRSFFVTETTFQKNRLLFPYRKSVWSKLSQIGIRHQLKRVQRE 600
QY 601 LSEAVROHREARPAALLSRFLFKPKDGLRPIVNDYVVGARTFRERKRAERLTSRYKA 660
DB 601 LSEAVROHREARPAALLSRFLFKPKDGLRPIVNDYVVGARTFRERKRAERLTSRYKA 660
QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFKVDVTCAYDTI 720
DB 661 LFSVLNTERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFKVDVTCAYDTI 720
QY 721 PQDRLTEVIASIIKPNQTYCVRRYAVQKAAHGHVVKAFKSHVSTLTDLPYMRQFVAHL 780
DB 721 PQDRLTEVIASIIKPNQTYCVRRYAVQKAAHGHVVKAFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSLRDAVITEQSSLINEASSGLFDVFLPMCHAVRIRCKSVYQCGIPOQSILSTL 840
DB 781 QETSLRDAVITEQSSLINEASSGLFDVFLPMCHAVRIRCKSVYQCGIPOQSILSTL 840
QY 841 LCSLCYGMENKLFAGIRDDGLLLRLVDVDFLLVTPHLTHAKTFLTLVRGPEYCCVNL 900
DB 841 LCSLCYGMENKLFAGIRDDGLLLRLVDVDFLLVTPHLTHAKTFLTLVRGPEYCCVNL 900
QY 901 RKTVVNPFVEDBALGGAFTVQMPAHLFPWCGLLDDTRLEQSDYSYARTSIRASLTF 960
DB 901 RKTVVNPFVEDBALGGAFTVQMPAHLFPWCGLLDDTRLEQSDYSYARTSIRASLTF 960
QY 961 NRGFKAGNRMRKLFGLVKLCHSIFLDLQVNSLQTVCTNIYKILLQAYRPHACVLQIP 1020
DB 961 NRGFKAGNRMRKLFGLVKLCHSIFLDLQVNSLQTVCTNIYKILLQAYRPHACVLQIP 1020
QY 1021 FHOQVWKNTFFLRVIDSTASLCYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
DB 1021 FHOQVWKNTFFLRVIDSTASLCYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
QY 1081 KLTHRVTVTVPLGLSLRTAQTLRSKLPQTTLTALAAANPALPSDFKTILD 1132
```

```
DB 1081 KLTHRVTVTVPLGLSLRTAQTLRSKLPQTTLTALAAANPALPSDFKTILD 1132
RESULT 11
AAE29226
ID AAE29226 standard; protein; 1132 AA.
XX
AC AAE29226;
XX
DT 27-JAN-2003 (first entry)
XX
DE Human telomerase reverse transcriptase (TERT).
XX
KW Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT; TERT;
transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;
telomerase reverse transcriptase.
XX
OS Homo sapiens.
XX
FN WO200274948-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002MO-CA000378.
XX
PR 21-MAR-2001; 2001US-0277811P.
XX
PA (GERO-) GERON CORP.
XX
PI Denning C, Clark AJ, Schiff JM;
XX
DR WPI; 2002-759895/82.
XX
N-PSDB; AAD46821.
XX
PT Mammalian cells, useful for producing animal tissues with carbohydrate
antigens that are compatible for transplantation into human patients.
XX
PS Disclosure; Page 34; 7ipp; English.
XX
CC The invention relates to animal tissues with carbohydrate antigens that
are compatible for transplantation into human patients. The mammalian
cell is inactivated homozygously for expression of alpha(1,3)galactosyl-
transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-
fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue
with carbohydrate antigens that are compatible for transplantation into
human patients. The present sequence is human telomerase reverse
transcriptase (TERT) used in the invention
SQ Sequence 1132 AA;
Query Match 100.0%; Score 5961; DB 5; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVQRGDPAAFRALVAQCILVCVPM 60
DB 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVQRGDPAAFRALVAQCILVCVPM 60
QY 61 DARPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFFGALLDARGGPPPEAFTTSVR 120
DB 61 DARPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFFGALLDARGGPPPEAFTTSVR 120
QY 121 SYLNTVNTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
DB 121 SYLNTVNTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLCERAWNHSVREAGVPLGLPAPGARRRGGASRSILPKRPRR 240
DB 181 ATQARPPPHASGPRRLCERAWNHSVREAGVPLGLPAPGARRRGGASRSILPKRPRR 240
QY 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVVSAPAEAEATSLGALSGRHSHPSVG 300
DB 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVVSAPAEAEATSLGALSGRHSHPSVG 300
```

Db 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSCTRSHPSVG 300
Qy 301 RQHAGPSTSRPPRPWDTPCPVYAETHKFLYSGDKEQLRPSFLSSLRPSLTGARRL 360
Db 301 RQHAGPSTSRPPRPWDTPCPVYAETHKFLYSGDKEQLRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRPWMPGTPRRLPRLPQRYQWMDPLFLELLGNHAQCYPVLLKTHCPLRAVT 420
Db 361 VETIFLGSRPWMPGTPRRLPRLPQRYQWMDPLFLELLGNHAQCYPVLLKTHCPLRAVT 420
Qy 421 PAAVCAREKQGSVAAAEEDDTPRRLVQLLRHSSPWQVYGFVRACLRRLVPPGLWGS 480
Db 421 PAAVCAREKQGSVAAAEEDDTPRRLVQLLRHSSPWQVYGFVRACLRRLVPPGLWGS 480
Qy 481 RHNERRFLNRTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLREI 540
Db 481 RHNERRFLNRTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLREI 540
Qy 541 LAKTFLHLMWSVVVELLSFFVTTTTFQKNRLLPFYKSVMSKLSIGIRQHLKRVQVRE 600
Db 541 LAKTFLHLMWSVVVELLSFFVTTTTFQKNRLLPFYKSVMSKLSIGIRQHLKRVQVRE 600
Qy 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRKA 660
Db 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRKA 660
Qy 661 LFSVLNYSRARPPGLLGASVIGLDDIHRAMRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYSRARPPGLLGASVIGLDDIHRAMRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPNQTYCYRRYAVQKAAGHVRAKFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPNQTYCYRRYAVQKAAGHVRAKFKSHVSTLTDLPYMRQFVAHL 780
Qy 781 QETSLRDAVIEQSSSINEASSGLFDFVLFPMCHHAVIRGKSVQCOGIPQGSILSTL 840
Db 781 QETSLRDAVIEQSSSINEASSGLFDFVLFPMCHHAVIRGKSVQCOGIPQGSILSTL 840
Qy 841 LCSLCYGMENKLFAGIRRDGLLRDLVDLFTPLTHAKTFLRTLVRGVPYGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRRDGLLRDLVDLFTPLTHAKTFLRTLVRGVPYGCVVNL 900
Qy 901 RKTVNFVEDEALGGTAPVQMPAHGLFPMCGLLDITLTVQSDYSSYARTSRASLTF 960
Db 901 RKTVNFVEDEALGGTAPVQMPAHGLFPMCGLLDITLTVQSDYSSYARTSRASLTF 960
Qy 961 NRGFKAGRNMRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGRNMRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Qy 1021 FHQQWKNPTFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAPLL 1080
Db 1021 FHQQWKNPTFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAPLL 1080
Qy 1081 KLTHRRVTVPLGLSLRTAQOLSRKLPGLTTLTALEAAANPALSPDFKTIID 1132
Db 1081 KLTHRRVTVPLGLSLRTAQOLSRKLPGLTTLTALEAAANPALSPDFKTIID 1132

RESULT 12

AAU72735

ID AAU72735 standard; protein; 1132 AA.

XX

AC AAU72735;

XX 09-APR-2002 (first entry)

XX Human telomerase reverse transcriptase (TERT).

DE

XX Telomerase reverse transcriptase; TERT; cytostatic; apoptosis;

KW cell growth inhibitor; antisense oligonucleotide; antisense technology.

XX

OS Homo sapiens.

XX

FN WO200188198-A1.

XX 22-NOV-2001.

PD

XX 15-MAY-2001; 2001WO-US015774.

XX

XX 16-MAY-2000; 2000US-00572423.

PR 07-DEC-2000; 2000US-00733294.

PR

XX (ISIS-) ISIS PHARM INC.

PA

XX Monia BP, Gaarde WA, Freier SM, Wanciewicz B;

XX

XX WPI; 2002-075321/10.

DR N-PSDB; AAS96607.

XX

PT New compound targeted to nucleic acid molecule encoding telomerase transcriptase (TERT), which specifically hybridizes with and inhibits expression of TERT, useful for modulating apoptosis and inhibiting cell growth.

PT

XX Disclosure; Page 100-105; 154pp; English.

PS

XX The invention describes a compound, 8-50 nucleobases in length targeted to a nucleic acid molecule encoding human TERT (telomerase reverse transcriptase), where the compound specifically hybridizes with and inhibits the expression of TERT. A series of oligonucleotides were designed to target different regions of the human TERT RNA. These were 20 nucleotides in length and composed of a central gap region consisting of ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions) by five-nucleotide wings. The wings were composed of 2'-methoxyethyl (2'-MOE) nucleotides. The compounds were analysed for their effect on human TERT mRNA levels by reverse transcriptase (RT)-polymerase chain reaction (PCR). The compound is useful for inhibiting the expression of TERT in cells or tissues, for treating a human having disease or condition associated with TERT, for modulating apoptosis, for inhibiting cell growth (preferably, cancer cell growth), in antisense therapy and for diagnostics and therapeutics. This is the amino acid sequence of human telomerase reverse transcriptase (TERT), described in the method of the invention

XX

SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 5; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLPGQWRLVQRGDPAAPRALVAQCLVCVPW 60

Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLPGQWRLVQRGDPAAPRALVAQCLVCVPW 60

Qy 61 DARPPPPAAPSFROVSCLELVARVLQRLCERGAKNVLAFAFALLDARGGPEAFTTSVR 120

Db 61 DARPPPPAAPSFROVSCLELVARVLQRLCERGAKNVLAFAFALLDARGGPEAFTTSVR 120

Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy 181 ATQARPPPHASGPRRLRGCCERANNHVSREAGVPLGLPAGNRRRGGSASRLPLKPRRR 240

Db 181 ATQARPPPHASGPRRLRGCCERANNHVSREAGVPLGLPAGNRRRGGSASRLPLKPRRR 240

Qy 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSCTRSHPSVG 300

Db 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSCTRSHPSVG 300

Qy 301 RQHAGPSTSRPPRPWDTPCPVYAETHKFLYSGDKEQLRPSFLSSLRPSLTGARRL 360

Db 301 RQHAGPSTSRPPRPWDTPCPVYAETHKFLYSGDKEQLRPSFLSSLRPSLTGARRL 360

Qy 361 VETIFLGSRPWMPGTPRRLPRLPQRYQWMDPLFLELLGNHAQCYPVLLKTHCPLRAAVT 420

361 VETIFLGRSPPWPGTFRRLPRLPQRYWQRPFLFELLLGNHQAQCPYGVLLKTHCPLRAAVT 420
 421 PAAGVCAREKPGQSVAAPEEEDTDRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
 421 PAAGVCAREKPGQSVAAPEEEDTDRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
 481 RHNERFLRNTKFIISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAEAHLRREI 540
 481 RHNERFLRNTKFIISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAEAHLRREI 540
 541 LAKFLHMLSVVYVVELLSRFFVYTTTQKNRLLPFRKSVWSKLSQIGIRQHLKRVQLRE 600
 541 LAKFLHMLSVVYVVELLSRFFVYTTTQKNRLLPFRKSVWSKLSQIGIRQHLKRVQLRE 600
 601 LSEAEVROHREARPAALLSRFLPKPDLRLPVMNDYVVGARTFRREKRAERLSRVKA 660
 601 LSEAEVROHREARPAALLSRFLPKPDLRLPVMNDYVVGARTFRREKRAERLSRVKA 660
 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFKVDVTGAYDTI 720
 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFKVDVTGAYDTI 720
 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
 781 QETSLRDAVTEQSSSNEASSGLPDVFLRPMCHHAVRIRGKSVVQCGIPQGSILSTL 840
 781 QETSLRDAVTEQSSSNEASSGLPDVFLRPMCHHAVRIRGKSVVQCGIPQGSILSTL 840
 841 LCSLCYGMENKLFAGIRRDGLLLRLVDVDFLLVTPHLTHAKTFLRLVRGVPYGCNVNL 900
 841 LCSLCYGMENKLFAGIRRDGLLLRLVDVDFLLVTPHLTHAKTFLRLVRGVPYGCNVNL 900
 901 RKTVPNPFVEBALGGTAFVQMPAHLFPWCGLLDDTRTLEVSQSYSSYARTSIRASLTF 960
 901 RKTVPNPFVEBALGGTAFVQMPAHLFPWCGLLDDTRTLEVSQSYSSYARTSIRASLTF 960
 961 NRGFKAGNRMRKLPGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
 961 NRGFKAGNRMRKLPGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
 1021 FHQVWKNTPTFLRVISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
 1021 FHQVWKNTPTFLRVISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
 1081 KLTHRVTVVPLGLSLRTAQTLRSKLPGLTTLTALAAANPALPSDFKTILD 1132
 1081 KLTHRVTVVPLGLSLRTAQTLRSKLPGLTTLTALAAANPALPSDFKTILD 1132

RESULT 13
 ABR42384
 ID ABR42384 standard; protein; 1132 AA.
 AC ABR42384;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Human telomerase reverse transcriptase.
 KW Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
 KW short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
 KW immunosuppressive; antiinfertility; fungicide; antiparasitic;
 KW antiinflammatory; human; gene therapy.
 OS Homo sapiens.
 XX
 PN WO2003035667-A2.
 XX
 PD 01-MAY-2003.
 XX

16-OCT-2002; 2002WO-US033065.
 22-OCT-2001; 2001US-0345326P.
 20-FEB-2002; 2002US-0359196P.
 22-MAY-2002; 2002US-0383195P.
 (UVRP) UNIV ROCHESTER.
 Rowley PT;
 WPI: 2003-403336/38.
 N-PSDB; ACC58039.
 Novel double-stranded short interfering RNA having sense and antisense
 nucleic acids which are complementary to each other and to target nucleic
 acid e.g., telomerase RNA or mRNA encoding telomerase reverse
 transcriptase.
 Disclosure; Fig 4; 37pp; English.
 The present sequence is the protein sequence of human telomerase reverse
 transcriptase (TERT). The invention relates to the discovery that double-
 stranded interfering RNAs, such as short interfering RNAs (siRNA), which
 target telomerase RNA or TERT mRNA are capable of inhibiting telomerase
 activity. Inhibition of telomerase in cancer cells leads to telomere
 shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
 telomerase activity can also be used for treatment of infertility, for
 contraception or sterilisation, for immunosuppression, for treatment of
 yeast, parasite and fungal infections, and in antiinflammatory therapies.
 As telomerase is active in a limited number of cell types, e.g. tumour
 cells, germline cells, certain stem cells of the haematopoietic system, T
 and B cells, sun-damaged skin, and proliferative cervix, most normal
 cells are not affected by telomerase RNA interference therapy

Query Match 100.0%; Score 5961; DB 6; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPQWRLLVQRGDPAAFALVAQCLVCPW 60
 Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPQWRLLVQRGDPAAFALVAQCLVCPW 60
 QY 61 DARPPAPSPROVSCLEKELVARVLQRCERAKNVLAFFGALLDAGRGPPPEAFTTSVR 120
 Db 61 DARPPAPSPROVSCLEKELVARVLQRCERAKNVLAFFGALLDAGRGPPPEAFTTSVR 120
 QY 121 SYLNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 Db 121 SYLNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 QY 181 ATQARPPHAGSPRRRLGCERAWNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRPRR 240
 Db 181 ATQARPPHAGSPRRRLGCERAWNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRPRR 240
 QY 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARAEATSLGALSCTGTHSHSPVG 300
 Db 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARAEATSLGALSCTGTHSHSPVG 300
 QY 301 RQHAGPPSTRPRPMDTPCPVVAETKHFYSSGDKQLRPSPLSLRPSLTGARRL 360
 Db 301 RQHAGPPSTRPRPMDTPCPVVAETKHFYSSGDKQLRPSPLSLRPSLTGARRL 360
 QY 361 VETIFLGRSPPWPGTFRRLPRLPQRYWQRPFLFELLLGNHQAQCPYGVLLKTHCPLRAAVT 420
 Db 361 VETIFLGRSPPWPGTFRRLPRLPQRYWQRPFLFELLLGNHQAQCPYGVLLKTHCPLRAAVT 420
 QY 421 PAAGVCAREKPGQSVAAPEEEDTDRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
 Db 421 PAAGVCAREKPGQSVAAPEEEDTDRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
 QY 481 RHNERFLRNTKFIISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAEAHLRREI 540

Db 481 RHNERFLRNTKFKISLGKHAQLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Qy 541 LAKFLHLMMSVYVVELLSRFFYVTTTQKNRLFFYRKSVMSKLSQSIGIRQHLKRVQURE 600
Db 541 LAKFLHLMMSVYVVELLSRFFYVTTTQKNRLFFYRKSVMSKLSQSIGIRQHLKRVQURE 600
Qy 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMODYVVGARTFRKRERLTSRVKA 660
Db 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMODYVVGARTFRKRERLTSRVKA 660
Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRATEVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRATEVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPNQTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPYMQFVAHL 780
Db 721 PODRLTEVIASIIKPNQTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPYMQFVAHL 780
Qy 781 QETSPRLDAVIEQSSSLNEASSGLFDVFLRPFMCHHAVIRKGSYVQCQGIPOGSIILSTL 840
Db 781 QETSPRLDAVIEQSSSLNEASSGLFDVFLRPFMCHHAVIRKGSYVQCQGIPOGSIILSTL 840
Qy 841 LCSLCYGMENKLPAGIRRDGLLRLVDDFLVTPHLTHAKTFLRVLVRGVPYGCVVNL 900
Db 841 LCSLCYGMENKLPAGIRRDGLLRLVDDFLVTPHLTHAKTFLRVLVRGVPYGCVVNL 900
Qy 901 RKTVVNPFVEALGGTAFVQMPAHGLFPWCGLLDTRTLQVNSLQTSYARTSIRASITF 960
Db 901 RKTVVNPFVEALGGTAFVQMPAHGLFPWCGLLDTRTLQVNSLQTSYARTSIRASITF 960
Qy 961 NRGKAGNMRKLPGLVRLKCHSLFDLQVNSLQTSYARTSIRASITF 1020
Db 961 NRGKAGNMRKLPGLVRLKCHSLFDLQVNSLQTSYARTSIRASITF 1020
Qy 1021 FHQQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAAGPLPSEAVOWLCHOAFL 1080
Db 1021 FHQQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAAGPLPSEAVOWLCHOAFL 1080
Qy 1081 KLTHRRVTVYVPLGLSLRTAQOLSRKLPGLTTLTALEAAANPALPSPDKTILD 1132
Db 1081 KLTHRRVTVYVPLGLSLRTAQOLSRKLPGLTTLTALEAAANPALPSPDKTILD 1132

RESULT 14
ID ABR42063 standard; protein; 1132 AA.
AC ABR42063;
XX
XX
DT 28-JUL-2003 (first entry)
XX
XX Human telomerase reverse transcriptase.
DE
DE Telomerase reverse transcriptase; TERT: enzyme; RNA interference;
KW short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
KW immunosuppressive; antinfertility; fungicide; anticancer; antiparasitic;
KW antinflammatory; human; gene therapy.
XX
OS Homo sapiens.
XX
XX WO2003034985-A2.
XX
XX
PD 01-MAY-2003.
XX
XX 16-OCT-2002; 2002WO-US033146.
XX
XX 22-OCT-2001; 2001US-0345326P.
PR 20-FEB-2002; 2002US-0359196P.
PR 22-MAY-2002; 2002US-0383195P.
XX
XX (UVRP) UNIV ROCHESTER.
XX
XX

PI Rowley PT;
XX WPI; 2003-403289/38.
DR N-PSDB; ACC57552.
XX
PT Novel nucleic acid encoding or comprising interfering RNAs which target
PT telomerase RNA, useful for inhibiting telomerase activity for treating
XX cancer, infertility and disorders of the immune system.
XX Disclosure; Fig 4; 52pp; English.
XX
CC The present sequence is that of human telomerase reverse transcriptase
CC (TERT). The invention relates to the discovery that double-stranded
CC interfering RNAs, such as short interfering RNAs (siRNA), which target
CC telomerase RNA or TERT mRNA are capable of inhibiting telomerase
CC activity. Inhibition of telomerase in cancer cells leads to telomere
CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
CC telomerase activity can also be used for treatment of infertility, for
CC contraception or sterilisation, for immunosuppression, for treatment of
CC yeast, parasite and fungal infections, and in antiinflammatory therapies.
CC As telomerase is active in a limited number of cell types, e.g. tumour
CC cells, germline cells, certain stem cells of the haematopoietic system, T
CC and B cells, sun-damaged skin, and proliferative cervix, most normal
CC cells are not affected by telomerase RNA interference therapy
XX
SQ Sequence 1132 AA;
Query Match 100.0%; Score 5961; DB 6; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATVRLRPGQWRLVQSGDPAAFRALVAQCLVCPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATVRLRPGQWRLVQSGDPAAFRALVAQCLVCPW 60
Qy 61 DARPPPPAAPSFRQVSCLEIARVQLRCLRGKAGNVLAFGALLDARGGPEAFTTSVR 120
Db 61 DARPPPPAAPSFRQVSCLEIARVQLRCLRGKAGNVLAFGALLDARGGPEAFTTSVR 120
Qy 121 SYLPTNTVDALRGSGAWGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVDALRGSGAWGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPRRLRGCRANVHVRAGVPLGLPAGARRRGGSASRLPKRPRR 240
Db 181 ATQARPPPHASGPRRLRGCRANVHVRAGVPLGLPAGARRRGGSASRLPKRPRR 240
Qy 241 GAAPEPERTVPGQSWAHPCRTGSDRGFCVSPARPAEATSLGALSCTRHSHPSVG 300
Db 241 GAAPEPERTVPGQSWAHPCRTGSDRGFCVSPARPAEATSLGALSCTRHSHPSVG 300
Qy 301 ROHHAGPSTSRPPRWDPTFCPPVYAEKHFYSSGDKQLRPSFLSSRLPSLTGARRL 360
Db 301 ROHHAGPSTSRPPRWDPTFCPPVYAEKHFYSSGDKQLRPSFLSSRLPSLTGARRL 360
Qy 361 VETIFLGSRWPMCTPRRLRPLQRYQWMPRLFLELLGNHACQPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRWPMCTPRRLRPLQRYQWMPRLFLELLGNHACQPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRLVOLLROHSSPWQVYGFVRACLRLVPPGLMGS 480
Db 421 PAAGVCAREKPGQSVAAPEEDTDPRLVOLLROHSSPWQVYGFVRACLRLVPPGLMGS 480
Qy 481 RHNERFLRNTKFKISLGKHAQLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Db 481 RHNERFLRNTKFKISLGKHAQLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Qy 541 LAKFLHLMMSVYVVELLSRFFYVTTTQKNRLFFYRKSVMSKLSQSIGIRQHLKRVQURE 600
Db 541 LAKFLHLMMSVYVVELLSRFFYVTTTQKNRLFFYRKSVMSKLSQSIGIRQHLKRVQURE 600
Qy 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMODYVVGARTFRKRERLTSRVKA 660
Db 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMODYVVGARTFRKRERLTSRVKA 660

Db 601 LSEAEVQHRREARPPALLTSRLRIFPKPDGLRPIVMDYVVGARTPRRKRERLTSRVKA 660
Qy 661 LFSVLNERRARRPGLGASVLGLDDIHRARTFVLVRVRAQPPPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNERRARRPGLGASVLGLDDIHRARTFVLVRVRAQPPPPPELYFVKVDVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPNQTYCYVRRYAVVQKAAGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPNQTYCYVRRYAVVQKAAGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
Qy 781 QETSPLRDVAVIEQSSSNEASSGLFDVFLRFMCHHVRIRGKSVVQCGIPQGSILSTL 840
Db 781 QETSPLRDVAVIEQSSSNEASSGLFDVFLRFMCHHVRIRGKSVVQCGIPQGSILSTL 840
Qy 841 LCSLCYGMENKLFAGIRRDGILLRLVDDPFLVTPHLTHAKTFLRTLVRGPEYGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRRDGILLRLVDDPFLVTPHLTHAKTFLRTLVRGPEYGCVVNL 900
Qy 901 RKTWNFFVEDEALGCTAFVQMPAHLFPWCGLLDITLTVQSDYSSYARTSTRASLTF 960
Db 901 RKTWNFFVEDEALGCTAFVQMPAHLFPWCGLLDITLTVQSDYSSYARTSTRASLTF 960
Qy 961 NRGFKAGNRMRKLFGLVRLKCHSLFLDLQVNSLQVCTNIIKILLQAYRPHACVQLQP 1020
Db 961 NRGFKAGNRMRKLFGLVRLKCHSLFLDLQVNSLQVCTNIIKILLQAYRPHACVQLQP 1020
Qy 1021 FHQQWKNPTFFLRVISDTASILCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQQWKNPTFFLRVISDTASILCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTHRVTVYVPLGLSLRTAQTLRSKLPGLTTLTALAAANPALPSDFKTIID 1132
Db 1081 KLTHRVTVYVPLGLSLRTAQTLRSKLPGLTTLTALAAANPALPSDFKTIID 1132

RESULT 15

ABP56676
ID ABP56676 standard; protein; 1132 AA.
XX
AC ABP56676;
XX
DT 25-MAR-2003 (first entry)
XX
DE Human telomerase reverse transcriptase protein SEQ ID NO:2.
XX
KW Human; telomerase reverse transcriptase; enzyme; hTERT; chromosome 5;
KW vulnery; antiulcer; epithelial cell migration promoter; wound;
KW epithelisation; skin wound; lesion; burn; surgical incision; ulcer;
KW epithelial cell; keratinocyte; epidermal; mucosal.
XX
OS Homo sapiens.
XX
FN WO200291999-A2.
XX
PD 21-NOV-2002.
XX
PF 09-MAY-2002; 2002WO-US014867.
XX
PR 09-MAY-2001; 2001US-0289903P.
XX
PA (GERO-) GERON CORP.
XX
PI Jiang X, Chiu C, Harley CB;
XX
DR WPI; 2003-120591/11.
DR N-PSDB; ABZ22474.
XX
PT Composition for treating wounds and enhancing epithelization of a skin
PT surface, comprises vector encoding telomerase reverse transcriptase or
PT telomerized epithelial cells on a microparticle or a matrix.
XX
PS Disclosure; Page 32; 68pp; English.
XX

CC The present invention describes a pharmaceutical composition (I)
CC comprising a vector encoding telomerase reverse transcriptase (TERT) in
CC an exipient or device, or comprises telomerized epithelial cells on a
CC microparticle or a matrix suitable for topical administration or
CC administration to a wound site. (I) has vulnery and antiulcer
CC activities and can be used to promote epithelial cell migration. (I) is
CC useful for treating a wound and enhancing epithelisation of a skin
CC surface. The wound is especially skin wound including acute lesion such
CC as traumatic lesion, burn, or surgical incision, chronic lesion such as
CC chronic venous ulcer, diabetic ulcer or compression ulcer and the wound
CC is further monitored for closure. The telomerase activity or TERT
CC expression is increased in epithelial cells at the site of treatment and
CC also in fibroblasts or endothelial cells at the site of treatment. The
CC epithelial cells are especially keratinocytes. A polynucleotide encoding
CC TERT is useful for the preparation of a medicament for treatment of a
CC wound or an epithelial surface in a human or animal. An epithelial cell
CC with increased telomerase activity or increased expression of TERT is
CC useful for preparation of a medicament for the treatment of a wound in a
CC human or animal. (I) is also useful for treating wounds of other
CC epidermal surfaces including mucosal surfaces such as bronchus, mouth,
CC nose, oesophagus, stomach, or intestine. The present sequence represents
CC human TERT (hTERT), which is given in the exemplification of the present
CC invention. hTERT is located to chromosome 5
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 6; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLLGPGQWRLVQRGDPAPAFALVAQCLVCVPM 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLLGPGQWRLVQRGDPAPAFALVAQCLVCVPM 60
Qy 61 DARPPAPSPFQVSCIKELVARVLQRLCERAGKAVLAFGALLDARGGPEAFTTSVR 120
Db 61 DARPPAPSPFQVSCIKELVARVLQRLCERAGKAVLAFGALLDARGGPEAFTTSVR 120
Qy 121 SYLPTNTVDALRGSGAWGLLRRVDDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVDALRGSGAWGLLRRVDDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPRRLGCEPANHVSREAGVPLGPAPGARRRGGSASRSLPLPKRPRR 240
Db 181 ATQARPPPHASGPRRLGCEPANHVSREAGVPLGPAPGARRRGGSASRSLPLPKRPRR 240
Qy 241 GAAPEPRTPVQGSWAHPGTRGDRGFCVSPAPAEATSLGALSCTRHSHPVG 300
Db 241 GAAPEPRTPVQGSWAHPGTRGDRGFCVSPAPAEATSLGALSCTRHSHPVG 300
Qy 301 RQHAGPPSTSRPPRPWDTPCPVYAEKTFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
Db 301 RQHAGPPSTSRPPRPWDTPCPVYAEKTFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRLLPQRYQMRLPFLLELGNHQAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRLLPQRYQMRLPFLLELGNHQAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRLVQLLRHSSSPWQVYGFVACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEDTDPRLVQLLRHSSSPWQVYGFVACLRRLVPPGLWGS 480
Qy 481 RHNERRFLNRTKFIISLGKAKLSLOELTWKMSVRDCAWLRSPGVGCVPAEHRLEEI 540
Db 481 RHNERRFLNRTKFIISLGKAKLSLOELTWKMSVRDCAWLRSPGVGCVPAEHRLEEI 540
Qy 541 LAKELHLMWSVYVVELLRSFFYVTTTFQKNRLFYFKSVMSKLSQSIGIRQHLKRVQURE 600
Db 541 LAKELHLMWSVYVVELLRSFFYVTTTFQKNRLFYFKSVMSKLSQSIGIRQHLKRVQURE 600
Qy 601 LSEAEVQHRREARPPALLTSRLRIFPKPDGLRPIVMDYVVGARTPRRKRERLTSRVKA 660
Db 601 LSEAEVQHRREARPPALLTSRLRIFPKPDGLRPIVMDYVVGARTPRRKRERLTSRVKA 660

QY 661 LFSVLNVERARRPGLLGASVGLDDIHRARTFVLVRQAQPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVGLDDIHRARTFVLVRQAQPPPELYFVKVDVTGAYDTI 720
QY 721 PQDLTEVIASIIKPNQTYCVRRAVAVQKAAGHVRKAFKSHVSTLTDLPYMQFVAHL 780
Db 721 PQDLTEVIASIIKPNQTYCVRRAVAVQKAAGHVRKAFKSHVSTLTDLPYMQFVAHL 780
QY 781 QETSLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVVQCGIPOGSILSTL 840
Db 781 QETSLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVVQCGIPOGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLTRVGRVPEYGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLTRVGRVPEYGCVVNL 900
QY 901 RKTUVNFEDEALGGTAFVOMPAHGLFPWCGLLLDTRTLEVSQSDYSSYARTSIRASITF 960
Db 901 RKTUVNFEDEALGGTAFVOMPAHGLFPWCGLLLDTRTLEVSQSDYSSYARTSIRASITF 960
QY 961 NRGFKAGNMRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNMRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
QY 1021 FHQQWKQPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGBLPSEAVOWLCHQAFLL 1080
Db 1021 FHQQWKQPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGBLPSEAVOWLCHQAFLL 1080
QY 1081 KLTHRRVTVPLGLSLRTAQTLQRKLPQTTLTALAAANPALSDPKTILTD 1132
Db 1081 KLTHRRVTVPLGLSLRTAQTLQRKLPQTTLTALAAANPALSDPKTILTD 1132

RESULT 16

ABR58045
ID ABR58045 standard; protein; 1132 AA.
XX
AC ABR58045;
XX
DT 29-AUG-2003 (first entry)
XX
DE Human telomerase reverse transcriptase.
XX
KW Enzyme; human; telomerase reverse transcriptase; adipogenic capacity;
KW primary preadipocyte cell; adipogenesis; obesity; adipocytokine;
KW anorectic; adiponectin; insulin.
XX
OS Homo sapiens.
XX
FN WO2003031640-A2.
XX
PD 17-APR-2003.
XX
PF 07-OCT-2002; 2002WO-US031635.
XX
PR 06-OCT-2001; 2001US-0327650P.
PR 06-OCT-2001; 2001US-0327651P.
XX
PA (BOST-) BOSTON MEDICAL CENT CORP.
XX
PI Kirkland J, Tchkonja T;
XX
DR WPI; 2003-421278/39.
DR N-PSDB; ACC44482.
XX
PT New primary preadipocyte strain expressing telomerase reverse
PT transcriptase, useful in research applications, screening assays,
PT clinical applications, and in the administration of therapeutic agents,
PT particularly for obesity.
XX
PS Disclosure; Page 13; 53pp; English.
XX

CC The invention relates to the generation of primary preadipocyte cell
CC strains that expresse telomerase reverse transcriptase (TERT- the
CC catalytic subunit of telomerase), and maintain and/or enhance replicative
CC potential and maintain adipogenic capacity of the cell. This sequence
CC represents the TERT protein. The cell strain can be used in research to
CC study all aspect of adipogenesis, especially in relation to reseaching
CC treatments for e.g. obesity. The cell can also be used to identify
CC adipogenesis modulators for use as therapeutic agents such as hormones,
CC growth factors, cytokines, enzymes, cholesterol binding proteins,
CC cholesterol removing proteins or their combinations. Alternatively, the
CC therapeutic agent may be an adipocytokine, preferably adiponectin, or
CC insulin
XX

QY Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 6; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGWRLVORGDPAPRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGWRLVORGDPAPRALVAQCLVCVPW 60
QY 61 DARPPPAAPSPROVSCUKELVARVQLCERGAKNVLAFGALDARGGPPPEAFTTSVR 120
Db 61 DARPPPAAPSPROVSCUKELVARVQLCERGAKNVLAFGALDARGGPPPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPLYQLGA 180
Db 121 SYLPTNTVDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPLYQLGA 180
QY 181 ATQARPPPHASGPRRRLGCERANWHSVREAGVPLGLPAPGARRRGGSASRSLPLPKPRR 240
Db 181 ATQARPPPHASGPRRRLGCERANWHSVREAGVPLGLPAPGARRRGGSASRSLPLPKPRR 240
QY 241 GAAPPEPTVPGGSAWHPGTRGSDRGFCVVSPPARBEATSEALSTRSHSVG 300
Db 241 GAAPPEPTVPGGSAWHPGTRGSDRGFCVVSPPARBEATSEALSTRSHSVG 300
QY 301 RQHHAGPSTSRPPRMDTTPCPVYAEHTKHFLLSYSSGDKQLRPSFLSSRLPSLTGARRL 360
Db 301 RQHHAGPSTSRPPRMDTTPCPVYAEHTKHFLLSYSSGDKQLRPSFLSSRLPSLTGARRL 360
QY 361 VETIFLGSRRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAVT 420
Db 361 VETIFLGSRRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVOLLRQHSPPQVGVFVRACTLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVOLLRQHSPPQVGVFVRACTLRRLVPPGLWGS 480
QY 481 RHNERRFLRNTKXFIISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVGCPAAEHLRBEI 540
Db 481 RHNERRFLRNTKXFIISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVGCPAAEHLRBEI 540
QY 541 LAKFLHLMMSVYVVELLRSFFYVTTTFOKNRLLPFYKSVWSKLQSGTGIROHLKRVQURE 600
Db 541 LAKFLHLMMSVYVVELLRSFFYVTTTFOKNRLLPFYKSVWSKLQSGTGIROHLKRVQURE 600
QY 601 LSEAEVRQHREARPAALLTSRLRFTPKPDGLRPIVNMDDYVVGARTFREKRAERTLSRKA 660
Db 601 LSEAEVRQHREARPAALLTSRLRFTPKPDGLRPIVNMDDYVVGARTFREKRAERTLSRKA 660
QY 661 LFSVLNVERARRPGLLGASVGLDDIHRARTFVLVRQAQPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVGLDDIHRARTFVLVRQAQPPPELYFVKVDVTGAYDTI 720
QY 721 PQDLTEVIASIIKPNQTYCVRRAVAVQKAAGHVRKAFKSHVSTLTDLPYMQFVAHL 780
Db 721 PQDLTEVIASIIKPNQTYCVRRAVAVQKAAGHVRKAFKSHVSTLTDLPYMQFVAHL 780
QY 781 QETSLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVVQCGIPOGSILSTL 840

Db 781 QETSLRDVAVIEQSSSINEASSGLFVDFLRFMCHAVIRKSVQCGIPQGSILSTL 840
Qy 841 LCSLCYGDVAVIEQSSSINEASSGLFVDFLRFMCHAVIRKSVQCGIPQGSILSTL 900
Db 841 LCSLCYGDVAVIEQSSSINEASSGLFVDFLRFMCHAVIRKSVQCGIPQGSILSTL 900
Qy 901 RKTVNVFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSYSSYARTSTRASITF 960
Db 901 RKTVNVFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSYSSYARTSTRASITF 960
Qy 961 NRGFKAGNMRKLFVGLKCHSLFLOLVNSLQTVCTNLYKILLQAYRPHACVLQLP 1020
Db 961 NRGFKAGNMRKLFVGLKCHSLFLOLVNSLQTVCTNLYKILLQAYRPHACVLQLP 1020
Qy 1021 FHQVWKNPTFFLRVISDTASICYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQVWKNPTFFLRVISDTASICYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTHRVTVYVLLGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTIILD 1132
Db 1081 KLTHRVTVYVLLGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTIILD 1132

RESULT 17

ADD21420
ID ADD21420 standard; protein; 1132 AA.

XX AC ADD21420;

XX DT 15-JAN-2004 (first entry)

XX DE Human TERT protein related to continual cell growth.

XX KW continual growth; cultured cell; cyclin dependent kinase; cdk4; cdk2;

XX KW cdk6; activating mutation; cell growth; cell division; cell cycle;

XX KW cancer-causing agent; continual growth-induced cell; enzyme; TERT;

XX KW telomerase; human.

XX OS Homo sapiens.

XX PN WO200304169-A2.

XX PD 30-MAY-2003.

XX PF 15-NOV-2002; 2002WO-US036729.

XX PR 15-NOV-2001; 2001US-0334760P.

XX PA (UTEM) UNIV TEMPLE.

XX PI Reddy PE, Rane SG, Mettuss RV;

XX DR WPI; 2003-449813/42.

XX PT A composition for reversibly inducing continual growth in normal cells
XX PT comprises a cyclin dependent kinase protein (e.g. cdk4, cdk2 or cdk6) or
XX PT its active fragment, derivative, homolog or analog, having an activating
XX PT mutation.

XX PS Claim 16; Page 135-138; 77pp; English.

XX CC This invention relates to a novel composition for inducing a reversible
XX CC state of a continual growth in cultured cells and comprises at least one
XX CC compound comprising a cyclin dependent kinase (cdk)4, cdk2 or cdk6
XX CC protein having an activating mutation. Growth and division of living
XX CC cells involve a regular series of events and processes that comprise the
XX CC cell cycle. Cyclin dependent kinases cdk2, cdk4 and cdk6 are involved in
XX CC the control of G1, the point at which cells irrevocably commit to DNA
XX CC synthesis and thus enter the cell cycle. The invention is useful in
XX CC reversibly inducing continual growth in normal cells and may allow the
XX CC screening of cancer-causing agents with the continual growth-induced
XX CC cells. The present sequence is that of the human TERT protein, the
XX CC catalytic subunit of telomerase, related to the invention. Note: Due to

CC an error in the specification or sequence listing, the Seq ID numbers
CC given in the disclosure do not correspond to those given in the sequence
CC listing. It is therefore unclear which Seq ID number corresponds to which
CC sequence and exactly which sequence is being claimed.
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 7; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCRAVRSLSRSHVREVLPLATFVRRLLGPOGWRVLRGDPAAFPALVAQCVCVPM 60

Db 1 MPAPRCRAVRSLSRSHVREVLPLATFVRRLLGPOGWRVLRGDPAAFPALVAQCVCVPM 60

Qy 61 DARPPPAAPSPROVSCCLKELVARVQLRCERGAKNVLAFFGALLDARGGPEAFTTSVR 120

Db 61 DARPPPAAPSPROVSCCLKELVARVQLRCERGAKNVLAFFGALLDARGGPEAFTTSVR 120

Qy 121 SYLPTNTVDALRGSGAWGLLLRRVDDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Db 121 SYLPTNTVDALRGSGAWGLLLRRVDDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy 181 ATQARPPPHASGPRRRLLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLLPKRPRR 240

Db 181 ATQARPPPHASGPRRRLLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLLPKRPRR 240

Qy 241 GAAPEPERTVPGQGSWAHPGTRGDRGFCVSPARPAEATSLLEGALSSTRHSHPSVG 300

Db 241 GAAPEPERTVPGQGSWAHPGTRGDRGFCVSPARPAEATSLLEGALSSTRHSHPSVG 300

Qy 301 RQHHAGPPSTSRPPMDTPCPPVYAEYKHFLLYSSGDKQLRPSFLLSSLPSTGARRL 360

Db 301 RQHHAGPPSTSRPPMDTPCPPVYAEYKHFLLYSSGDKQLRPSFLLSSLPSTGARRL 360

Qy 361 VETIFLGSRPMPGTPRRLLPRLPQRYQWMPRLFLELGNHACQPYGVLLKTHCPLRAAVT 420

Db 361 VETIFLGSRPMPGTPRRLLPRLPQRYQWMPRLFLELGNHACQPYGVLLKTHCPLRAAVT 420

Qy 421 PAAGVCAREKPOGSAVAAPPEEDTPRRLVOLLROHSSPWQVYGFVRACLRLVPPGLWGS 480

Db 421 PAAGVCAREKPOGSAVAAPPEEDTPRRLVOLLROHSSPWQVYGFVRACLRLVPPGLWGS 480

Qy 481 RHNERFLRNTKFIISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCVPAEHLRESEI 540

Db 481 RHNERFLRNTKFIISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCVPAEHLRESEI 540

Qy 541 LAKFLHLMMSVYVVELLRSFFYVTTETTFQKRLFFYRKSVWSKLSQSIGIRQHLKRVQURE 600

Db 541 LAKFLHLMMSVYVVELLRSFFYVTTETTFQKRLFFYRKSVWSKLSQSIGIRQHLKRVQURE 600

Qy 601 LSEAEVRQHRERAPALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660

Db 601 LSEAEVRQHRERAPALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660

Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720

Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720

Qy 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780

Db 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780

Qy 781 QETSPLRDADVIEQSSSINEASSGLFVDFLRFMCHAVIRKSVQCGIPQGSILSTL 840

Db 781 QETSPLRDADVIEQSSSINEASSGLFVDFLRFMCHAVIRKSVQCGIPQGSILSTL 840

Qy 841 LCSLCYGDVAVIEQSSSINEASSGLFVDFLRFMCHAVIRKSVQCGIPQGSILSTL 900

Db 841 LCSLCYGDVAVIEQSSSINEASSGLFVDFLRFMCHAVIRKSVQCGIPQGSILSTL 900

Qy 901 RKTVNVFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSYSSYARTSTRASITF 960

Db 901 RKTVNVFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSYSSYARTSTRASITF 960

Ds 901 RKTVPFVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSRASLTF 960
Qy 961 NRGFKAGNNRRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVILQLP 1020
Ds 961 NRGFKAGNNRRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVILQLP 1020
Qy 1021 FHQOVKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOWLCHQAFLL 1080
Ds 1021 FHQOVKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOWLCHQAFLL 1080
Qy 1081 KLTRHRTVTVPLLSLRTAQOLSKLPCTTTLTALAAANPALPSDFKTILD 1132
Ds 1081 KLTRHRTVTVPLLSLRTAQOLSKLPCTTTLTALAAANPALPSDFKTILD 1132

RESULT 18

ADH72743

ID ADH72743 standard; protein; 1132 AA.

XX AC ADH72743;

XX DT 25-MAR-2004 (first entry)

XX DE Human protein of the invention SEQ ID NO:19.

XX KW stem cell; cardiant; hepatotropic; nephrotropic; cytostatic; neurotropic;

XX KW neuroprotective; antiarthritic; antidiabetic; antiarteriosclerotic;

XX KW heart failure; leukaemia; neurodegenerative disease; diabetes;

XX KW arteriosclerosis; skeletal muscle; human.

XX OS Homo sapiens.

XX FN WO2003027281-A2.

XX PD 03-APR-2003.

XX PF 20-SEP-2002; 2002WO-JP009702.

XX PR 20-SEP-2001; 2001JP-00286332.

XX PR 09-MAY-2002; 2002JP-00133575.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PA (TAMA/) TAMAKI T.

XX PA (ANDO/) ANDO K.

XX PI Tamaki T, Ando K, Akatsuka A, Nakamura Y, Hotta T, Sakurada K;

XX DR WPI; 2003-371925/35.

XX PT Pluripotent stem cells originating in skeletal muscle interstitial

XX PT tissue, useful in drugs for regenerating tissues and cells e.g. in

XX PT treating heart failure, leukemia, neurodegenerative diseases, and

XX PT diabetes.

XX PS Disclosure; SEQ ID NO 19; 29pp; Japanese.

XX CC The invention relates to novel pluripotent stem cells originating from a

XX CC skeletal muscle interstitial tissue. A cell of the invention has

XX CC cardiant, hepatotropic, nephrotropic, cytostatic, neurotropic,

XX CC neuroprotective, antiarthritic, antidiabetic, and antiarteriosclerotic

XX CC activity. The cells are useful in drugs for regenerating tissues and

XX CC cells e.g. in treating heart failure, leukaemia, neurodegenerative

XX CC diseases, diabetes and arteriosclerosis. The pluripotent stem cells were

XX CC isolated from rat skeletal muscles after analysis of the various

XX CC components by culturing and staining, as well as by other biochemical

XX CC analysis. The present sequence is used in the exemplification of the

XX CC invention.

XX CC Sequence 1132 AA;

XX CC Query Match 100.0%; Score 5961; DB 7; Length 1132;

XX CC Best Local Similarity 100.0%; Pred. No. 0;

XX CC Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPLATEFVRRLPGQWRLVQRGDPAAAFRALVAQCLVCVPW 60

Ds 1 MPRAPRCRAVRSLLRSHYREVLPLATEFVRRLPGQWRLVQRGDPAAAFRALVAQCLVCVPW 60

Qy 61 DARPPPAAPSFQVSCUKELVARVLQRLCERGAKNVLAFGFALLDGGAGGPEAFTTSVR 120

Ds 61 DARPPPAAPSFQVSCUKELVARVLQRLCERGAKNVLAFGFALLDGGAGGPEAFTTSVR 120

Qy 121 SYLPTNTVTDALRGSGAWGLLLRRVGDDVLAHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180

Ds 121 SYLPTNTVTDALRGSGAWGLLLRRVGDDVLAHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180

Qy 181 ATQARPPPHASGPRRRLLGCERANWHSVREAGVPLGLPAPGARRRGGSASRSLPKRPRR 240

Ds 181 ATQARPPPHASGPRRRLLGCERANWHSVREAGVPLGLPAPGARRRGGSASRSLPKRPRR 240

Qy 241 GAAPERTPVGOGSWAHRCRTRGSPDRGFCVVSPPAPAEATSEALSGSTRSHPSVG 300

Ds 241 GAAPERTPVGOGSWAHRCRTRGSPDRGFCVVSPPAPAEATSEALSGSTRSHPSVG 300

Qy 301 RQHHAGPPSTSRPPRMDTFCPPVYAEKHFLLSSGDKQLRPSFLLSSLRPSLTGARRL 360

Ds 301 RQHHAGPPSTSRPPRMDTFCPPVYAEKHFLLSSGDKQLRPSFLLSSLRPSLTGARRL 360

Qy 361 VETIFLGSRRPMPGTPLRLPRLPQRYQWMLRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Ds 361 VETIFLGSRRPMPGTPLRLPRLPQRYQWMLRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy 421 PAAGVCAREKPOGSVAAPPEEDTDLRLVOLLQHSPPQWYGVFVACLRRLVPPGLWS 480

Ds 421 PAAGVCAREKPOGSVAAPPEEDTDLRLVOLLQHSPPQWYGVFVACLRRLVPPGLWS 480

Qy 481 RHNERRFLNRTKFIKSLGKAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Ds 481 RHNERRFLNRTKFIKSLGKAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy 541 LAKFLHLMMSVYVVELLRSFFYVTEFTFQKNRFFYRKSVMSKLSQSIGIRQHLKRVOLRE 600

Ds 541 LAKFLHLMMSVYVVELLRSFFYVTEFTFQKNRFFYRKSVMSKLSQSIGIRQHLKRVOLRE 600

Qy 601 LSEAEVRQHEARPPALLTSRLRTPKPDGLRPINMDYVVGARTFREKKAERLTSRKA 660

Ds 601 LSEAEVRQHEARPPALLTSRLRTPKPDGLRPINMDYVVGARTFREKKAERLTSRKA 660

Qy 661 LFSVLNVERARRPGLLGASVGLGDDIHRANRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720

Ds 661 LFSVLNVERARRPGLLGASVGLGDDIHRANRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy 721 PQDLRTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780

Ds 721 PQDLRTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780

Qy 781 QETSPLRDAVIEOSSSLNEASSGLFDVLFMRCHHVRIRGKSYVOCQIPQSGIISLTL 840

Ds 781 QETSPLRDAVIEOSSSLNEASSGLFDVLFMRCHHVRIRGKSYVOCQIPQSGIISLTL 840

Qy 841 LCSLCYGDMMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900

Ds 841 LCSLCYGDMMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy 901 RKTVPFVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSRASLTF 960

Ds 901 RKTVPFVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSRASLTF 960

Qy 961 NRGFKAGNNRRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVILQLP 1020

Ds 961 NRGFKAGNNRRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVILQLP 1020

Qy 1021 FHQOVKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOWLCHQAFLL 1080

Ds 1021 FHQOVKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOWLCHQAFLL 1080

QY 1081 KLTHRVTVYVPLGLSLRTAQQLSRKLPGLTTLTALAAANPALPSDFKTLID 1132
 DB 1081 KLTHRVTVYVPLGLSLRTAQQLSRKLPGLTTLTALAAANPALPSDFKTLID 1132

RESULT 19

ID ADG70114 standard; protein; 1132 AA.

AC ADG70114;

DT 11-MAR-2004 (first entry)

XX HTERT protein.

XX cytostatic; gene therapy; reverse transcriptase-inhibitor; HIV-1;
 KW human telomerase reverse transcriptase; hTERT; chimeric; catalytic site;
 KW unregulated cellular growth; cancer; tumor.

XX Homo sapiens.

OS WO2003095605-A2.

PN 20-NOV-2003.

XX 14-APR-2003; 2003WO-EP003874.

XX 08-MAY-2002; 2002US-0378820P.

XX (PHAA) PHARMACIA ITAL SPA.

XX Moll J, Schmuchel A, Stouten P;

XX WPI; 2004-012095/01.

DR N-PSDB; ADG70113.

XX New HIV-1 Reverse Transcriptase and human Telomerase Reverse
 PT Transcriptase proteins and nucleic acids, useful in gene therapy or for
 PT treating or preventing unregulated cellular growth, e.g. cancer cell or
 PT tumor growth.

XX Example 1; SEQ ID NO 4; 141pp; English.

XX The invention relates to the isolation of compounds that bind and inhibit
 CC the activity of HIV-1 reverse transcriptase (RT) or human telomerase
 CC reverse transcriptase (hTERT). The method involves determining these
 CC compounds using a HIV-1 RT/hTERT chimeric construct containing these
 CC catalytic sites of each enzyme. The nucleic acid is useful for treating
 CC or preventing unregulated cellular growth, including cancer cell and
 CC tumor growth. It is also useful in gene therapy. Compounds that inhibit
 CC telomerase activity can be used to treat cancer. The vectors of the
 CC invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
 CC express DNA which encodes HIV-RT/hTERT. This sequence corresponds to the
 CC human TERT protein.

XX Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 8; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPCRAVSLRSHRYEVLPLATFVRRRLGPGQWRVLVQRGDPAAPALVAQCILVCVPW 60
 DB 1 MPRAPCRAVSLRSHRYEVLPLATFVRRRLGPGQWRVLVQRGDPAAPALVAQCILVCVPW 60

QY 61 DARPPAAPSPFQVSCLELVARVLQRLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120
 DB 61 DARPPAAPSPFQVSCLELVARVLQRLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120

QY 121 SYLPNTVTDALRGSGAWGLLRVGVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 DB 121 SYLPNTVTDALRGSGAWGLLRVGVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRRRLGCERAMNHSVREAGVPLGLPAPGARRRGGSSASRSLPLPKRPRR 240
 DB 181 ATQARPPPHASGPRRRRLGCERAMNHSVREAGVPLGLPAPGARRRGGSSASRSLPLPKRPRR 240
 QY 241 GAAPERTPVGQSWAHPGRTGRPSDRGFCVSPARPAEATSLLEGALSCTRHSHPVG 300
 DB 241 GAAPERTPVGQSWAHPGRTGRPSDRGFCVSPARPAEATSLLEGALSCTRHSHPVG 300
 QY 301 ROHHAGPSTSRPPRPMDTTPCPVYAEYTKHFLYSGDKEQLRPSFLSSLSLPSLTGARRL 360
 DB 301 ROHHAGPSTSRPPRPMDTTPCPVYAEYTKHFLYSGDKEQLRPSFLSSLSLPSLTGARRL 360
 QY 361 VETIFLGSRPMMPTGTPRRRLPRLPQRYWOMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
 DB 361 VETIFLGSRPMMPTGTPRRRLPRLPQRYWOMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
 QY 421 PAAGVCAREKPOGSAVAPEEEDTPRLVOLLROHSSPWQYVGFVACLRRLVPPGLWGS 480
 DB 421 PAAGVCAREKPOGSAVAPEEEDTPRLVOLLROHSSPWQYVGFVACLRRLVPPGLWGS 480
 QY 481 RHNERRFLRNTKFIISLGKIAKLSLOBLTWMSVRDCAWLRRSPGVCPAAEHLRREEI 540
 DB 481 RHNERRFLRNTKFIISLGKIAKLSLOBLTWMSVRDCAWLRRSPGVCPAAEHLRREEI 540
 QY 541 LAKFLHLMMSVYVVELLRSFFYVTTFTFQKNRLFYRKSVMKLSQSIGIRQHLKRVQURE 600
 DB 541 LAKFLHLMMSVYVVELLRSFFYVTTFTFQKNRLFYRKSVMKLSQSIGIRQHLKRVQURE 600
 QY 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFREKRAERLTSRVKA 660
 DB 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFREKRAERLTSRVKA 660
 QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRWRTFVLVRQAQDPPPELVKVDVTGAYDTI 720
 DB 661 LFSVLNTERARRPGLLGASVLGLDDIHRWRTFVLVRQAQDPPPELVKVDVTGAYDTI 720
 QY 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMQRFVAHL 780
 DB 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMQRFVAHL 780
 QY 781 QETSPLRDAVIEQSSSINEASSGLFDVFLRFMCHHAVIRGKSYVQCGIPQGSILSTL 840
 DB 781 QETSPLRDAVIEQSSSINEASSGLFDVFLRFMCHHAVIRGKSYVQCGIPQGSILSTL 840
 QY 841 LCSLCYGDMEKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
 DB 841 LCSLCYGDMEKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
 QY 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTTLEVSQSDYSYARTSIRASLTF 960
 DB 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTTLEVSQSDYSYARTSIRASLTF 960
 QY 961 NRGFKAGRNMRRLFGVLRUKCHSLFLDLQVNSLQTVCTNIYKILLQAVRHFACVLQLP 1020
 DB 961 NRGFKAGRNMRRLFGVLRUKCHSLFLDLQVNSLQTVCTNIYKILLQAVRHFACVLQLP 1020
 QY 1021 PHQOVWKNPTFFLVRISDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHOAPLL 1080
 DB 1021 PHQOVWKNPTFFLVRISDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHOAPLL 1080
 QY 1081 KLTHRVTVYVPLGLSLRTAQQLSRKLPGLTTLTALAAANPALPSDFKTLID 1132
 DB 1081 KLTHRVTVYVPLGLSLRTAQQLSRKLPGLTTLTALAAANPALPSDFKTLID 1132

RESULT 20
 ID ADG90599 standard; protein; 1132 AA.
 XX ADG90599;
 AC ADG90599;
 XX 25-MAR-2004 (first entry)
 DT 25-MAR-2004 (first entry)
 XX

Human TERT SEQ ID NO:2.
DE human; immune response; telomerase reverse transcriptase; TERT;
KW cytostatic; immunostimulant; cancer; cytotoxic T cell response.
XX
XX Homo sapiens.
XX WO2004002408-A2.
XX
XX 08-JAN-2004.
XX
XX 24-JUN-2003; 2003WO-US019844.
XX
XX 27-JUN-2002; 2002US-0393295P.
XX
XX (GERO-) GERON CORP.
XX
XX Majumdar A, Ferber IA, Frolkis M, Wang Z;
XX
XX WPI; 2004-071946/07.
XX
XX N-PSDB; ADG90598.
XX
XX Eliciting an immune response in a mammal specific for its own telomerase
PT reverse transcriptase (TERT), useful for treating or preventing cancer,
PT comprises administering a composition containing TERT of another
PT mammalian species.
XX
XX Claim 66; SEQ ID NO 2; 44pb; English.
XX
XX The invention relates to a novel method for eliciting an immune response
XX in a mammalian subject that is specific for its own telomerase reverse
XX transcriptase (TERT), comprising administering an immunogenic composition
XX containing a protein with at least 20 consecutive amino acids of TERT of
XX another mammalian species, or a nucleic acid encoding the protein. A
XX composition of the invention has cytostatic, and immunostimulant
XX activity. The protein or the nucleic acid encoding the protein is useful
XX in the manufacture of a medicament for the treatment of cancer in a human
XX or for eliciting a cytotoxic T cell response in a human.
XX
XX Query Match 100.0%; Score 5961; DB 8; Length 1132;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRIGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRIGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
Qy 61 DARPPAPSPROVSCLEKELVARVLORLCERGAKNVLAFGFALLDGGAGGPEAFTTSVR 120
Db 61 DARPPAPSPROVSCLEKELVARVLORLCERGAKNVLAFGFALLDGGAGGPEAFTTSVR 120
Qy 121 SYLNTVTDALRGSGAWGLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
Db 121 SYLNTVTDALRGSGAWGLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
Qy 181 ATQARPPHAGSPRRRLGRCERAWNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRPRR 240
Db 181 ATQARPPHAGSPRRRLGRCERAWNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRPRR 240
Qy 241 GAAPEPRTVQGSWAHPGTRGDRGFCVSPAPAEATSLGALSCTRHSFVS 300
Db 241 GAAPEPRTVQGSWAHPGTRGDRGFCVSPAPAEATSLGALSCTRHSFVS 300
Qy 301 ROHAGPSTSRPRPMDTPCPVVAETKFLYSYGDKQLRPSFLSSLRPSLTGARRL 360
Db 301 ROHAGPSTSRPRPMDTPCPVVAETKFLYSYGDKQLRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGRPWPMPGTTPRRLPRLPQRYQMWRPLFLELLGNHQAQCPYGVLLKTHCFLRAAVT 420
Db 361 VETIFLGRPWPMPGTTPRRLPRLPQRYQMWRPLFLELLGNHQAQCPYGVLLKTHCFLRAAVT 420

Qy 421 PAAGVCAREKPOGSAAPBEEDTDPRLLVOLLROHSSPQWYGFVACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPOGSAAPBEEDTDPRLLVOLLROHSSPQWYGFVACLRRLVPPGLWGS 480
Qy 481 RHNERFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCPAAEHLREEI 540
Db 481 RHNERFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCPAAEHLREEI 540
Qy 541 LAKFLHLMMSVYVVELLRSFFYVTTETTFQKNRLFYFKSVMSKLSQSIGIRHLKRVQRE 600
Db 541 LAKFLHLMMSVYVVELLRSFFYVTTETTFQKNRLFYFKSVMSKLSQSIGIRHLKRVQRE 600
Qy 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFREKRAERLTSRVKA 660
Db 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFREKRAERLTSRVKA 660
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRADPPPELYFVKVDVTGAVDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRADPPPELYFVKVDVTGAVDTI 720
Qy 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMEQFVAHL 780
Db 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMEQFVAHL 780
Qy 781 QETSPLEDAVVIQSSSLNEASSGLFDVFLRFMCHHVRIRGKSYVQCGIPIQSILSTL 840
Db 781 QETSPLEDAVVIQSSSLNEASSGLFDVFLRFMCHHVRIRGKSYVQCGIPIQSILSTL 840
Qy 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVEYGCVVNL 900
Db 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVEYGCVVNL 900
Qy 901 RKTWNPPVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVDQSDYSYARTSIRASLTF 960
Db 901 RKTWNPPVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVDQSDYSYARTSIRASLTF 960
Qy 961 NRGFKAGRNMRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIYKILLLOAQRFHACVQLP 1020
Db 961 NRGFKAGRNMRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIYKILLLOAQRFHACVQLP 1020
Qy 1021 FHOQVKNPTFFLRVSDTASLCYSILKXNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHOQVKNPTFFLRVSDTASLCYSILKXNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTRHRVTVYVPLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTVYVPLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTILD 1132
RESULT 21
ADI82172
ID ADI82172 standard; protein; 1132 AA.
XX AC ADI82172;
XX AC ADI82172;
XX DT 22-APR-2004 (first entry)
XX XX
XX Human telomerase reverse transcriptase.
XX DE Human; embryonic stem cell; pluripotent stem cell; abnormal cell growth;
XX KW malignancy; differentiation.
XX XX Homo sapiens.
XX OS US2003224411-A1.
XX FN 04-DEC-2003.
XX PD 13-MAR-2003; 2003US-00388578.
XX PF 13-MAR-2003; 2003US-00388578.
XX PR 13-MAR-2003; 2003US-00388578.
XX XX (STAN/) STANTON L W.

Db 1081 KLTRHRTYVPLGSLRTAQQLSKRLPGTTLTALRAANPALPSDFKTLID 1132

RESULT 22

ID ADR70482

XX ADR70482 standard; protein; 1132 AA.

XX AC ADR70482;

XX DT 02-DEC-2004 (first entry)

XX DE Human telomerase reverse transcriptase, TERT.

XX KW Human; telomerase reverse transcriptase; TERT;

XX KW POU domain, class 5 transcription factor; POU5F1; Oct3; Oct4;

XX KW teratocarcinoma-derived growth factor; Cripto; podocalyxin-like; PODXL;

XX KW gastrin-releasing peptide receptor; GRPR; human embryonic stem cell; hES;

XX KW primate pluripotent stem cell; cancer; gene expression; cell separation;

XX KW differentiation.

XX OS Homo sapiens.

XX PN US2004180347-A1.

XX PD 16-SEP-2004.

XX PF 13-MAR-2003; 2003US-00389431.

XX PR 13-MAR-2003; 2003US-00389431.

XX PA (STAN/) STANTON L W.

XX PA (BRAN/) BRANDENBERGER R.

XX PA (GOLD/) GOLD J D.

XX PA (IRVI/) IRVING J M.

XX PA (MAND/) MANDALAM R.

XX PA (MOKM/) MOK M.

XX ST Stanton LW, Brandenberger R, Gold JD, Irving JM, Mandalam R;

XX PI Mok M;

XX DR WPI; 2004-675599/66.

XX DR N-PSDB; ADR70481.

XX AS Assessing culture of undifferentiated human embryonic stem cells or their

XX PT progeny, by detecting Cripto, gastrin-releasing peptide (GRP) receptor

XX PT and podocalyxin-like protein markers, and either hTERT and/or Oct3/4, or

XX PT GRP receptor.

XX PS Disclosure; SEQ ID NO 2; 57pp; English.

XX CC The invention relates to assessing a culture of undifferentiated human

XX CC embryonic stem (hES) cells (undifferentiated primate pluripotent stem

XX CC cells) or their progeny, involves detecting or measuring a marker such as

XX CC Cripto (teratocarcinoma-derived growth factor), gastrin-releasing peptide

XX CC (GRP) receptor and podocalyxin-like protein, and either hTERT (telomerase

XX CC reverse transcriptase) and/or Oct3/4 (also known as POU domain, class 5,

XX CC transcription factor 1(POU5F1)), or GRP receptor. The method involves

XX CC detecting or measuring at least two markers, and detecting or measuring

XX CC hTERT and/or Oct3/4. The expression of the marker(s) is detected or

XX CC measured at mRNA level by PCR amplification. The expression of the

XX CC marker(s) is detected or measured at the protein level by antibody assay.

XX CC The method involves quantifying the proportion of undifferentiated hES

XX CC cells or differentiated cells in the culture from the marker expression.

XX CC The level of the marker is determined to be at least 100-fold higher than

XX CC the level of the marker in BJ fibroblasts or is determined to be no less

XX CC than 100-fold lower than the level of the marker in hES cells, cultured

XX CC on an extracellular matrix in medium conditioned with mouse embryonic

XX CC fibroblasts and containing 4 ng/ml basic fibroblast growth factor. The

XX CC method further involves modifying the culture conditions so as to cause

XX CC the hES cells to increase expression of the marker detected or measured

XX CC in the culture. The method is useful for assessing a culture of

XX CC undifferentiated hES cells or their progeny. The marker used in the above

XX CC method is useful for characterising pluripotent stem cells and their

CC differentiated progeny, for clinical diagnosis of cancer, for assessing

CC and manipulating culture conditions, regulating gene expression, cell

CC separation and purification, and to influence differentiation. The

CC present sequence is a marker protein of the invention for

CC undifferentiated stem cells.

XX SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 8; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLRGLPGQWRLVORGDDPAAAFALVAQCLVCVPW 60

Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLRGLPGQWRLVORGDDPAAAFALVAQCLVCVPW 60

Qy 61 DARPPPPAAPSFRVSCLELVARVQLRCLCRGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

Db 61 DARPPPPAAPSFRVSCLELVARVQLRCLCRGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy 181 ATQARPPPHASGPRRLRGCERANWHSVREAGVPLGLPAGARRRGGSASRSLPLPKRPRR 240

Db 181 ATQARPPPHASGPRRLRGCERANWHSVREAGVPLGLPAGARRRGGSASRSLPLPKRPRR 240

Qy 241 GAAPEPERTVPGGSAWHPGRTGPDSDRGFCVVSPPARPAEEATSEALSGALSTRHSHSVG 300

Db 241 GAAPEPERTVPGGSAWHPGRTGPDSDRGFCVVSPPARPAEEATSEALSGALSTRHSHSVG 300

Qy 301 RQHHAGPPSTSRPPRMDTPCPPVYAEHTKHFLYSSGDKQLRPSFLSSRLSPSLTGARRL 360

Db 301 RQHHAGPPSTSRPPRMDTPCPPVYAEHTKHFLYSSGDKQLRPSFLSSRLSPSLTGARRL 360

Qy 361 VETIFLGSRWPMFGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Db 361 VETIFLGSRWPMFGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy 421 PAAGVCAREKPOGSAVAPEEEDTPRRLVOLLRHSSPQWVYGVFVRACLRLRPVPLGLWS 480

Db 421 PAAGVCAREKPOGSAVAPEEEDTPRRLVOLLRHSSPQWVYGVFVRACLRLRPVPLGLWS 480

Qy 481 RHNERFLRNTKKFISLGHAKLSLQELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540

Db 481 RHNERFLRNTKKFISLGHAKLSLQELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540

Qy 541 LAKFLHLMSSVYVELLRSFFYVTTTFOKNLFFYRKSVWSKLOSIGIRQHLKRVQURE 600

Db 541 LAKFLHLMSSVYVELLRSFFYVTTTFOKNLFFYRKSVWSKLOSIGIRQHLKRVQURE 600

Qy 601 LSAEAVRQHRARPALLTSRLRFPKPDGLRPIVNMVYVVGARTFREKKAERLTSRVKA 660

Db 601 LSAEAVRQHRARPALLTSRLRFPKPDGLRPIVNMVYVVGARTFREKKAERLTSRVKA 660

Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRAQDPPPELFPVKVDVTGAYDTI 720

Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRAQDPPPELFPVKVDVTGAYDTI 720

Qy 721 PQDLRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLPYMQFVAHL 780

Db 721 PQDLRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLPYMQFVAHL 780

Qy 781 QETSPLRDADAVIIOSSSINEASSGLFDVFLRFMCHAVRIRGKSVYOCQIPQGSILSTL 840

Db 781 QETSPLRDADAVIIOSSSINEASSGLFDVFLRFMCHAVRIRGKSVYOCQIPQGSILSTL 840

Qy 841 LCSLCYGDMEKMLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900

Db 841 LCSLCYGDMEKMLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900

Qy 901 RKTWNFPVDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVDQSDYSSYARTSIRASITF 960

Db 901 RTVVNFVDEBALGTAFOVPAHGLFPWCCGLLDTRELVQSDYSSVARTSIRASLTFF 960
Qy 961 NRGFKAGNRMRKLGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRHACVLQLP 1020
Db 961 NRGFKAGNRMRKLGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRHACVLQLP 1020
Qy 1021 FHOQVKNPTFFLRVISDTASICYSLKAKNAGMSLGAKAAGPLPSEAVOMLCHQAFLL 1080
Db 1021 FHOQVKNPTFFLRVISDTASICYSLKAKNAGMSLGAKAAGPLPSEAVOMLCHQAFLL 1080
Qy 1081 KLTRHVVYVPLLSRLTAQTLQSLKLPGLTTLTALAAANPALPSDFKTILD 1132
Db 1081 KLTRHVVYVPLLSRLTAQTLQSLKLPGLTTLTALAAANPALPSDFKTILD 1132

RESULT 23
AAW61350
ID AAW61350 standard; protein; 1154 AA.
XX AC AAW61350;
XX AC AAW61350;
DT 25-MAR-2003 (revised)
DT 12-OCT-1998 (first entry)
XX Human telomerase protein 2 (TP2).
XX TP2; human; telomerase protein 2; cancer; AIDS; ageing; therapy.
XX Homo sapiens.
XX OS
XX PN WO9821343-A1.
XX PD 22-MAY-1998.
XX PF 13-NOV-1997; 97WO-US021248.
XX PR 15-NOV-1996* 96US-00751189.
PR 11-JUN-1997* 97US-00873039.
PR 16-OCT-1997; 97US-00951733.
XX (AMGE-) AMGEN INC.
XX (AMGE-) AMGEN CANADA INC.
XX Harrington LA, Robinson MO;
XX WPI; 1998-297946/26.
XX N-PSDB; AAV27876.
XX New nucleic acid encoding human telomerase protein-2 - used for
PT regulating telomerase activity, e.g. for treating cancer or acquired
PT immune deficiency syndrome.
XX Claim 1e; Fig 9; 150pp; English.

XX This polypeptide comprises human telomerase protein 2 (TP2), a novel
CC protein of the telomerase complex. Its amino acid sequence was deduced
CC from a composite (see AAV27876) of isolated cDNA clones 32 (see AAV27872)
CC and TP2-15 (see AAV27875), obtained from a human colon tumour cell line
CC LIM1863 cDNA. Expressing TP2 in a cell is used to increase telomerase
CC activity and thus proliferation for treatment of e.g. HIV infection, AIDS
CC and ageing disorders, while expressing an inactive mutant of TP2 (or
CC molecule antisense to the gene) is used to decrease telomerase activity,
CC e.g. for treatment of cancer. TP2 polypeptides can also be used to screen
CC for agents that inhibit TP2 activity or its binding to TRP1 (see
CC AAW61347) or telomerase RNA, potentially useful therapeutically, also to
CC raise specific antibodies useful in immunoassays and therapeutically as
CC inhibitors. Also contemplated are transgenic animals in which the TP2
CC gene has been inactivated or is overexpressed. TP2 polypeptides are
CC administered i.v., s.c. or orally, or they are delivered from engineered
CC cells or gene therapy vectors. (Updated on 25-MAR-2003 to correct PR
CC field.)
XX

SQ Sequence 1154 AA;
Query Match 100.0%; Score 5961; DB 2; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCASRLRLSHRYEVLPLATFVRRLLGPOQWRLLVQRGDPAAFRALVAQCLVCVPM 60
Db 23 MPRAPRCASRLRLSHRYEVLPLATFVRRLLGPOQWRLLVQRGDPAAFRALVAQCLVCVPM 82
Qy 61 DARPPAAPSPROVSLKELVARVLORLCERGAQKVLAFGFPALLDARGGPEAFTTSVR 120
Db 83 DARPPAAPSPROVSLKELVARVLORLCERGAQKVLAFGFPALLDARGGPEAFTTSVR 142
Qy 121 SYLPTNTVDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAVQCGPPLYQLGA 180
Db 143 SYLPTNTVDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAVQCGPPLYQLGA 202
Qy 181 ATQARPPPHASGPRRLRGCEAWNHSVREAGVPLGLPAPGARRRRGSSASRSLPLKPRPR 240
Db 203 ATQARPPPHASGPRRLRGCEAWNHSVREAGVPLGLPAPGARRRRGSSASRSLPLKPRPR 262
Qy 241 GAAPERTPVQGSWAHPGTRGSDRGFCVVSAPAEATSLGALSGRHSHPSVG 300
Db 263 GAAPERTPVQGSWAHPGTRGSDRGFCVVSAPAEATSLGALSGRHSHPSVG 322
Qy 301 ROHAGAPPTSRPPRMDTPCPVVAETKHFLYSSGDKQLRPSFLLSLSPSLTGAREL 360
Db 323 ROHAGAPPTSRPPRMDTPCPVVAETKHFLYSSGDKQLRPSFLLSLSPSLTGAREL 382
Qy 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHACQPGVLLKTHCPRAAAT 420
Db 383 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHACQPGVLLKTHCPRAAAT 442
Qy 421 PAAGVCAREKPCQGSVAAPPEEDTDPRLVQLLRQHSWPQVYGFVRACLRRLVPGLWGS 480
Db 443 PAAGVCAREKPCQGSVAAPPEEDTDPRLVQLLRQHSWPQVYGFVRACLRRLVPGLWGS 502
Qy 481 RHNERFLRNTHKFIISLGHAKLSIQELTWKMSVRDCAWLRRSPGCVGCPAAEHLRREI 540
Db 503 RHNERFLRNTHKFIISLGHAKLSIQELTWKMSVRDCAWLRRSPGCVGCPAAEHLRREI 562
Qy 541 LAKFLHLMSSVYVVELLSFFVTTTQKNRLFFYRKSVMKLSQIGIRQHLKRVQLE 600
Db 563 LAKFLHLMSSVYVVELLSFFVTTTQKNRLFFYRKSVMKLSQIGIRQHLKRVQLE 622
Qy 601 LSEAFVROHREARPAALTSRLRFLPKDGLRPIVNMVYVVGARTPRREKRAERLTSRVKA 660
Db 623 LSEAFVROHREARPAALTSRLRFLPKDGLRPIVNMVYVVGARTPRREKRAERLTSRVKA 682
Qy 661 LFSVLNYERARRPGLIGASVLGLDDIHRAWTFVLRVAQDPPPELYFVKVDVTGAYDTI 720
Db 683 LFSVLNYERARRPGLIGASVLGLDDIHRAWTFVLRVAQDPPPELYFVKVDVTGAYDTI 742
Qy 721 PQDLTEVIASIIKPNQTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
Db 743 PQDLTEVIASIIKPNQTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 802
Qy 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRPMCHHAVIRKGSYVQCGIPQGSILSTL 840
Db 803 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRPMCHHAVIRKGSYVQCGIPQGSILSTL 862
Qy 841 LCSICYGDMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLTLVRGPEYCVNVL 900
Db 863 LCSICYGDMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLTLVRGPEYCVNVL 922
Qy 901 RKTVMNPFVEALGCTAFVQMPAHGLFPWCCGLLDTRELVQSDYSSVARTSIRASLTFF 960
Db 923 RKTVMNPFVEALGCTAFVQMPAHGLFPWCCGLLDTRELVQSDYSSVARTSIRASLTFF 982
Qy 961 NRGFKAGNRMRKLGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRHACVLQLP 1020
Db 983 NRGFKAGNRMRKLGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRHACVLQLP 1042

QY 1021 FHQVWKNTFLRVIDSTASLCYSILKAKNAGSLGAKGAGLPSEAVQWLCHQAPLL 1080
 Db 1043 FHQVWKNTFLRVIDSTASLCYSILKAKNAGSLGAKGAGLPSEAVQWLCHQAPLL 1102
 QY 1081 KLTHRVTVYVLLGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTIILD 1132
 Db 1103 KLTHRVTVYVLLGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTIILD 1154

RESULT 24
 AAW47008
 ID AAW47008 standard; protein; 1189 AA.
 XX AAW47008;
 AC AAW47008;
 DT 13-AUG-1998 (first entry)
 XX Glutathione-S-transferase and hTERT fusion protein 8.
 DE Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
 KW cell proliferation; cancer; ageing; ribonucleoprotein.
 XX Synthetic.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Misc-difference 22..23
 FT /note=" enterokinase cleavage site"
 FT
 XX GB2317891-A.
 XX 08-APR-1998.
 XX 01-OCT-1997; 97GB-00020890.
 XX 01-OCT-1996; 96US-00724643.
 PR 18-APR-1997; 97US-00844419.
 PR 25-APR-1997; 97US-00846017.
 PR 06-MAY-1997; 97US-00851843.
 PR 09-MAY-1997; 97US-00854050.
 PR 14-AUG-1997; 97US-00911312.
 PR 14-AUG-1997; 97US-00912951.
 PR 14-AUG-1997; 97US-00915503.
 XX (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
 PI Andrews WH;
 PI WPI; 1998-171633/16.
 DR Pure and recombinant human Telomerase Reverse Transcriptase and its
 XX variants - are useful in the diagnosis, prognosis and treatment of cell
 PT proliferation conditions especially cancer and ageing.
 XX Example 6; Page 234-235; 387pp; English.

The present sequence represents a fusion protein from an example of the
 present invention which describes human telomerase reverse transcriptase
 (hTERT). The present invention also describes the following methods: (A)
 determining whether a test compound is a modulator of hTERT, by detecting
 the change in hTERT recombinant protein or polynucleotide, on
 administration of the compound; (B) preparation of recombinant telomerase
 by contacting a protein preparation of hTERT with a telomerase RNA
 component; (C) detection of the hTERT RNA or protein in a sample by
 binding a relevant probe to the sample and detecting the complex formed
 or in the case of RNA detection, amplifying the product and correlating
 the presence of complex or amplification product with presence of hTERT in
 the sample; and (D) increasing the proliferation of a vertebrate cell by
 increasing hTERT expression; and (E) the use of an agent that causes an
 increase in cell vertebrate cell proliferation to create a medicament

CC that inhibits ageing. A protein preparation of hTERT and the
 CC polynucleotide encoding hTERT can be used in the manufacture of
 CC medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
 CC telomerase activity can be used to treat conditions that are associated
 CC with high telomerase activity. A protein preparation of hTERT can also be
 CC used in the new methods
 XX Sequence 1189 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1189;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPRAPCRAVRSLLRSHYREVLPATFVRRLGPGWRLVORGDPAAAFRALVAQCLVCPW 60
 Db 58 MPRAPCRAVRSLLRSHYREVLPATFVRRLGPGWRLVORGDPAAAFRALVAQCLVCPW 117
 QY 61 DARPPPAAPSPFVSCIKELVARVLQRLCERGANVLAFGPALDARGGPEAFTTSVR 120
 Db 118 DARPPPAAPSPFVSCIKELVARVLQRLCERGANVLAFGPALDARGGPEAFTTSVR 177
 QY 121 SYLPTNTVDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLQLGA 180
 Db 178 SYLPTNTVDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLQLGA 237
 QY 181 ATOARPPPHASGPRRLGRCERANVHVSREAGVPLGLPAPGARRRGGSASRLPKRRPR 240
 Db 238 ATOARPPPHASGPRRLGRCERANVHVSREAGVPLGLPAPGARRRGGSASRLPKRRPR 297
 QY 241 GAAPEPERTVPGGSGWAHPGRTGSDRGFCVVSPPARPEATSLGALSCTRSHPSVG 300
 Db 298 GAAPEPERTVPGGSGWAHPGRTGSDRGFCVVSPPARPEATSLGALSCTRSHPSVG 357
 QY 301 RQHHAGPSTSRPPRWDTPCPVYAEYTHFLYSSGDKQLRPSFLSSRLPSLTGARRL 360
 Db 358 RQHHAGPSTSRPPRWDTPCPVYAEYTHFLYSSGDKQLRPSFLSSRLPSLTGARRL 417
 QY 361 VETIFGSRPMPGTPRRRLPRLPQRYWQMPRLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
 Db 418 VETIFGSRPMPGTPRRRLPRLPQRYWQMPRLFLELGNHAQCPYGVLLKTHCPLRAAVT 477
 QY 421 PAAGVCAREKPOGSVAAPREEDTDPRLLVOLLROHSSPMQVYGVFVRACLRLVPPGLWGS 480
 Db 478 PAAGVCAREKPOGSVAAPREEDTDPRLLVOLLROHSSPMQVYGVFVRACLRLVPPGLWGS 537
 QY 481 RHNERRFLRNTKPFISLGHAKLSQLBTWKMSVRDCAWLRRSPGVGCPVAAEHLREEI 540
 Db 538 RHNERRFLRNTKPFISLGHAKLSQLBTWKMSVRDCAWLRRSPGVGCPVAAEHLREEI 597
 QY 541 LAKFLHLMVSVYVVELLSRFFVYVTEITFQKRLFFYRKSVMWSKLSQSIGIRQHLKRVQURE 600
 Db 598 LAKFLHLMVSVYVVELLSRFFVYVTEITFQKRLFFYRKSVMWSKLSQSIGIRQHLKRVQURE 657
 QY 601 LSAEVRQHREARPAALTSRLRFPKPDGLRPIVMDYVVGARTFREKRAERLTSRKA 660
 Db 658 LSAEVRQHREARPAALTSRLRFPKPDGLRPIVMDYVVGARTFREKRAERLTSRKA 717
 QY 661 LFSVLNRYERARRPCLLGASVLGLDDIHRWRTFVLVRAQDPPPELVFVKVDVTGAYDTI 720
 Db 718 LFSVLNRYERARRPCLLGASVLGLDDIHRWRTFVLVRAQDPPPELVFVKVDVTGAYDTI 777
 QY 721 PQRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLQPMRQFVAHL 780
 Db 778 PQRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLQPMRQFVAHL 837
 QY 781 QETSPLRDADVIVSQSSSLNEASSGLFDVLFMFCHHAVIRGKSYVOCQIPQGSILSTL 840
 Db 838 QETSPLRDADVIVSQSSSLNEASSGLFDVLFMFCHHAVIRGKSYVOCQIPQGSILSTL 897
 QY 841 LCSLCYGDMMENKLFAGIRRDGLLLRLVDDFLVLTTPHLTHAKTFLRITLVRGVPYGCVVNL 900
 Db 898 LCSLCYGDMMENKLFAGIRRDGLLLRLVDDFLVLTTPHLTHAKTFLRITLVRGVPYGCVVNL 957

QY 901 RKTVVNPFVEBALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASITF 960
 Db 958 RKTVVNPFVEBALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASITF 1017
 QY 961 NRGPKAGNRMRKLFGLVRLKCHSLFDLOVNSLQTVCTNIIKILLQAYRPHACVQLP 1020
 Db 1018 NRGFKAGNRMRKLFGLVRLKCHSLFDLOVNSLQTVCTNIIKILLQAYRPHACVQLP 1077
 QY 1021 FHQQVWKNPTFLRIVISDTASICYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
 Db 1078 FHQQVWKNPTFLRIVISDTASICYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1137
 QY 1081 KLTHRVTVVPLGLSLRQAQOLSKLPGTTLTALEAAANPALPSDFKTILD 1132
 Db 1138 KLTHRVTVVPLGLSLRQAQOLSKLPGTTLTALEAAANPALPSDFKTILD 1189

RESULT 25

AAW47000
 ID AAW47000 standard; protein; 1285 AA.
 XX
 AC AAW47000;
 XX
 DT 13-AUG-1998 (first entry)
 XX
 DE HIS tagged thioredoxin moiety and full length hTERT fusion protein.
 XX
 KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
 XX cell proliferation; cancer; ageing; ribonucleoprotein.
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 119..120
 FT /note= "enterokinase cleavage site"
 FT 120..1285
 FT /label= hTERT
 FT /note= "full length human telomerase reverse
 FT transcriptase"
 XX
 FN GB2317891-A.
 XX
 XX 08-APR-1998.
 XX
 XX 01-OCT-1997; 97GB-00020890.
 XX
 PR 01-OCT-1996; 96US-00724643.
 PR 18-APR-1997; 97US-00844419.
 PR 25-APR-1997; 97US-00846017.
 PR 06-MAY-1997; 97US-00851843.
 PR 09-MAY-1997; 97US-00854050.
 PR 14-AUG-1997; 97US-00911312.
 PR 14-AUG-1997; 97US-00912951.
 PR 14-AUG-1997; 97US-00915503.
 XX
 PA (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX
 XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
 PI Andrews WH;
 XX
 DR WPI; 1998-171633/16.
 XX
 XX Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of cell
 PT proliferation conditions especially cancer and ageing.
 XX
 XX Example 6; Page 223; 387pp; English.
 PS
 XX The present sequence represents a fusion protein from an example of the
 CC present invention which describes human telomerase reverse transcriptase
 CC (hTERT). The present invention also describes the following methods: (A)

CC determining whether a test compound is a modulator of hTERT, by detecting
 CC the change in hTERT recombinant protein or polynucleotide, on
 CC administration of the compound; (B) preparation of recombinant telomerase
 CC by contacting a protein preparation of hTERT with a telomerase RNA
 CC component; (C) detection of the hTERT RNA or protein in a sample by
 CC binding a relevant probe to the sample and detecting the complex formed
 CC or in the case of RNA detection, amplifying the product and correlating
 CC the presence of complex or amplification product with presence of hTERT in
 CC the sample; and (D) increasing the proliferation of a vertebrate cell by
 CC increasing hTERT expression; and (E) the use of an agent that causes an
 CC increase in cell vertebrate cell proliferation to create a medicament
 CC that inhibits ageing. A protein preparation of hTERT and the
 CC polynucleotide encoding hTERT can be used in the manufacture of
 CC medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
 CC telomerase activity can be used to treat conditions that are associated
 CC with high telomerase activity. A protein preparation of hTERT can also be
 CC used in the new methods
 XX
 SQ Sequence 1285 AA;
 Query Match 99.9%; Score 5955; DB 2; Length 1285;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPOGRLVQRGDPAAPRALVAQCLVCPW 60
 Db 154 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPOGRLVQRGDPAAPRALVAQCLVCPW 213
 QY 61 DARPPPAAPSPROVSCLELVARVLQRLCERGAKNVLAFGFALLDGGGPPPEAFTTSVR 120
 Db 214 DARPPPAAPSPROVSCLELVARVLQRLCERGAKNVLAFGFALLDGGGPPPEAFTTSVR 273
 QY 121 SYLPTNTVTDALRGSGAWGLLLRRVGGDDVLVLLARCALFVLVAPSCAYQVCGPPYQLGA 180
 Db 274 SYLPTNTVTDALRGSGAWGLLLRRVGGDDVLVLLARCALFVLVAPSCAYQVCGPPYQLGA 333
 QY 181 ATQARPPPHASGPRRRRLGGERAWNHSVREAGVPLGLPAGARRRGGSSASRLPLKRRR 240
 Db 334 ATQARPPPHASGPRRRRLGGERAWNHSVREAGVPLGLPAGARRRGGSSASRLPLKRRR 393
 QY 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSGPARPAEATSLEGALSCTRHSHPVSG 300
 Db 394 GAAPERTPVQGSWAHPGTRGSDRGFCVSGPARPAEATSLEGALSCTRHSHPVSG 453
 QY 301 ROHAGBPSTSRPRPMDTPCPVYAEYTKHLYSGDKEQLRPSLLSLRPSLTGARRL 360
 Db 454 ROHAGBPSTSRPRPMDTPCPVYAEYTKHLYSGDKEQLRPSLLSLRPSLTGARRL 513
 QY 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPLRAAVT 420
 Db 514 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPLRAAVT 573
 QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSHPWYGVFVRACLRRLVPPGLWGS 480
 Db 574 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSHPWYGVFVRACLRRLVPPGLWGS 633
 QY 481 RHNERFLRNTKPTISLCKHAKLSLOELTWKSVRDCAWLRSPOGVCVPAEHLRREI 540
 Db 634 RHNERFLRNTKPTISLCKHAKLSLOELTWKSVRDCAWLRSPOGVCVPAEHLRREI 693
 QY 541 LAKFLHLMSSVYVVELLRSFFYVTTTFOKRLFFYKSVMSKLQSIGIRHQLKRVQURE 600
 Db 694 LAKFLHLMSSVYVVELLRSFFYVTTTFOKRLFFYKSVMSKLQSIGIRHQLKRVQURE 753
 QY 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
 Db 754 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 813
 QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELFFVKVDVTGAYDTI 720
 Db 814 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELFFVKVDVTGAYDTI 873
 QY 721 PQDRLTEVIAISIIKPNQTYCVRRVAVVQKAAHGHVRKAFKSHVSTLTLDLPQYMRQFVAHL 780

Db 874 PQRDLTEVIASIIIPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMQFVNAHL 933
Qy 781 QETSPRLDAVVIQSSSLEASSGLFDVFLRPMCHHAVIRGKSYVQCGIPQGSII STL 840
Db 934 QETSPRLDAVVIQSSSLEASSGLFDVFLRPMCHHAVIRGKSYVQCGIPQGSII STL 993
Qy 841 LCSLCYGDMEKLFAGIRGDLIRLAVDDFLIVTPHLTHAKTFLRTLVGRVPEYGCVVNL 900
Db 994 LCSLCYGDMEKLFAGIRGDLIRLAVDDFLIVTPHLTHAKTFLRTLVGRVPEYGCVVNL 1053
Qy 901 RKTIVNPFVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLLEVSQSDYSSYARTISRASLTF 960
Db 1054 RKTIVNPFVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLLEVSQSDYSSYARTISRASLTF 1113
Qy 961 NRGFKAGNMRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 1114 NRGFKAGNMRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1173
Qy 1021 FHOQVWKNPTFLRIVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAFL 1080
Db 1174 FHOQVWKNPTFLRIVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAFL 1233
Qy 1081 KLTRHRVTYVPLLSRLTAQOLSRKLPCTTTLTALEAAANPALPDPFTILD 1132
Db 1234 KLTRHRVTYVPLLSRLTAQOLSRKLPCTTTLTALEAAANPALPDPFTILD 1285

RESULT 26

AAW71376
ID AAW71376 standard; protein; 1132 AA.
XX
AC AAW71376;
XX
DT 04-DEC-1998 (first entry)
XX
DE Human telomerase catalytic subunit referred to as hEST2.
XX
KW Catalytic subunit; human; telomerase; telomere maintenance; diagnosis;
KW treatment; cancer.
XX
OS Homo sapiens.
XX
PN W03837181-A2.
XX
PD 27-AUG-1998.
XX
PF 20-FEB-1998; 98WO-US003404.
XX
PR 20-FEB-1997; 97US-0038750P.
PR 20-MAY-1997; 97US-0047151P.
PR 01-AUG-1997; 97US-0054549P.
PR 14-AUG-1997; 97US-0055762P.
PR 30-OCT-1997; 97US-0064322P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Counter CM, Meyerson M, Weinberg RA;
XX
DR WPI; 1998-495367/42.
DR N-PSDB; AAV60320.
XX
PT New isolated human telomerase catalytic sub-unit gene - used to develop
PT products for increasing or reducing the life span of cells such as cancer
PT cells or transformed cells.
XX
PS Claim 5; Fig 6; 96pp; English.
XX
CC The present sequence represents the catalytic subunit of a human
CC telomerase holoenzyme. Disruption of the telomerase gene alters telomere
CC maintenance. The DNA is essential for telomerase activity, and the
CC protein is physically associated with telomerase and a constituent of
CC active telomerase complex. The products can be used for increasing or

CC reducing the lifespan of cells such as cancer cells or transformed cells.
CC They can also be used in the diagnosis and treatment of malignancies. In
CC addition, cells with a longer lifespan can be transplanted into or
CC grafted onto an individual (e.g. as skin grafts, as systems for delivery
CC of therapeutic proteins, such as hormones and enzymes), to whom they
CC provide therapeutic benefit

XX Sequence 1132 AA;

Query Match 99.9%; Score 5954; DB 2; Length 1132;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSYREVLPATFVRRLGPGCWRLLVQRGDPAAPRALVAQCLVCPW 60
Db 1 MPRAPRCRAVRSLLRSYREVLPATFVRRLGPGCWRLLVQRGDPAAPRALVAQCLVCPW 60
Qy 61 DARPPAPSPFVSCLEIVARVLQRLCERGAKNVLAFGPALDARGGPEAFTTSVR 120
Db 61 DARPPAPSPFVSCLEIVARVLQRLCERGAKNVLAFGPALDARGGPEAFTTSVR 120
Qy 121 SYLPTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPRRLGCRANVHSVREAGVPLGLPAGARRGGASRSLPLPKRPRR 240
Db 181 ATQARPPPHASGPRRLGCRANVHSVREAGVPLGLPAGARRGGASRSLPLPKRPRR 240
Qy 241 GAAPEPERTVGGQSWAHPCRTGRGSDRGFCVSPARPABEATSLGALSSTRHSHSVG 300
Db 241 GAAPEPERTVGGQSWAHPCRTGRGSDRGFCVSPARPABEATSLGALSSTRHSHSVG 300
Qy 301 ROHHAGPPSTRPPRMDTFCPPVYAEKHFXYSSGDKQLRPSFLSSRLPSLTGARRL 360
Db 301 ROHHAGPPSTRPPRMDTFCPPVYAEKHFXYSSGDKQLRPSFLSSRLPSLTGARRL 360
Qy 361 VETIFLGSRRPMGTPRRLPRLPQRYQWMPRLFLELLGNHAQCYPYGVLLKTHCPLRAVT 420
Db 361 VETIFLGSRRPMGTPRRLPRLPQRYQWMPRLFLELLGNHAQCYPYGVLLKTHCPLRAVT 420
Qy 421 PAAGVCAREKPOGSVAAPPEEDTDPRLLVOLLRHSSPQWVGVFVRACLRLVPGLWGS 480
Db 421 PAAGVCAREKPOGSVAAPPEEDTDPRLLVOLLRHSSPQWVGVFVRACLRLVPGLWGS 480
Qy 481 RHNERREFLRNTKCFISLGKHAQLSLQELTWKMSVRGCAWLRSSPGVCPAAEHLRBEI 540
Db 481 RHNERREFLRNTKCFISLGKHAQLSLQELTWKMSVRGCAWLRSSPGVCPAAEHLRBEI 540
Qy 541 LAKFLHLMSSVYVELLSRFFYVTTTFOKNRLFYRKSVWSKLSQSGIRQHLKRVQLRE 600
Db 541 LAKFLHLMSSVYVELLSRFFYVTTTFOKNRLFYRKSVWSKLSQSGIRQHLKRVQLRE 600
Qy 601 LSEAEVRQHREARPAALLTSRLRFLPKDGLRPIVNMVYVVGARTFRREKRAELTSRKA 660
Db 601 LSEAEVRQHREARPAALLTSRLRFLPKDGLRPIVNMVYVVGARTFRREKRAELTSRKA 660
Qy 661 LFSVLYNERARRPGLLGASVLGLDDIHRWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLYNERARRPGLLGASVLGLDDIHRWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PQDLRTBVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMQFVNAHL 780
Db 721 PQDLRTBVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMQFVNAHL 780
Qy 781 QETSPRLDAVVIQSSSLEASSGLFDVFLRPMCHHAVIRGKSYVQCGIPQGSII STL 840
Db 781 QETSPRLDAVVIQSSSLEASSGLFDVFLRPMCHHAVIRGKSYVQCGIPQGSII STL 840
Qy 841 LCSLCYGDMEKLFAGIRRDLRLVDDFLIVTPHLTHAKTFLRTLVGRVPEYGCVVNL 900
Db 841 LCSLCYGDMEKLFAGIRRDLRLVDDFLIVTPHLTHAKTFLRTLVGRVPEYGCVVNL 900

QY 901 RKTVMNPFVEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 960
 Db 901 RKTVMNPFVEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 960
 QY 961 NRGFKAGNMRKLGVLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
 Db 961 NRGFKAGNMRKLGVLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
 QY 1021 FHQQWKNPFTFLRVISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
 Db 1021 FHQQWKNPFTFLRVISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
 QY 1081 KLTHRVTVYVPLGLSLRTAQTSLSKLPGLTTLTALAAANPALPSDFKTLTD 1132
 Db 1081 KLTHRVTVYVPLGLSLRTAQTSLSKLPGLTTLTALAAANPALPSDFKTLTD 1132

RESULT 27
 AAY00627
 ID AAY00627 standard; protein; 1132 AA.
 XX AC AAY00627;
 XX DT 26-JUL-1999 (first entry)
 XX DE Human telomerase protein sequence.
 XX KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 XX OS Homo sapiens.
 XX PN WO9901560-A1.
 XX PD 14-JAN-1999.
 XX PF 01-JUL-1998; 98WO-US013835.
 XX PR 01-JUL-1997; 97US-0051410P.
 XX PR 21-JUL-1997; 97US-0053018P.
 XX PR 21-JUL-1997; 97US-0053329P.
 XX PR 04-AUG-1997; 97US-0054642P.
 XX PR 09-SEP-1997; 97US-0058287P.
 XX PA (CAMP-) CAMBIA BIOSYSTEMS LLC.
 XX PI Killian A, Bowtell D;
 XX WPI: 1999-106060/09.
 XX DR N-PSDB; AAX18254.
 XX PT New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PT growth following injury or bone marrow transplantation.
 XX PS Claim 19; Fig 1; 134pp; English.
 XX CC This sequence is the human telomerase of the invention. Primers that
 CC amplify the telomerase coding sequence can be used in a method for
 CC diagnosing cancer in a patient. The telomerase can be used for detection,
 CC diagnosis and drug screening. Inhibitors of telomerase activity can be
 CC used to treat cancers such as melanomas, other skin cancers,
 CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
 CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
 CC growths. Enhancers of telomerase may be used to stimulate stem cell
 CC proliferation and differentiation (expansion of haematopoietic stem cells
 CC could be administered in the bone marrow transplant context). As well,
 CC many tissues have stem cells. Proliferation of these cells may be useful
 CC in wound healing, hair growth, treatment of disease such as Wilms'
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury

XX SQ Sequence 1132 AA;
 Query Match
 Best Local Similarity 99.9%; Score 5954; DB 2; Length 1132;
 Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPRAPCRVRSLRSHYREVLPATFVRRLLPGQWRVLVQRGDPAAFPALVAQCLVCVFW 60
 Db 1 MPRAPCRVRSLRSHYREVLPATFVRRLLPGQWRVLVQRGDPAAFPALVAQCLVCVFW 60
 QY 61 DARPPAAPSPQVSCIKELVARVLOLRCERGAKNVLAFFGALLDARGGPEAFTTSVR 120
 Db 61 DARPPAAPSPQVSCIKELVARVLOLRCERGAKNVLAFFGALLDARGGPEAFTTSVR 120
 QY 121 SYLNTVTDALRGSGAWGLLRLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 Db 121 SYLNTVTDALRGSGAWGLLRLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 QY 181 ATQARPPPHASGPRRRRLGCERAMNHSVREAGVPLGLPAPGARRRGGASASRLPLPKRPRR 240
 Db 181 ATQARPPPHASGPRRRRLGCERAMNHSVREAGVPLGLPAPGARRRGGASASRLPLPKRPRR 240
 QY 241 GAAPERTPVQGSWAHPGRTGPRSDRGFCVSPARPABEATSLGALSSTRHSHPSVG 300
 Db 241 GAAPERTPVQGSWAHPGRTGPRSDRGFCVSPARPABEATSLGALSSTRHSHPSVG 300
 QY 301 ROHAGPSTSRPPRMDTPCPVYAEKHFYSSGDKQLRPSFLSSLRPSLTGARRL 360
 Db 301 ROHAGPSTSRPPRMDTPCPVYAEKHFYSSGDKQLRPSFLSSLRPSLTGARRL 360
 QY 361 VETIFLGSRRPMPGTPRRRLPRLPQRYQMRPLFLELLGNHAQCYPYVLLKTHCPLRAAVT 420
 Db 361 VETIFLGSRRPMPGTPRRRLPRLPQRYQMRPLFLELLGNHAQCYPYVLLKTHCPLRAAVT 420
 QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYVGFVRACLRRLVPPGLWGS 480
 Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYVGFVRACLRRLVPPGLWGS 480
 QY 481 RHNERRRFLRNTKFTISLGHAKLSLQELTWKMSVYRDCAWLRSPGVGCPVAAEHLRBEI 540
 Db 481 RHNERRRFLRNTKFTISLGHAKLSLQELTWKMSVYRDCAWLRSPGVGCPVAAEHLRBEI 540
 QY 541 LAKFLHMLMSVYVVELLRSFFYVTTFTFQKNRLFYFRKSVMSKLSQSIGIRHQLKEVQLRE 600
 Db 541 LAKFLHMLMSVYVVELLRSFFYVTTFTFQKNRLFYFRKSVMSKLSQSIGIRHQLKEVQLRE 600
 QY 601 LSEAEVRQHREARPAALLTSRLRPIPKPDGLRPIVNM DYVVGARTPRRKRERLTSRVKA 660
 Db 601 LSEAEVRQHREARPAALLTSRLRPIPKPDGLRPIVNM DYVVGARTPRRKRERLTSRVKA 660
 QY 661 LFSVLNYERARRPGILGASVLGLDDIHRAWETFLVRVRAQDPPPELYFVKVDVTGAYDTI 720
 Db 661 LFSVLNYERARRPGILGASVLGLDDIHRAWETFLVRVRAQDPPPELYFVKVDVTGAYDTI 720
 QY 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
 Db 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
 QY 781 QETSPLRDADVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSVYVQCGIIPQGSILSTL 840
 Db 781 QETSPLRDADVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSVYVQCGIIPQGSILSTL 840
 QY 841 LCSLCYGDMEKMLFAGIRRDGLLRLVDDFLIVTFLHNTAKTFLRTLVRGPEYGCNVNL 900
 Db 841 LCSLCYGDMEKMLFAGIRRDGLLRLVDDFLIVTFLHNTAKTFLRTLVRGPEYGCNVNL 900
 QY 901 RKTVMNPFVEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 960
 Db 901 RKTVMNPFVEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 960
 QY 961 NRGFKAGNMRKLGVLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
 Db 961 NRGFKAGNMRKLGVLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020

Db 961 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLIQAYRFHACVQLP 1020
 QY 1021 FHQQWKNPTFPLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
 Db 1021 FHQQWKNPTFPLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
 QY 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
 Db 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132

RESULT 28
 AAY00638
 ID AAY00638 standard; protein; 1132 AA.
 XX AC AAY00638;
 XX DT 26-JUL-1999 (first entry)
 XX DE Truncated telomerase protein sequence.
 XX KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 XX OS Homo sapiens.
 OS Synthetic.
 XX OS WO9901560-A1.
 XX PN 14-JAN-1999.
 XX PD 01-JUL-1998; 98WO-US013835.
 XX PF 01-JUL-1997; 97US-0051410P.
 XX PR 21-JUL-1997; 97US-0053018P.
 XX PR 21-JUL-1997; 97US-0053329P.
 XX PR 04-AUG-1997; 97US-0054642P.
 XX PR 09-SEP-1997; 97US-0058287P.
 XX PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
 XX PI Kilian A, Bowtell D;
 XX WI WI; 1999-106060/09.
 XX DR N-PSDB; AAX18266.
 XX PT New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PT growth following injury or bone marrow transplantation.
 XX PS Claim 4; Fig 11f-i; 134pp; English.
 XX CC This sequence is a truncated human telomerase of the invention. Primers
 CC that amplify the telomerase coding sequence can be used in a method for
 CC diagnosing cancer in a patient. The telomerase can be used for detection,
 CC diagnosis and drug screening. Inhibitors of telomerase activity can be
 CC used to treat cancers such as melanomas, other skin cancers,
 CC neuroblastomas, breast carcinomas, colon carcinomas, leukemias,
 CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
 CC growths. Enhancers of telomerase may be used to stimulate stem cell
 CC proliferation and differentiation (expansion of haematopoietic stem cells
 CC could be administered in the bone marrow transplant context). As well,
 CC many tissues have stem cells. Proliferation of these cells may be useful
 CC in wound healing, hair growth, treatment of disease such as Wilm's
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury
 XX SQ Sequence 1132 AA;
 Query Match 99.9%; Score 5954; DB 2; Length 1132;
 Best Local Similarity 99.9%; Pred. No. 0;

	Matches 1131;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	MPRAPRCRAVRSLLRSHYREVLPLATEVRLRGLPGQWELVORGDPAAFRALVAOCLVCVPM	60						
Db	1	MPRAPRCRAVRSLLRSHYREVLPLATEVRLRGLPGQWELVORGDPAAFRALVAOCLVCVPM	60						
QY	61	DARPPPAAPSPFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDARGAGGPEAFTTSVR	120						
Db	61	DARPPPAAPSPFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDARGAGGPEAFTTSVR	120						
QY	121	SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA	180						
Db	121	SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA	180						
QY	181	ATQARPPPHASGPRRLRGCEANWHSVREAGVPLGLPAPGARRRGGGSASRSLPLPKPRR	240						
Db	181	ATQARPPPHASGPRRLRGCEANWHSVREAGVPLGLPAPGARRRGGGSASRSLPLPKPRR	240						
QY	241	GAAPERTPVGQSWAHPCGTRGSDRGFCVVSPPARPAEABEATSGALSGTRHSHPSVG	300						
Db	241	GAAPERTPVGQSWAHPCGTRGSDRGFCVVSPPARPAEABEATSGALSGTRHSHPSVG	300						
QY	301	ROHHAGPSTSRPRPMDTPCPVYAEKHFLYSSGDKQOLRPSFLLSSLRPSLTGARRL	360						
Db	301	ROHHAGPSTSRPRPMDTPCPVYAEKHFLYSSGDKQOLRPSFLLSSLRPSLTGARRL	360						
QY	361	VETIFLGSRPMPFGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT	420						
Db	361	VETIFLGSRPMPFGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT	420						
QY	421	PAAGVCAREKPOGSVAAPSEEDTPRLVOLLQHSFPWQYGVFVRACLRLVPPGLWGS	480						
Db	421	PAAGVCAREKPOGSVAAPSEEDTPRLVOLLQHSFPWQYGVFVRACLRLVPPGLWGS	480						
QY	481	RHNERFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVAAEHLREEI	540						
Db	481	RHNERFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVAAEHLREEI	540						
QY	541	LAKFLHWSVYVVELLSFFYVTTTFFQKNRLFYFKRSVMSKLSQIGIRQLKRVQLRE	600						
Db	541	LAKFLHWSVYVVELLSFFYVTTTFFQKNRLFYFKRSVMSKLSQIGIRQLKRVQLRE	600						
QY	601	LSEAEVRQHRARPALLTSRLRPIPKDGLRPIVNM DYVVGARTFREKRAERLTSRKA	660						
Db	601	LSEAEVRQHRARPALLTSRLRPIPKDGLRPIVNM DYVVGARTFREKRAERLTSRKA	660						
QY	661	LFSVLNVERARRPGLLGASVLGLDDIHRWRTFVLVRADQPPPELYFVKVDVTGADTI	720						
Db	661	LFSVLNVERARRPGLLGASVLGLDDIHRWRTFVLVRADQPPPELYFVKVDVTGADTI	720						
QY	721	PDRLTEVIASIIKPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLQPMRQFVAHL	780						
Db	721	PDRLTEVIASIIKPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLQPMRQFVAHL	780						
QY	781	QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGSKSVOCIGIPQGSILSTL	840						
Db	781	QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGSKSVOCIGIPQGSILSTL	840						
QY	841	LCSLCYGDMENKLPAGIRRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL	900						
Db	841	LCSLCYGDMENKLPAGIRRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL	900						
QY	901	RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEQSDYSYARTSIRSLTF	960						
Db	901	RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEQSDYSYARTSIRSLTF	960						
QY	961	NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLIQAYRFHACVQLP	1020						
Db	961	NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLIQAYRFHACVQLP	1020						
QY	1021	FHQQWKNPTFPLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL	1080						
Db	1021	FHQQWKNPTFPLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL	1080						

QY 1081 KLTHRVTVYVPLGSLRTAQTLQSLRKLPGTTLTALAAANPALPDSDFKTILD 1132
 DB 1081 KLTHRVTVYVPLGSLRTAQTLQSLRKLPGTTLTALAAANPALPDSDFKTILD 1132

RESULT 29
 AAY28401
 ID AAY28401 standard; protein; 1132 AA.
 XX AAY28401;
 XX 22-SEP-1999 (first entry)
 XX Human EST2 protein sequence.
 DE EST2: proliferative capacity; cellular proliferation; decubitus ulcer;
 KW telomerase-activating therapeutic agent; cell life-span extension;
 KW venous disease; venous stasis ulcer; excessive pressure; arterial ulcer;
 KW tissue regeneration enhancer; atherosclerosis; therapy.
 XX Homo sapiens.
 OS
 XX
 PN W09935243-A2.
 XX
 PD 15-JUL-1999.
 XX
 PF 12-JAN-1999; 99WO-US000682.
 XX
 PR 12-JAN-1998; 98US-0071220P.
 PR 13-JAN-1998; 98US-0071455P.
 PR 21-APR-1998; 98US-00063657.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 XX
 XX Hannon GJ, Wang J, Beach DH;
 XX N-PSDB; AAX89424.
 DR WPI; 1999-444196/37.
 XX
 PT Increasing proliferative capacity of cells useful for promoting wound
 healing.
 XX
 PS Claim 3; Page 65-70; 73pp; English.
 XX
 CC This sequence is the human EST2 protein, and can be used in the method of
 the invention. The method is for increasing the proliferative capacity of
 cells, and comprises contacting the cell with a telomerase-activating
 therapeutic agent (TATA). The method can be used for extending the life-
 span of cells, e.g. by increasing the number of mitotic divisions. They
 can be used for e.g. the extension of skin or other epithelial cell
 cultures or grafts, the expansion of mesenchymal cell cultures or grafts,
 and the expansion of chondrocyte or osteocyte cultures or grafts. They
 can be applied to e.g. neuronal, haematopoietic, epithelial, pancreatic,
 hepatic, chondrocytic and osteocytic stem and progenitor cells in in
 vivo, in vitro or ex vivo protocols. The methods can be used for
 promoting the healing of wounds resulting from e.g. surgery, burns,
 inflammation or irritation or ulcers resulting from e.g. venous disease
 (venous stasis ulcers), excessive pressure (decubitus ulcers) or arterial
 ulcers. They can also be used to enhance tissue regeneration processes,
 e.g. of the skin, hair and/or fingernails. They can also be used for
 treating age-related conditions, e.g. atrophy of the skin through loss of
 extracellular matrix homeostasis in dermal fibroblasts, age-related
 macular degeneration caused by accumulation of lipofuscin and
 downregulation of a neuronal survival factor in retinal pigmented
 epithelial (RPE) cells, and atherosclerosis caused by loss of
 proliferative capacity and overexpression of hypertensive and thrombotic
 factors in endothelial cells. Expanded populations of normal or
 genetically engineered rejuvenated cells could be used for autologous or
 allogeneic cell and gene therapy. They can also be used for prolonging
 the lifespan of a culture of normal cells or tissue being used to secrete
 therapeutic or other commercially significant proteins and products

SQ Sequence 1132 AA;		Query Match	99.9%; Score 5954; DB 2; Length 1132;
		Best Local Similarity	99.9%; Pred. No. 0;
		Matches 1131; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLLGPGQWRLLVQRGDP
DB	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLLGPGQWRLLVQRGDP
QY	61	DARPPAPSPROVSCUKELVARVL	ORLCERGAKNVLAFFGALLDARGG
DB	61	DARPPAPSPROVSCUKELVARVL	ORLCERGAKNVLAFFGALLDARGG
QY	121	SYLPTNTVDALRGSGAWGLLRL	RVGDDVLVHLLARCALFVLVAPSC
DB	121	SYLPTNTVDALRGSGAWGLLRL	RVGDDVLVHLLARCALFVLVAPSC
QY	181	ATQARPPPHASGPRRLRGCE	RAMNHSVREAGVPLGAPGARRRG
DB	181	ATQARPPPHASGPRRLRGCE	RAMNHSVREAGVPLGAPGARRRG
QY	241	GAAPERTPVQSGSWAHPCGR	TRGSDRGFCVSPARPAEATSLE
DB	241	GAAPERTPVQSGSWAHPCGR	TRGSDRGFCVSPARPAEATSLE
QY	301	ROHAGPPSTSRPPRWDTPCP	PVYAEYKHYLYSSGDKQLRPS
DB	301	ROHAGPPSTSRPPRWDTPCP	PVYAEYKHYLYSSGDKQLRPS
QY	361	VETIFLGSRPMMCTPRRLP	RLPQRYQMRLFLLELGNHAQCP
DB	361	VETIFLGSRPMMCTPRRLP	RLPQRYQMRLFLLELGNHAQCP
QY	421	PAAGVCAREKPGQSVAAPEE	EDTPRLVQLLRHSSPWQYVGF
DB	421	PAAGVCAREKPGQSVAAPEE	EDTPRLVQLLRHSSPWQYVGF
QY	481	RHNERRFLRNTKFKISLGH	AKAKLSLOELTWKMSVRDCAW
DB	481	RHNERRFLRNTKFKISLGH	AKAKLSLOELTWKMSVRDCAW
QY	541	LAKFLHLMSSVYVVELLS	EFYVTTETTFQKNRLFYRKS
DB	541	LAKFLHLMSSVYVVELLS	EFYVTTETTFQKNRLFYRKS
QY	601	LSEAEVQHRERAPALLTS	RLRFTPKDGLRPIVNMVVG
DB	601	LSEAEVQHRERAPALLTS	RLRFTPKDGLRPIVNMVVG
QY	661	LFSVLNYERARRPCLLG	ASVLGLDDIHRWRTFVLVRAQ
DB	661	LFSVLNYERARRPCLLG	ASVLGLDDIHRWRTFVLVRAQ
QY	721	PQDRLTEVIASIIKPQNT	YCVRRYAVVQKAHGHVRKA
DB	721	PQDRLTEVIASIIKPQNT	YCVRRYAVVQKAHGHVRKA
QY	781	QETSPLRDADVIEOSS	SINERASSGLFDVFLRFMCH
DB	781	QETSPLRDADVIEOSS	SINERASSGLFDVFLRFMCH
QY	841	LCSCICYGDMENKLFAG	TRRDLGLRLVDDFLVTPH
DB	841	LCSCICYGDMENKLFAG	TRRDLGLRLVDDFLVTPH
QY	901	RKTVMNPFVEDEALG	TAFTVQMPAHGLFPWCG
DB	901	RKTVMNPFVEDEALG	TAFTVQMPAHGLFPWCG
QY	961	NRGFKAGNNRRKLF	GVRLKCHSLFLDLQVNS
DB	961	NRGFKAGNNRRKLF	GVRLKCHSLFLDLQVNS

QY 1021 FHQVWKNPTFLRVISDTASLCYSILKAKVAGMSLGAKGAGPLPSEAVOWLCHQAPLL 1080
Db 1021 FHQVWKNPTFLRVISDTASLCYSILKAKVAGMSLGAKGAGPLPSEAVOWLCHQAPLL 1080
QY 1081 KLTRHRVTYVPLGLSLRTAQQLSRKLPQTTLTALAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLGLSLRTAQQLSRKLPQTTLTALAAANPALPSDFKTILD 1132

RESULT 30

AA96566
ID AA96566 standard; protein; 1132 AA.

XX AA96566;

DT 12-SEP-2000 (first entry)

XX hEST2, a human telomerase catalytic subunit homologue.

XX hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
KW retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
KW proliferation; immortal; tumour therapy; macular degeneration;
KW activator. INK4.

XX Homo sapiens.

XX WO200031238-A2.

XX 02-JUN-2000.

XX 24-NOV-1999; 99WO-US027907.

XX 25-NOV-1998; 98US-0109891P.

PR 17-FEB-1999; 98US-0120549P.

XX (GENE-) GENETICA INC.

XX Hannon GJ, Beach DH;

XX WPI; 2000-400055/34.

DR N-PSDB; AAA29388.

XX New method for increasing the proliferative capacity of cell lines
PT comprises administering agents reversibly activating telomerase activity
PT and reversibly inactivating Rb/INK4 and/or p53 pathways useful in
PT treating age related diseases.

XX Claim 14; Page 116-119; 123pp; English.

XX This protein, designated hEST2, is a human telomerase catalytic subunit
CC homologue of yeast EST2p and Euplotes p123. hEST2 is a member of the
CC reverse transcriptase family of enzymes. The invention concerns methods
CC and reagents for extending the life-span, e.g. the number of mitotic
CC divisions, of a cell. The method relies on activation of a telomerase
CC activity and inhibition of one or both of a retinoblastoma (Rb)/INK4
CC pathway or a p53 pathway. Phosphorylation of Rb by cyclin-dependent
CC kinases, cdk4 and cdk6, releases the cells into the division cycle.
CC Binding of INK4 family members, e.g. the tumour suppressor p16INK4a,
CC inhibits kinase activity and results in growth arrest. Rb inactivators
CC can selectively and reversibly inactivate an Rb/INK4 pathway, especially
CC an Rb/p16INK4a pathway. The oncoprotein MDM2 is a cellular inhibitor of
CC Rb/E2F function and the p53 tumour suppressor and can also be used in the
CC methods. Other molecules which can be used include cdk4 or cdk6 mutants.
CC In particular, a cdk4 mutant is one which differs from at one or more of
CC residues K22, R24, H95 and/or D97. Additional constructs include a
CC papilloma virus E7 protein, or other viral oncoprotein which bypasses Rb
CC and/or p53. Antisense constructs of the Rb and p16INK4a genes may also be
CC used. The methods are useful for increasing the proliferative capacity of
CC cells. The cells are subsequently of use in pharmaceutical and cosmetic
CC preparations used to treat conditions related to (premature) ageing, e.g.
CC macular degeneration and arteriosclerosis. The cells can also be used to
CC replace tumour cell lines in vitro and for studies on biochemical and

CC physiological aspects of growth and differentiation. Long lived
CC (immortal) cells could also be of use in the production of normal or
CC genetically engineered biotechnology products

SQ Sequence 1132 AA;

Query Match 99.9%; Score 5954; DB 3; Length 1132;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLPGOGWRLVORGDDPAAAFALVAQCILVCVPW 60

Db 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLPGOGWRLVORGDDPAAAFALVAQCILVCVPW 60

QY 61 DARPPPAAPSFQVSCCLKELVARVQLRCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

Db 61 DARPPPAAPSFQVSCCLKELVARVQLRCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

QY 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180

Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180

QY 181 ATQARPPPHASGPRRLRGCCERAWNHSVREAGVPLGLPAGARRRGGSASRLPLPKPRR 240

Db 181 ATQARPPPHASGPRRLRGCCERAWNHSVREAGVPLGLPAGARRRGGSASRLPLPKPRR 240

QY 241 GAAPEPERTVGGGSAHAPGRTGRGSDRGFCVVSAPARPAEATSELEGALSSTRHSHPVG 300

Db 241 GAAPEPERTVGGGSAHAPGRTGRGSDRGFCVVSAPARPAEATSELEGALSSTRHSHPVG 300

QY 301 ROHHAGPSTSRPPRWDTPCPVYATKIFLVSDDKEQLRPSFLSSRLPSLTGARRL 360

Db 301 ROHHAGPSTSRPPRWDTPCPVYATKIFLVSDDKEQLRPSFLSSRLPSLTGARRL 360

QY 361 VETIFLGSRRPMPGTGTPRLPRLPQRYWQMPPLFLELLGNHAQCPYGVLLKTHCPLRAVT 420

Db 361 VETIFLGSRRPMPGTGTPRLPRLPQRYWQMPPLFLELLGNHAQCPYGVLLKTHCPLRAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVLQRLHQHSSPWQYGVFVRACLRLVPPGLWGS 480

Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVLQRLHQHSSPWQYGVFVRACLRLVPPGLWGS 480

QY 481 RHNERFLRNTKFIKSLGKIAKLSQLBLTWKMSVRDCAWLRSPGVCVCPAAEHLRBEI 540

Db 481 RHNERFLRNTKFIKSLGKIAKLSQLBLTWKMSVRDCAWLRSPGVCVCPAAEHLRBEI 540

QY 541 LAKFLHLMMSVYVVELLRSFFYVTTTFOKNRLFYFKSVMSKLSQSIGIRQHLKRVQURE 600

Db 541 LAKFLHLMMSVYVVELLRSFFYVTTTFOKNRLFYFKSVMSKLSQSIGIRQHLKRVQURE 600

QY 601 LSAEVRQHRERAPALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFREKRAERLTSRKA 660

Db 601 LSAEVRQHRERAPALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFREKRAERLTSRKA 660

QY 661 LFSVLNVERARRPGLLGASVLGLDDIHRNWRFLVLRVRAQDPPPELFPVKVDVTGADTI 720

Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRNWRFLVLRVRAQDPPPELFPVKVDVTGADTI 720

QY 721 PQRLTEVIASIIKPNQTYCVRYAVVQKAAGHVRKAFKSHVSTLTDLPYMQFVAHL 780

Db 721 PQRLTEVIASIIKPNQTYCVRYAVVQKAAGHVRKAFKSHVSTLTDLPYMQFVAHL 780

QY 781 QETSPLRDADVIFQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCGIPQGSILSTL 840

Db 781 QETSPLRDADVIFQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCGIPQGSILSTL 840

QY 841 LCSLCYGDMEKLPAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTVLRGPEYGCVVNL 900

Db 841 LCSLCYGDMEKLPAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTVLRGPEYGCVVNL 900

QY 901 RKTWNFPVDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVDSDYSYARTSIRASLTF 960

Db 901 RKTWNFPVDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVDSDYSYARTSIRASLTF 960

```
QY 961 NRGFKAGNRNRKLFVGLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
DB 961 NRGFKAGNRNRKLFVGLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
QY 1021 FHQQVWKNPTFFLRVLTSDTASLCYSTLKAKNAGMSLGAKGAGPLPSEAVOMLCHOAFLL 1080
DB 1021 FHQQVWKNPTFFLRVLTSDTASLCYSTLKAKNAGMSLGAKGAGPLPSEAVOMLCHOAFLL 1080
QY 1081 KLTHRVTVVPLLSRLTAQTSLSKLPCTTLTALAAANPALPSDFKTILD 1132
DB 1081 KLTHRVTVVPLLSRLTAQTSLSKLPCTTLTALAAANPALPSDFKTILD 1132

RESULT 31
ID ADC47061 standard; protein; 1132 AA.
XX ADC47061;
AC ADC47061;
DT 18-DEC-2003 (first entry)
DE Human TERT amino acid sequence #SEQ ID 2.
KW Human; TERT; telomerase; antibody; reverse transcriptase; tumour;
KW autoimmune disease; liver cancer.
OS Homo sapiens.
XX WO2003054545-A1.
XX 03-JUL-2003.
XX 19-DEC-2002; 2002WO-JP013310.
XX 21-DEC-2001; 2001JP-00390050.
XX (MITS-) MITSUBISHI KAGAKU MEDICAL INC.
XX (MURA/) MURAKAMI S.
XX (KANE/) KANEKO S.
XX Murakami S, Kaneko S, Masutomi K;
XX WPI; 2003-569289/53.
XX N-PSDB; ADC47060.
XX Detecting anti-telomerase antibody for detecting tumors and autoimmune
XX disease.
XX Example Examples; Page 36-41; 45pp; Japanese.
XX The invention relates to a method for detecting an anti-telomerase
XX antibody. The method of the invention comprises reacting telomerase
XX producing protein and a fragment or complex of template RNA with anti-
XX telomerase antibody in a sample, and analysing the product. The
XX telomerase producing protein is preferably telomerase reverse
XX transcriptase, and the analysis method is preferably western blot. The
XX method can be used to detect for tumours and autoimmune disease. The
XX method can also be used for detecting liver cancer. The current
XX sequence represents the human TERT amino acid sequence.
XX Sequence 1132 AA;
XX Query Match 99.9%; Score 5954; DB 7; Length 1132;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSLLSHREVLPATFVRRLGPGQWRVLVQRGDPAAFRALVAQCLVCPW 60
DB 1 MPRAPRCRAVRSLLSHREVLPATFVRRLGPGQWRVLVQRGDPAAFRALVAQCLVCPW 60
QY 61 DARPPPAAPSPFQVSLKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
DB 61 DARPPPAAPSPFQVSLKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
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DB 61 DARPPPAAPSPFQVSLKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGAWGLLRRVGDVLLVHLARCALFVLVAPSCAYQVCGPPYQLCA 180
DB 121 SYLPTNTVDALRGSGAWGLLRRVGDVLLVHLARCALFVLVAPSCAYQVCGPPYQLCA 180
QY 181 ATQARPPPHASGRRRLGCERAWNHSVREAGVPLGLPAPGARRRRGSGASRSRLPKRPRR 240
DB 181 ATQARPPPHASGRRRLGCERAWNHSVREAGVPLGLPAPGARRRRGSGASRSRLPKRPRR 240
QY 241 GAAPPEPTPVCGSGWAHPGTRGSPDRGFCVSPARPAEATSLGEGALSGTRHSHPSVG 300
DB 241 GAAPPEPTPVCGSGWAHPGTRGSPDRGFCVSPARPAEATSLGEGALSGTRHSHPSVG 300
QY 301 ROHAGAPSTSRPPRMDTPCPVYAEKHFYSSGDKQLRPSFLLSSLRPSLTGARRL 360
DB 301 ROHAGAPSTSRPPRMDTPCPVYAEKHFYSSGDKQLRPSFLLSSLRPSLTGARRL 360
QY 361 VETIFLGSRRPMMPTPRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRRPMMPTPRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGSGVAAPPEEDTDRRLVOLLROHSSPWQVYGFVRACLRLVPLGWS 480
DB 421 PAAGVCAREKPGSGVAAPPEEDTDRRLVOLLROHSSPWQVYGFVRACLRLVPLGWS 480
QY 481 RHNERRFLRNTKKTIFSLGKHAKLSLOELTWMSVRDCAWLRSPGVGCVPAEHLRBEI 540
DB 481 RHNERRFLRNTKKTIFSLGKHAKLSLOELTWMSVRDCAWLRSPGVGCVPAEHLRBEI 540
QY 541 LAKFLHLMWSVYVVELLSFFYVTTTFOKNRLFYRKSVMKLSQSIGIRQHLKRVQURE 600
DB 541 LAKFLHLMWSVYVVELLSFFYVTTTFOKNRLFYRKSVMKLSQSIGIRQHLKRVQURE 600
QY 601 LSEAEVRQREARPAALLTSRLRFTPKDGLRPIVNMVYVVGARTFRREKRAERLTSRKA 660
DB 601 LSEAEVRQREARPAALLTSRLRFTPKDGLRPIVNMVYVVGARTFRREKRAERLTSRKA 660
QY 661 LFSVLNVERARRPGLLGASVLGLDDIHRAWTFVLRVRAQDPPPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNVERARRPGLLGASVLGLDDIHRAWTFVLRVRAQDPPPPPELYFVKVDVTGAYDTI 720
QY 721 PDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVKAFKSHVSTLTDLPQYMRQFVAHL 780
DB 721 PDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVKAFKSHVSTLTDLPQYMRQFVAHL 780
QY 781 QETSPLRDAVIEQSSSLNEASSGLFDVFLRFMCHHAVRIKGSYVQCGIPQGSILSTL 840
DB 781 QETSPLRDAVIEQSSSLNEASSGLFDVFLRFMCHHAVRIKGSYVQCGIPQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLLVTPHLTHAKTFLTLVRGVPEYCVNVL 900
DB 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLLVTPHLTHAKTFLTLVRGVPEYCVNVL 900
QY 901 RKTVNVFEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 960
DB 901 RKTVNVFEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 960
QY 961 NRGFKAGNRNRKLFVGLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
DB 961 NRGFKAGNRNRKLFVGLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
QY 1021 FHQQVWKNPTFFLRVLTSDTASLCYSTLKAKNAGMSLGAKGAGPLPSEAVOMLCHOAFLL 1080
DB 1021 FHQQVWKNPTFFLRVLTSDTASLCYSTLKAKNAGMSLGAKGAGPLPSEAVOMLCHOAFLL 1080
QY 1081 KLTHRVTVVPLLSRLTAQTSLSKLPCTTLTALAAANPALPSDFKTILD 1132
DB 1081 KLTHRVTVVPLLSRLTAQTSLSKLPCTTLTALAAANPALPSDFKTILD 1132
```

ID ADE40482 standard; protein; 1132 AA.
XX
AC ADE40482;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human telomerase reverse transcriptase (hTERT).
XX
KW Immortal porcine cell; telomerase reverse transcriptase; epithelial cell;
KW uterine endometrial glandular tissue; virus quantification;
KW virus production; porcine reproductive and respiratory syndrome virus;
KW PRRSV; toxicity evaluation; human; hTERT; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003077853-A2.
XX
PD 25-SEP-2003.
XX
PF 11-MAR-2003; 2003WO-US007526.
XX
PR 11-MAR-2002; 2002US-0363129P.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Farris JA, Foster DN, O'grady SM;
XX
DR WPI; 2003-779075/73.
DR N-PSDB; ADE40481.
XX
PT New immortal porcine cell comprising a polynucleotide encoding an
PT exogenous telomerase reverse transcriptase polypeptide, useful for
PT measuring the amount of virus in a sample or for evaluating toxicity of a
PT compound.
XX
PS Claim 4; SEQ ID NO 2; 42pp; English.
XX
CC The invention relates to immortal porcine cells comprising a
CC polynucleotide encoding an exogenous telomerase reverse transcriptase
CC (TERT). The invention also encompasses the method of making immortal
CC porcine cells, and the use of the immortal porcine cells for measuring
CC the amount of virus in a sample, producing a virus, and evaluating the
CC toxicity of a compound. The cells of the invention may be diploid or
CC aneuploid, and may be an epithelial cell obtained from uterine
CC endometrial glandular tissue. The exogenous telomerase reverse
CC transcriptase expressed by the cells of the invention is preferably human
CC telomerase reverse transcriptase (ADE40482). The immortal porcine cells
CC are useful for measuring an amount of a virus in a sample, producing a
CC virus (especially porcine reproductive and respiratory syndrome virus
CC (PRRSV)), or for evaluating toxicity of a compound. The present sequence
CC represents human telomerase reverse transcriptase (hTERT), which is
CC claimed for use in the immortal cells of the invention.
XX
SQ Sequence 1132 AA;

Query Match 99.9%; Score 5954; DB 7; Length 1132;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPCRAVRLSLRSHREVLPVPLATFVRRLLGPGQWRVLVQRGDPAAPRALVAQCILVCVPW 60
DB 1 MPRAPCRAVRLSLRSHREVLPVPLATFVRRLLGPGQWRVLVQRGDPAAPRALVAQCILVCVPW 60

QY 61 DARPPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDGGAGGPPPEAFTTSVR 120
DB 61 DARPPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDGGAGGPPPEAFTTSVR 120

QY 121 SYLPNTVTDALRGSGAWGLLRVGDVVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPNTVTDALRGSGAWGLLRVGDVVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLLPLPKRPRR 240
XX

DB 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLLPLPKRPRR 240
QY 241 GAAPEPERTVPGQGSWAHPGRTGRPSDRGFCVVPSPAPAEATSLLEGALSGTRHSHPSVG 300
DB 241 GAAPEPERTVPGQGSWAHPGRTGRPSDRGFCVVPSPAPAEATSLLEGALSGTRHSHPSVG 300
QY 301 ROHHAGPSTSRPRPMDTCCPPVYAEKHFLLVSSGDKQELRPSFLSSLRPSLTGARRL 360
DB 301 ROHHAGPSTSRPRPMDTCCPPVYAEKHFLLVSSGDKQELRPSFLSSLRPSLTGARRL 360
QY 361 VETIFGSRPWPCTPRRLPRLPQRYWQMPPLFELIGNHAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFGSRPWPCTPRRLPRLPQRYWQMPPLFELIGNHAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKXPOGSVAAPPEEDTDPRLVQLLRQHSPPWQYGVFVACLRRLVPPGLWGS 480
DB 421 PAAGVCAREKXPOGSVAAPPEEDTDPRLVQLLRQHSPPWQYGVFVACLRRLVPPGLWGS 480
QY 481 RHNERFLRNTKKFISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
DB 481 RHNERFLRNTKKFISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
QY 541 LAKFLHLMMSVYVVELLRSPFFYVTTTFOKNRLFYFRKSVMSKLSQSIGIRQHLKRVOLRE 600
DB 541 LAKFLHLMMSVYVVELLRSPFFYVTTTFOKNRLFYFRKSVMSKLSQSIGIRQHLKRVOLRE 600
QY 601 LSEAEVQHQREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVQHQREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNVERARRPGLIGASVLGLDDIHRARWTFVLVRAQDPPPELVFKVDVDTGAYDTI 720
DB 661 LFSVLNVERARRPGLIGASVLGLDDIHRARWTFVLVRAQDPPPELVFKVDVDTGAYDTI 720
QY 721 PQDLTEVIAIIKPONTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMQFVAHL 780
DB 721 PQDLTEVIAIIKPONTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMQFVAHL 780
QY 781 QETSPLRDADVIBQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPOGSIILSTL 840
DB 781 QETSPLRDADVIBQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPOGSIILSTL 840
QY 841 LCSLCYGDMMENKLPAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVEYGCVVNL 900
DB 841 LCSLCYGDMMENKLPAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVEYGCVVNL 900
QY 901 RKTVMNPPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSIRASLTF 960
DB 901 RKTVMNPPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSIRASLTF 960
QY 961 NRGFKAGRNRRKLFVLRLLKCHSLFLDLQVNSLQTVCTNLYKILLQAVRFHACVILQLP 1020
DB 961 NRGFKAGRNRRKLFVLRLLKCHSLFLDLQVNSLQTVCTNLYKILLQAVRFHACVILQLP 1020
QY 1021 FHOQVKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAWMLCHOAFLL 1080
DB 1021 FHOQVKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAWMLCHOAFLL 1080
QY 1081 KLTRHRTVYVPLLGSLRTAQTLQSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
DB 1081 KLTRHRTVYVPLLGSLRTAQTLQSRKLPGLTTLTALEAAANPALPSDFKTILD 1132

RESULT 33
AAW56113
ID AAW56113 standard; protein; 1132 AA.
XX
AC AAW56113;
XX
DT 13-AUG-1998 (first entry)
XX
DE Human telomerase reverse transcriptase protein refined sequence.
XX

KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.
XX Homo sapiens.
XX GB23117891-A.
XX 08-APR-1998.
XX 01-OCT-1997; 97GB-00020890.
XX 01-OCT-1996; 96US-00724643.
XX 18-APR-1997; 97US-00844419.
XX 25-APR-1997; 97US-00846017.
XX 06-MAY-1997; 97US-00851843.
XX 09-MAY-1997; 97US-00854050.
XX 14-AUG-1997; 97US-00911312.
XX 14-AUG-1997; 97US-00912951.
XX 14-AUG-1997; 97US-00915503.
XX (GERO-) GERON CORP.
XX (UYTE-) UNIV TECHNOLOGY CORP.
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB; Andrews WH;
XX WPI; 1998-171633/16.
XX N-PSDB; AA22428.
XX Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.
XX Example 1; Fig 74; 387pp; English.
XX The present sequence represents human telomerase reverse transcriptase (hTERT), which is a ribonucleoprotein. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTERT, by detecting the change in hTERT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTERT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTERT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTERT and the polynucleotide encoding hTERT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of hTERT can also be used in the new methods
SQ Sequence 1132 AA;
Query Match 99.8%; Score 5952; DB 2; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRLSLRSHYREVLPATFVRRLPQCGWRLVQRGDPAAFRALVAQCILVCPW 60
DB 1 MPRAPRCRAVRLSLRSHYREVLPATFVRRLPQCGWRLVQRGDPAAFRALVAQCILVCPW 60
QY 61 DARPPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDGAAGGPEAFTTSVR 120
DB 61 DARPPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDGAAGGPEAFTTSVR 120
QY 121 SYLPTNTVTDALRGSGAWGILLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPTNTVTDALRGSGAWGILLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRRRLGCERAWNHSVREAGVPLGPAGARRRGGSSASRSLPLPKRPRR 240
DB ATQARPPPHASGPRRRRLGCERAWNHSVREAGVPLGPAGARRRGGSSASRSLPLPKRPRR 240
QY 241 GAAPERTPVGQGSWAHPGTRGSDRGFCVSPARPAEATSLLEGALSCTRHHSPSVG 300
DB GAAPERTPVGQGSWAHPGTRGSDRGFCVSPARPAEATSLLEGALSCTRHHSPSVG 300
QY 301 RQHAGPPESTSRPPRPMDTPCPVVAETKFLYSSGDEQRLRPSFLLSLSPSLTGARRL 360
DB RQHAGPPESTSRPPRPMDTPCPVVAETKFLYSSGDEQRLRPSFLLSLSPSLTGARRL 360
QY 361 VETIFLGSRPWMPGTPRRRLPRLPORYQWMDPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
DB VETIFLGSRPWMPGTPRRRLPRLPORYQWMDPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPOGSAVAPEEEDTPRRLVOLLROHSSPMQVYGFVACLRRLVPPGLWGS 480
DB PAAGVCAREKPOGSAVAPEEEDTPRRLVOLLROHSSPMQVYGFVACLRRLVPPGLWGS 480
QY 481 RHNERRFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLRBEI 540
DB RHNERRFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLRBEI 540
QY 541 LAKFLHLMMSVYVVELLRSFFVTETTPQKNRLFYRKSVMKLSQSIGIROHLKRVQLRE 600
DB LAKFLHLMMSVYVVELLRSFFVTETTPQKNRLFYRKSVMKLSQSIGIROHLKRVQLRE 600
QY 601 LSEAEVRQHREARPAALITSLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
DB LSEAEVRQHREARPAALITSLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNVERARRPGLLGASVLGLDDIHRAMTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
DB LFSVLNVERARRPGLLGASVLGLDDIHRAMTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPQNTYCVRRYAVQKAAGHVHRKAFKSHVSTLTDLQPMRQFVAHL 780
DB PODRLTEVIASIIKPQNTYCVRRYAVQKAAGHVHRKAFKSHVSTLTDLQPMRQFVAHL 780
QY 781 QETSPLRDVAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSVYVQCGIPQGSILSTL 840
DB QETSPLRDVAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSVYVQCGIPQGSILSTL 840
QY 841 LCSLCYGDMEKNLPAFIRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGPEYCVVNL 900
DB LCSLCYGDMEKNLPAFIRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGPEYCVVNL 900
QY 901 RKTVVPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSDYSSYARTSIRASLTF 960
DB RKTVVPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSDYSSYARTSIRASLTF 960
QY 961 NRGFKAGNMRRKLFGLVRLKCHSLFDLQVNSLQTVCTNIIKILLQAYRPHACVQLQP 1020
DB NRGFKAGNMRRKLFGLVRLKCHSLFDLQVNSLQTVCTNIIKILLQAYRPHACVQLQP 1020
QY 1021 FHOQWKNPTFFLVRVSDTASLCYSILKAKNAGSLGAKGAGPLPSSAVOWLCHQAFLL 1080
DB FHOQWKNPTFFLVRVSDTASLCYSILKAKNAGSLGAKGAGPLPSSAVOWLCHQAFLL 1080
QY 1081 KLTRHRTVYVPLLSGLRSLTAQTLRSLKPLGTTTLTALEAAANPALPSDFKTIID 1132
DB KLTRHRTVYVPLLSGLRSLTAQTLRSLKPLGTTTLTALEAAANPALPSDFKTIID 1132
RESULT 34
RAY00647
ID RAY00647 standard; protein; 1166 AA.
XX RAY00647;
XX 26-JUL-1999 (first entry)
XX

DE	Telomerase (ver. 2) protein sequence.	
XX		
KW	Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;	Db
KW	neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;	Qy
KW	smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;	Db
KW	stem cell differentiation; organ regeneration; organ differentiation.	Qy
XX		
OS	Homo sapiens.	Db
OS	Synthetic.	Qy
XX		
PN	WO9901560-A1.	Db
XX		
PD	14-JAN-1999.	Qy
XX		
PF	01-JUL-1998; 98WO-US013835.	Db
XX		
PR	01-JUL-1997; 97US-0051410P.	Qy
PR	21-JUL-1997; 97US-0053018P.	Db
PR	21-JUL-1997; 97US-0053329P.	Qy
PR	04-AUG-1997; 97US-0054642P.	Db
PR	09-SEP-1997; 97US-0056287P.	Qy
XX		
PA	(CAMB-) CAMBIA BIOSYSTEMS LLC.	Db
XX		
PI	Kilian A, Bowtell D;	Qy
XX		
DR	WPI; 1999-106060/09.	Db
XX	N-PSDB; AAX18275.	Qy
XX		
PT	New isolated vertebrate telomerase genes - used to develop products for	Db
PT	treating cancers or for organ regeneration, nerve cell or brain cell	Qy
PT	growth following injury or bone marrow transplantation.	Db
XX		
PS	Claim 4; Fig 11z-ac; 134pp; English.	Qy
XX		
CC	This sequence is a truncated human telomerase of the invention. Primers	Db
CC	that amplify the telomerase coding sequence can be used in a method for	Qy
CC	diagnosing cancer in a patient. The telomerase can be used for detection,	Db
CC	diagnosis and drug screening. Inhibitors of telomerase activity can be	Qy
CC	used to treat cancers such as melanomas, other skin cancers,	Db
CC	neuroblastomas, breast carcinomas, colon carcinomas, leukemias,	Qy
CC	lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin	Db
CC	growths. Enhancers of telomerase may be used to stimulate stem cell	Qy
CC	proliferation and differentiation (expansion of haematopoietic stem cells	Db
CC	could be administered in the bone marrow transplant context). As well,	Qy
CC	many tissues have stem cells. Proliferation of these cells may be useful	Db
CC	in wound healing, hair growth, treatment of disease such as Wilm's	Qy
CC	tumour, organ regeneration or differentiation after injury or diseases,	Db
CC	nerve cell or brain cell growth following injury	Qy
XX		
SQ	Sequence 1166 AA;	Db
	Query Match 99.4%; Score 5927; DB 2; Length 1166;	Qy
	Best Local Similarity 97.0%; Pred. No. 0;	Db
	Matches 1131; Conservative 0; Mismatches 1; Indels 34; Gaps 1;	Qy
Qy	1 MPRAPRCRAVRLSHRYREVLPVPLATFVRRLGPGQWRVLVQRGDPAAPALVAQCLVCPW 60	Db
Db	1 MPRAPRCRAVRLSHRYREVLPVPLATFVRRLGPGQWRVLVQRGDPAAPALVAQCLVCPW 60	Qy
Qy	61 DARPPPAAPSPROV-----SCLKELVARVLQ 86	Db
Db	61 DARPPPAAPSPROVGLPGVRLGLRAAGNQRUAESSAGSGRPPRSCUKELVARVLQ 120	Qy
Qy	87 RLCERGAKNVLAFGFALLDARGGPPPEAFTTSVRSLPNTVTDALRGSGAWGLLRRVGD 146	Db
Db	121 RLCERGAKNVLAFGFALLDARGGPPPEAFTTSVRSLPNTVTDALRGSGAWGLLRRVGD 180	Qy
Qy	147 DVLVHLLARCALFVLVAPSCAYQVCGPPLYQIGAATQARPPPHASGPRRLGCRANWHS 206	Db
Db	181 DVLVHLLARCALFVLVAPSCAYQVCGPPLYQIGAATQARPPPHASGPRRLGCRANWHS 240	Qy
Qy	207 VREAGVPLGLPAPGARRRGGASRSPLPKPRRGAAPERTPVGQGSWAHPGRTGRPS 266	Db

RESULT 35
AAW56101
ID AAW56101 standard; protein; 1405 AA.
XX
AC AAW56101;
XX
DT 13-AUG-1998 (first entry)
XX
DE Enhanced green fluorescent protein and hTERT fusion protein.

XX Human; telomerase reverse transcriptase; hTERT; TERT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein.

XX Synthetic.
OS Homo sapiens.

XX Key Location/Qualifiers
FH Region 1..250
FT /note= "enhanced green fluorescent protein fragment"
FT Region 276..1405
FT /note= "hTERT protein fragment"

XX GB2317891-A.

PN 08-APR-1998.

PD 01-OCT-1997; 97GB-00020890.

PF 01-OCT-1996; 96US-00724643.

PR 18-APR-1997; 97US-00844419.

PR 25-APR-1997; 97US-00846017.

PR 06-MAY-1997; 97US-00851843.

PR 09-MAY-1997; 97US-00854050.

PR 14-AUG-1997; 97US-00911312.

PR 14-AUG-1997; 97US-00912951.

PR 14-AUG-1997; 97US-00915503.

XX (GERO-) GERON CORP.

PA (UYTE-) UNIV TECHNOLOGY CORP.

XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;

XX WPI; 1998-171633/16.

XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.

XX Example 15; Page 269-270; 387pp; English.

XX The present sequence represents a fusion protein from an example of the
CC present invention which describes human telomerase reverse transcriptase
CC (hTERT). The present invention also describes the following methods: (A)
CC determining whether a test compound is a modulator of hTERT, by detecting
CC the change in hTERT recombinant protein or polynucleotide, on
CC administration of the compound; (B) preparation of recombinant telomerase
CC by contacting a protein preparation of hTERT with a telomerase RNA
CC component; (C) detection of the hTERT RNA or protein in a sample by
CC binding a relevant probe to the sample and detecting the complex formed
CC or in the case of RNA detection, amplifying the product and correlating
CC the presence of complex or amplification product with presence of hTERT in
CC the sample; and (D) increasing the proliferation of a vertebrate cell by
CC increasing hTERT expression; and (E) the use of an agent that causes an
CC increase in cell vertebrate cell proliferation to create a medicament
CC that inhibits ageing. A protein preparation of hTERT and the
CC polynucleotide encoding hTERT can be used in the manufacture of
CC medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
CC telomerase activity can be used to treat conditions that are associated
CC with high telomerase activity. A protein preparation of hTERT can also be
CC used in the new methods

XX Sequence 1405 AA;

Query Match 99.3%; Score 5918; DB 2; Length 1405;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1128; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY 1 MPAPRCRAVRSLLRSHREVLPATFVRRLGPGQWRLVQRGDDPAAFRALVAQCLVCPW 60
DB 276 MPAPRCRAVRSLLRSHREVLPATFVRRLGPGQWRLVQRGDDPAAFRALVAQCLVCPW 335

QY 61 DARPPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120
DB 336 DARPPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFFGALLDARGGPEAFTTSVR 395
QY 121 SYLNTNTVDALRGSGAWGLLRRYVDDVLVHLLARCALFVLVAPSCAYOVCGPPYQLGA 180
DB 396 SYLNTNTVDALRGSGAWGLLRRYVDDVLVHLLARCALFVLVAPSCAYOVCGPPYQLGA 455
QY 181 ATQARPPPHASGPRRRLLGCERAWNHSVREAGVPLGLPAGARRRRGGSSASRSLPLPKRRR 240
DB 456 ATQARPPPHASGPRRRLLGCERAWNHSVREAGVPLGLPAGARRRRGGSSASRSLPLPKRRR 515
QY 241 GAAPPERTPVQGSWAHPGTRGPDGRGFCVSPARPAEATSLEGALSGRHSHPSVG 300
DB 516 GAAPPERTPVQGSWAHPGTRGPDGRGFCVSPARPAEATSLEGALSGRHSHPSVG 575
QY 301 ROHAGBPSTSRPPRPMWDTCPVVAETKFLYSSGDKQELRPSPLLSLSPSLTGARRL 360
DB 576 ROHAGBPSTSRPPRPMWDTCPVVAETKFLYSSGDKQELRPSPLLSLSPSLTGARRL 634
QY 361 VETIFLGSRRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
DB 635 VETIFLGSRRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 694
QY 421 PAAGVCAREKPGQSVAAPEEDTDRRLVQLLRHSSPWQYGVFVRACLRRLVPPGLWGS 480
DB 695 PAAGVCAREKPGQSVAAPEEDTDRRLVQLLRHSSPWQYGVFVRACLRRLVPPGLWGS 754
QY 481 RHNERRLRNTKKEFISLGKHAKLISOLETWKMSVRDCAWLRSPGVCVPAEHLRREI 540
DB 755 RHNERRLRNTKKEFISLGKHAKLISOLETWKMSVRDCAWLRSPGVCVPAEHLRREI 814
QY 541 LAKFLHLMMSVYVVELLSRFPYVTTETTFQKNRLFYRKSVMKLSQSIGRQHLKRVQRE 600
DB 815 LAKFLHLMMSVYVVELLSRFPYVTTETTFQKNRLFYRKSVMKLSQSIGRQHLKRVQRE 874
QY 601 LSEAEVQRHREARPAALTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
DB 875 LSEAEVQRHREARPAALTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 934
QY 661 LFSVLNTERARRRPGILGASVGLDDIHRAWTFLVRVAQDPPPELYFVKVDVTGAYDTI 720
DB 935 LFSVLNTERARRRPGILGASVGLDDIHRAWTFLVRVAQDPPPELYFVKVDVTGAYDTI 994
QY 721 PODRLTEVIASIIIPQNTYCVRRYAVVOKAAGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
DB 995 PODRLTEVIASIIIPQNTYCVRRYAVVOKAAGHVRKAFKSHVSTLTDLQPMRQFVAHL 1054
QY 781 QETSPLRDAVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCGIPQGSILSTL 840
DB 1055 QETSPLRDAVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCGIPQGSILSTL 1114
QY 841 LCSLCYGDMEKMLFAGIRRDGLLLRLVDDFLVLTPTLTHAKTFLTLVRGPEYCVNL 900
DB 1115 LCSLCYGDMEKMLFAGIRRDGLLLRLVDDFLVLTPTLTHAKTFLTLVRGPEYCVNL 1174
QY 901 RKTVNPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSYSSYARTSTRASLTF 960
DB 1175 RKTVNPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSYSSYARTSTRASLTF 1234
QY 961 NRGFKAGRNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRHFACVLQUP 1020
DB 1235 NRGFKAGRNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRHFACVLQUP 1294
QY 1021 FHOQWKNPTPFLRIVSDTASLCYSILKAKVAGMSLGAKGAAGPLPSEAVOWLCHQAFLL 1080
DB 1295 FHOQWKNPTPFLRIVSDTASLCYSILKAKVAGMSLGAKGAAGPLPSEAVOWLCHQAFLL 1354
QY 1081 KLTRHRYTVYVPLLGSRLTAOTOLSRKLPCTTLTALEAAANPALPSDFKTILD 1132
DB 1355 KLTRHRYTVYVPLLGSRLTAOTOLSRKLPCTTLTALEAAANPALPSDFKTILD 1405

Db 1088 PFHQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHOAFL 1147
QY 1080 LKLTTHRVTVYVPLLSGLRTAQOLSKPLPGTTLTALEAAANPALPSDFKTILD 1132
Db 1148 LKLTTHRVTVYVPLLSGLRTAQOLSKPLPG-TLTALEAAANPALPSDFKTILD 1199

RESULT 37
ID AAY00641
AC AAY00641;
XX AAY00641;
XX AAY00641;
DT 26-JUL-1999 (first entry)
XX
DE Telomerase protein sequence lacking motif A.
XX
KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW stem cell differentiation; organ regeneration; organ differentiation.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9901560-A1.
XX
PD 14-JAN-1999.
XX
XX 01-JUL-1998; 98WO-US013835.
XX
PR 01-JUL-1997; 97US-0051410P.
PR 21-JUL-1997; 97US-0053018P.
PR 21-JUL-1997; 97US-0053329P.
PR 04-AUG-1997; 97US-0054642P.
PR 09-SEP-1997; 97US-0058287P.
XX
PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
XX Kilian A, Bowtell D;
XX
XX WPI; 1999-106060/09.
DR N-PSDB; AAX18269.
XX
XX New isolated vertebrate telomerase genes - used to develop products for
PT treating cancers or for organ regeneration, nerve cell or brain cell
PT growth following injury or bone marrow transplantation.
XX
XX Claim 4; Fig 11n-o; 134pp; English.
XX
XX This sequence is a truncated human telomerase of the invention. Primers
CC that amplify the telomerase coding sequence can be used in a method for
CC diagnosing cancer in a patient. The telomerase can be used for detection,
CC diagnosis and drug screening. Inhibitors of telomerase activity can be
CC used to treat cancers such as melanomas, other skin cancers,
CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC growths. Enhancers of telomerase may be used to stimulate stem cell
CC proliferation and differentiation (expansion of haematopoietic stem cells
CC could be administered in the bone marrow transplant context). As well,
CC many tissues have stem cells. Proliferation of these cells may be useful
CC in wound healing, hair growth, treatment of disease such as Wilm's
CC tumour, organ regeneration or differentiation after injury or diseases,
XX nerve cell or brain cell growth following injury
XX
XX Sequence 1120 AA;
XX

Query Match 98.7%; Score 5882; DB 2; Length 1120;
Best Local Similarity 98.9%; Pred No. 0;
Matches 1120; Conservative 0; Mismatches 0; Indels 12; Gaps 1;
QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRVLVQRGDPAAFRALVAQCLVCPW 60
|||||

Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRVLVQRGDPAAFRALVAQCLVCPW 60
QY 61 DARPPAAPSPQVSCSLKELVARVQLRCERCAKNVLAFGPALLDGAAGPPEAFTTSVR 120
Db 61 DARPPAAPSPQVSCSLKELVARVQLRCERCAKNVLAFGPALLDGAAGPPEAFTTSVR 120
QY 121 SYLPNTVTDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAVQVCPGPLYQLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAVQVCPGPLYQLGA 180
QY 181 ATOARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRRGSSASRSPLPKRPR 240
Db 181 ATOARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRRGSSASRSPLPKRPR 240
QY 241 GAAPEPRTVQGSWAHPGTRGSDRGFCVVSPPARPAEATSLEGALSGRHSHPSVG 300
Db 241 GAAPEPRTVQGSWAHPGTRGSDRGFCVVSPPARPAEATSLEGALSGRHSHPSVG 300
QY 301 RQHAGPSTSRPPRPMDTPCPVVAETKHFYSSGDKQLRPSFLLSLRPSLTGARRL 360
Db 301 RQHAGPSTSRPPRPMDTPCPVVAETKHFYSSGDKQLRPSFLLSLRPSLTGARRL 360
QY 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQGSVAAPDEEDTPRRLVQLLRHSSPWQVYGVFRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQGSVAAPDEEDTPRRLVQLLRHSSPWQVYGVFRACLRLVPPGLWGS 480
QY 481 RHNERFLRNTKCFISLGKHAKLSIQELTWKSVRDCAWLRSSPGVCPVAAEHLRBEI 540
Db 481 RHNERFLRNTKCFISLGKHAKLSIQELTWKSVRDCAWLRSSPGVCPVAAEHLRBEI 540
QY 541 LAKFLHLMVSVVVELLSFFVTTTFFQKRLFFYKRSVMSKLOSIGIRQHLKXVQURE 600
Db 541 LAKFLHLMVSVVVELLSFFVTTTFFQKRLFFYKRSVMSKLOSIGIRQHLKXVQURE 600
QY 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRERKABRLTSRVKA 660
Db 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRERKABRLTSRVKA 660
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYFVKVVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYFVKVVDVTGAYDTI 720
QY 721 PQDLTEVIASIIKPONTYCYRRYAVQKAAHGVKAFKSHVSTLTDLQPMRQFVAHL 780
Db 711 --DLTEVIASIIKPONTYCYRRYAVQKAAHGVKAFKSHVSTLTDLQPMRQFVAHL 768
QY 781 QETSPLRDAVVEOSSSLNEASSGLFDVFLRPMCHHAVIRGKSVQCGIPQGSILSTL 840
Db 769 QETSPLRDAVVEOSSSLNEASSGLFDVFLRPMCHHAVIRGKSVQCGIPQGSILSTL 828
QY 841 LCSLCYGMENKLFAGIRRDGLLRVDDFLVTPHLLTHAKTFLRTLVRGPEYCCVNL 900
Db 829 LCSLCYGMENKLFAGIRRDGLLRVDDFLVTPHLLTHAKTFLRTLVRGPEYCCVNL 888
QY 901 RKTVMNPFVEALGCTAFVQMPAHGLPPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 960
Db 889 RKTVMNPFVEALGCTAFVQMPAHGLPPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 948
QY 961 NRGFKAGNMRKLFVGLRLKCHSIFLDQVNSLQVCTNIYKILLQAYRHFACVLOLP 1020
Db 949 NRGFKAGNMRKLFVGLRLKCHSIFLDQVNSLQVCTNIYKILLQAYRHFACVLOLP 1008
QY 1021 FHQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHOAFL 1080
Db 1009 FHQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHOAFL 1068
QY 1081 KLTHRVTVYVPLLSGLRTAQOLSKPLPGTTLTALEAAANPALPSDFKTILD 1132
Db 1069 KLTHRVTVYVPLLSGLRTAQOLSKPLPGTTLTALEAAANPALPSDFKTILD 1120

RESULT 38
AA00650
ID AA00650 standard; protein; 1120 AA.
XX
XX
AC AA00650;
XX
DT 26-JUL-1999 (first entry)
XX
DE Telomerase (ver. 2) protein sequence lacking motif A.
XX
KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
KW stem cell differentiation; organ regeneration; organ differentiation.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9901560-A1.
XX
XX 14-JAN-1999.
XX
XX 01-JUL-1998; 98WO-US013835.
XX
XX 01-JUL-1997; 97US-0051410P.
PR 21-JUL-1997; 97US-0053018P.
PR 21-JUL-1997; 97US-0053329P.
PR 04-AUG-1997; 97US-0054642P.
PR 09-SEP-1997; 97US-0058287P.
XX
XX (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI Kilian A, Bowtell D;
XX
XX WPI: 1999-106060/09.
DR N-PSDB; AX18278.
XX
XX New isolated vertebrate telomerase genes - used to develop products for
PT treating cancers or for organ regeneration, nerve cell or brain cell
PT growth following injury or bone marrow transplantation.
XX
XX Claim 4; Fig 11ah-aj; 134pp; English.
XX
XX This sequence is a truncated human telomerase of the invention. Primers
CC that amplify the telomerase coding sequence can be used in a method for
CC diagnosing cancer in a patient. The telomerase can be used for detection,
CC diagnosis and drug screening. Inhibitors of telomerase activity can be
CC used to treat cancers such as melanomas, other skin cancers,
CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC growths. Enhancers of telomerase may be used to stimulate stem cell
CC proliferation and differentiation (expansion of haematopoietic stem cells
CC could be administered in the bone marrow transplant context). As well,
CC many tissues have stem cells. Proliferation of these cells may be useful
CC in wound healing, hair growth, treatment of disease such as Wilms'
CC tumour, organ regeneration or differentiation after injury or diseases,
CC nerve cell or brain cell growth following injury. Note: The N-terminus of
CC this sequence can be replaced by the sequences shown in AAY00656-Y00658
XX
SQ Sequence 1120 AA;

Query Match 98.5%; Score 5873; DB 2; Length 1120;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1119; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

QY 1 MPAPRCRAVRSLLSHREVULPLATFVRRLGPGQWRVLVQRGDPAAFRALVAQCLVCPW 60
DB 1 MPAPRCRAVRSLLSHREVULPLATFVRRLGPGQWRVLVQRGDPAAFRALVAQCLVCPW 60

QY 61 DARPPPAAPSPQVSCIKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
|||||

Db 61 DARPPPAAPSPQVSCIKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
QY 121 SYLPNTVTDALRGSGAWGLLLRRVGDVVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
|||||
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGDVVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAGARRRRGGASRSPLPKPRR 240
|||||
Db 181 ATQARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAGARRRRGGASRSPLPKPRR 240
QY 241 GAPEPERTVGGQSWAHPGRTGRPSDRGFCVSPARPABEATSEALGSTRSHSHSVG 300
|||||
Db 241 GAPEPERTVGGQSWAHPGRTGRPSDRGFCVSPARPABEATSEALGSTRSHSHSVG 300
QY 301 ROHHAGPSTSRPPRWDTPCPVYAEKTHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
|||||
Db 301 ROHHAGPSTSRPPRWDTPCPVYAEKTHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
QY 361 VETIFGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAOCYGVLLKTHCPLRAAVT 420
|||||
Db 361 VETIFGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAOCYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPOGSAVAPEEEDTPRRLVOLLROHSSPWOVYGFVRACLRLRVLPPGLWS 480
|||||
Db 421 PAAGVCAREKPOGSAVAPEEEDTPRRLVOLLROHSSPWOVYGFVRACLRLRVLPPGLWS 480
QY 481 RHNERRFLRNTKTFISLGKHAKLSQBLTWKMSVRDCAWLRRSPGVGCPAAEHLRPEI 540
|||||
Db 481 RHNERRFLRNTKTFISLGKHAKLSQBLTWKMSVRDCAWLRRSPGVGCPAAEHLRPEI 540
QY 541 LAKFLHLMMSVYVVELLRSPFYVTTETTFQKRLFFYKSVMSKLOSGIROLKRVOLRE 600
|||||
Db 541 LAKFLHLMMSVYVVELLRSPFYVTTETTFQKRLFFYKSVMSKLOSGIROLKRVOLRE 600
QY 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVMDYVVGARTFREKRAERLTSRVKA 660
|||||
Db 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVMDYVVGARTFREKRAERLTSRVKA 660
QY 661 LFSVLYNERARRPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELVFVKVDVTGAYDTI 720
|||||
Db 661 LFSVLYNERARRPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELVFVKVDVTGAYDTI 720
QY 721 PDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRAFKSHVSTLTDLOPMRQFVAHL 780
|||||
Db 721 PDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRAFKSHVSTLTDLOPMRQFVAHL 780
QY 781 QETSPRLDAVVEIOSSSINEASSGLFDVFLRFMCHHAVIRGKSVYVQCGIPQGSILSTL 840
|||||
Db 781 QETSPRLDAVVEIOSSSINEASSGLFDVFLRFMCHHAVIRGKSVYVQCGIPQGSILSTL 840
QY 841 LCSLCYGDMMENKLPAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLRVLVRGVPYGVVNL 900
|||||
Db 841 LCSLCYGDMMENKLPAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLRVLVRGVPYGVVNL 900
QY 901 RKTVNVPEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSIRASLTF 960
|||||
Db 901 RKTVNVPEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSIRASLTF 960
QY 961 NRGFKAGNNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQVAFHACVLQLP 1020
|||||
Db 961 NRGFKAGNNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQVAFHACVLQLP 1020
QY 999 NRGFKAGNNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQVAFHACVLQLP 1008
|||||
Db 999 NRGFKAGNNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQVAFHACVLQLP 1008
QY 1021 FHQGVKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVWLCHQAPLL 1080
|||||
Db 1021 FHQGVKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVWLCHQAPLL 1080
QY 1081 KLTHHRVTVYVPLIGSLRTAOTLSRKLPGTTLTALEAAANPALPSDEKTLID 1132
|||||
Db 1081 KLTHHRVTVYVPLIGSLRTAOTLSRKLPGTTLTALEAAANPALPSDEKTLID 1132
QY 1069 KLTHHRVTVYVPLIGSLRTAOTLSRKLPGTTLTALEAAANPALPSDEKTLID 1120
|||||
Db 1069 KLTHHRVTVYVPLIGSLRTAOTLSRKLPGTTLTALEAAANPALPSDEKTLID 1120

RESULT 39
AAW47006

DD	AAW47006 standard; protein; 1150 AA.	QY	61	DAREPPAAPSPQVSCLEKELVARVQLRCERAKNVLAFLGPFALLDARGGPPPEAFTTSVR	120
AC	AAW47006;	Db	61	DAREPPAAPSPQVSCLEKELVARVQLRCERAKNVLAFLGPFALLDARGGPPPEAFTTSVR	120
XX	13-AUG-1998 (first entry)	QY	121	SYLENTVTDALRGSGANGLLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQIGA	180
XX	Glutathione-S-transferase and hTERT fusion protein 6.	Db	121	SYLENTVTDALRGSGANGLLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQIGA	180
DE	Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;	QY	181	ATQARPPPHASGPPRRRLGCCERAWNHSVREACVPLGLPAPGARRRGGSSASRSLLPKRPRR	240
KW	cell proliferation; cancer; ageing; ribonucleoprotein.	Db	181	ATQARPPPHASGPPRRRLGCCERAWNHSVREACVPLGLPAPGARRRGGSSASRSLLPKRPRR	240
XX	Synthetic.	QY	241	GAPEPERTPVQGSWAHPGTRGSDRGFCVSPARPAEBEATSLGALSSTRHSPSVG	300
OS	Homo sapiens.	Db	241	GAPEPERTPVQGSWAHPGTRGSDRGFCVSPARPAEBEATSLGALSSTRHSPSVG	300
XX	GB2317891-A.	QY	301	ROHAGPPSTSRPPRWDTPCPVYAEKHLFYSGGDEQLRPSFLSSLRPSLTGARRL	360
XX	08-APR-1998.	Db	301	ROHAGPPSTSRPPRWDTPCPVYAEKHLFYSGGDEQLRPSFLSSLRPSLTGARRL	360
XX	01-OCT-1997; 97GB-00020890.	QY	361	VETIFLGSRRPMPGTPRRRLPORYWQMRPLFLELLGNHAQCPVGLLTKHCPRAAVT	420
PR	01-OCT-1996; 96US-00724643.	Db	361	VETIFLGSRRPMPGTPRRRLPORYWQMRPLFLELLGNHAQCPVGLLTKHCPRAAVT	420
PR	18-APR-1997; 97US-00844419.	QY	421	PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSPPQVYGFVRACLRLVPPGL-WG	479
PR	25-APR-1997; 97US-00846017.	Db	421	PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSPPQVYGFVRACLRLVPPGL-WG	479
PR	06-MAY-1997; 97US-00851843.	QY	480	SRHNERFLNNTKFIISLGKHAQLSLOELTWQMSVRDCAWLRSPGVCVGAEEHRLREE	539
PR	09-MAY-1997; 97US-00854050.	Db	480	SRHNERFLNNTKFIISLGKHAQLSLOELTWQMSVRDCAWLRSPGVCVGAEEHRLREE	539
PR	14-AUG-1997; 97US-00911312.	QY	540	ILAKFLHMLSVVYVELLSRPFYVTTETFOKNRFLFYRKSVWSKIQSIGIQLHKLKRVQLR	599
PR	14-AUG-1997; 97US-00912951.	Db	540	ILAKFLHMLSVVYVELLSRPFYVTTETFOKNRFLFYRKSVWSKIQSIGIQLHKLKRVQLR	599
XX	14-AUG-1997; 97US-00915503.	QY	600	ELSAEVRQHRARPALLTSRLRPIPKPDGLRPIVN-MDYVVGARTFREREKRAERLTSRV	658
PA	(GERO-) GERON CORP.	Db	600	ELSAEVRQHRARPALLTSRLRPIPKPDGLRPIVN-MDYVVGARTFREREKRAERLTSRV	658
PA	(UYTE-) UNIV TECHNOLOGY CORP.	QY	659	KALFSLVNYERARRPGLIGASVLGDDIHRARWTFVLVRQAQDPPPELYFKVDVTGAYD	718
XX	Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;	Db	659	KALFSLVNYERARRPGLIGASVLGDDIHRARWTFVLVRQAQDPPPELYFKVDVTGAYD	718
PI	Andrews WH;	QY	719	TIPQDRLEVTASIIKQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPYMRQFVA	778
XX	WPI; 1998-171633/16.	Db	719	TIPQDRLEVTASIIKQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPYMRQFVA	778
DR	Pure and recombinant human Telomerase Reverse Transcriptase and its	QY	779	HLQETSPDRADVTEQSSSLEASGLFVFLAFMCHAVE-RGKSW-QCQGIPOGSI	835
PT	variants - are useful in the diagnosis, prognosis and treatment of cell	Db	779	HLQETSPDRADVTEQSSSLEASGLFVFLAFMCHAVE-RGKSW-QCQGIPOGSI	835
PT	proliferation conditions especially cancer and ageing.	QY	838	STLLCSLCYGDMEKNLFGAIRRDDGLLRVDDFLVTPHLTHAKTFTLTVRGVPEYGCV	897
XX	Example 6; Page 231-232; 387pp; English.	Db	838	STLLCSLCYGDMEKNLFGAIRRDDGLLRVDDFLVTPHLTHAKTFTLTVRGVPEYGCV	897
CC	The present sequence represents a fusion protein from an example of the	QY	897	STLLCSLCYGDMEKNLFGAIRRDDGLLRVDDFLVTPHLTHAKTFTLTVRGVPEYGCV	897
CC	present invention which describes human telomerase reverse transcriptase	Db	897	STLLCSLCYGDMEKNLFGAIRRDDGLLRVDDFLVTPHLTHAKTFTLTVRGVPEYGCV	897
CC	(hTERT). The present invention also describes the following methods: (A)	QY	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	determining whether a test compound is a modulator of hTERT, by detecting	Db	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	the change in hTERT recombinant protein or polynucleotide, on	QY	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	administration of the compound; (B) preparation of recombinant telomerase	Db	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	by contacting a protein preparation of hTERT with a telomerase RNA	QY	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	component; (C) detection of the hTERT RNA or protein in a sample by	Db	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	binding a relevant probe to the sample and detecting the complex formed	QY	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	or in the case of RNA detection, amplifying the product and correlating	Db	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	the presence of complex or amplification product with presence of hTERT in	QY	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	the sample; and (D) increasing the proliferation of a vertebrate cell by	Db	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	increasing hTERT expression; and (E) the use of an agent that causes an	QY	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	increase in cell vertebrate cell proliferation to create a medicament	Db	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	that inhibits ageing. A protein preparation of hTERT and the	QY	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	polynucleotide encoding hTERT can be used in the manufacture of	Db	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	medicaments for inhibiting the effect of ageing or cancer. Inhibitors of	QY	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	telomerase activity can be used to treat conditions that are associated	Db	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	with high telomerase activity. A protein preparation of hTERT can also be	QY	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
CC	used in the new methods	Db	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
XX	Sequence 1150 AA;	QY	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
XX	Query Match 96.0%; Score 5721; DB 2; Length 1150;	Db	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
XX	Best Local Similarity 97.8%; Pred. No. 0;	QY	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
XX	Matches 1112; Conservative 6; Mismatches 5; Indels 14; Gaps 13;	Db	956	VNLKTTVNPVEDEALGGTAFVQMPAHGLFPW-CGILLDTTLEVSQDSSYARTSIRA	956
QY	1 MPAPRCRAVRSLLRSHYREVLPATFVRRRLGPGQWRVLVQRGDPAAPRALVAQCLVCPW 60	QY	1016	VQLPFFHQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCH	1075
Db	1 MPAPRCRAVRSLLRSHYREVLPATFVRRRLGPGQWRVLVQRGDPAAPRALVAQCLVCPW 60	Db	1016	VQLPFFHQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCH	1075
		QY	1076	QAFLLKLTTRHVTYVPLLGSLRTAQTSRLKPGTTLTALAAANPALPSDFKTILD 1132	
		Db	1076	QAFLLKLTTRHVTYVPLLGSLRTAQTSRLKPGTTLTALAAANPALPSDFKTILD 1132	

KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW stem cell differentiation; organ regeneration; organ differentiation.
OS Homo sapiens.
OS Synthetic.
XX
XX
XX WO9901560-A1.
XX
XX 14-JAN-1999.
XX
XX 01-JUL-1998; 98WO-US013835.
XX
XX 01-JUL-1997; 97US-0051410P.
PR 21-JUL-1997; 97US-0053018P.
PR 21-JUL-1997; 97US-0053329P.
PR 04-AUG-1997; 97US-0054642P.
PR 09-SEP-1997; 97US-0058287P.
XX
XX (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
XX
XX Kilian A, Bowtell D;
XX
XX WPI; 1999-106060/09.
XX N-PSDB; AAX18280.
XX
XX New isolated vertebrate telomerase genes - used to develop products for
XX treating cancers or for organ regeneration, nerve cell or brain cell
XX growth following injury or bone marrow transplantation.
XX
XX Claim 4; Fig 11am-an; 134pp; English.
XX
XX This sequence is a truncated human telomerase of the invention. Primers
XX that amplify the telomerase coding sequence can be used in a method for
XX diagnosing cancer in a patient. The telomerase can be used for detection,
XX diagnosis and drug screening. Inhibitors of telomerase activity can be
XX used to treat cancers such as melanomas, other skin cancers,
XX neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
XX lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
XX growths. Enhancers of telomerase may be used to stimulate stem cell
XX proliferation and differentiation (expansion of haematopoietic stem cells
XX could be administered in the bone marrow transplant context). As well,
XX many tissues have stem cells. Proliferation of these cells may be useful
XX in wound healing, hair growth, treatment of disease such as Wilm's
XX tumour, organ regeneration or differentiation after injury or diseases of
XX nerve cell or brain cell growth following injury. Note: The N-terminus of
XX this sequence can be replaced by the sequences shown in AAY00656-Y00658,
XX and the C-terminus can be replaced by the sequence shown in AAY00654
XX
XX Sequence 1041 AA;
XX
XX Query Match 91.7%; Score 5467; DB 2; Length 1041;
XX Best Local Similarity 98.8%; Pred. No. 0;
XX Matches 1039; Conservative 0; Mismatches 1; Indels 12; Gaps 1;
XX
XX 1 MPRAPCRVRSLRLSHRVREVLPLATFVRRLGPGQWRVLVQRGDPAAFRALVAQCLVCVPW 60
XX
XX 1 MPRAPCRVRSLRLSHRVREVLPLATFVRRLGPGQWRVLVQRGDPAAFRALVAQCLVCVPW 60
XX
XX 61 DARPPPAAPSPROVSCLELVARVLQRLCERGANVLAFFGALLDGGGPPPEAFTTSVR 120
XX
XX 61 DARPPPAAPSPROVSCLELVARVLQRLCERGANVLAFFGALLDGGGPPPEAFTTSVR 120
XX
XX 121 SYLPTNTVTDALRGSGAWGLLRLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
XX
XX 121 SYLPTNTVTDALRGSGAWGLLRLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
XX
XX 181 ATQARPPPHASGPPRRRLGCERAWNHSVREAGVPLGAPAGARRRGGSASRSLPLPKPRRR 240
XX
XX 181 ATQARPPPHASGPPRRRLGCERAWNHSVREAGVPLGAPAGARRRGGSASRSLPLPKPRRR 240
XX
XX 241 GAAPEPERTPVGQSWAHPGRTGRPSDRGFCVWSPARPAEATSLEGALSGTRHSHPSVG 300

Db
241 GAAPEPERTPVGQSWAHPGRTGRPSDRGFCVWSPARPAEATSLEGALSGTRHSHPSVG 300
Qy
301 RQHAGPPSTSRPRPMDTPCPVPYAEATHFLYSSGDKQQLRPSFLSSLRPSLTGARRL 360
Db
301 RQHAGPPSTSRPRPMDTPCPVPYAEATHFLYSSGDKQQLRPSFLSSLRPSLTGARRL 360
Qy
361 VETIFLGSRPMPGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db
361 VETIFLGSRPMPGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Qy
421 PAAGVCAREKPOGSVAAPPEEDTDPRLVQLLRQHSSPWQYGVFVRACLRLVPPGLWGS 480
Db
421 PAAGVCAREKPOGSVAAPPEEDTDPRLVQLLRQHSSPWQYGVFVRACLRLVPPGLWGS 480
Qy
481 RHNERRFLNRTKKFISLGKHAQLSLOBLTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
Db
481 RHNERRFLNRTKKFISLGKHAQLSLOBLTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
Qy
541 LAKFLHLMMSVYVVELLRSPFYVTETTFQKNRLFVYRKSVMSKLSQIGIRHLLKRVOLRE 600
Db
541 LAKFLHLMMSVYVVELLRSPFYVTETTFQKNRLFVYRKSVMSKLSQIGIRHLLKRVOLRE 600
Qy
601 LSAEVRQHREARPALITSLRFTPKDGLRPIVNMDDYVVGARTFREKRAERLTSRVKA 660
Db
601 LSAEVRQHREARPALITSLRFTPKDGLRPIVNMDDYVVGARTFREKRAERLTSRVKA 660
Qy
661 LFSVLNVERARRPGLLGASVLGLDDIHRAMWRTFVLVRAQDPPPELVFVVDVTGAYDTI 720
Db
661 LFSVLNVERARRPGLLGASVLGLDDIHRAMWRTFVLVRAQDPPPELVFVVDVTGAYDTI 720
Qy
721 PQRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
Db
711 --DRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 768
Qy
781 QETSPURDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYVOCQIGIPOGSIILSTL 840
Db
769 QETSPURDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYVOCQIGIPOGSIILSTL 828
Qy
841 LCSLCYGDGMENKLFAGTRRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYEGCVVNL 900
Db
829 LCSLCYGDGMENKLFAGTRRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYEGCVVNL 888
Qy
901 RKTVMFPVDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSSYARTSIRASLTFF 960
Db
889 RKTVMFPVDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSSYARTSIRASLTFF 948
Qy
961 NRGFKAGRNRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNLYKTLILQAYRFHACVLQLP 1020
Db
949 NRGFKAGRNRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNLYKTLILQAYRFHACVLQLP 1008
Qy
1021 FHOQVWKNPTFFLRVISDTSASLCYSILKAKNA 1052
Db
1009 FHOQVWKNPTFFLRVISDTSASLCYSILKAKNA 1040
XX
XX RESULT 43
XX ID AAY00643
XX AAY00643 standard; protein; 1041 AA.
XX
XX AC AAY00643;
XX
XX XX 26-JUL-1999 (first entry)
XX
XX DE Altered C-terminus telomerase protein sequence lacking motif A.
XX
XX KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
XX KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
XX KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
XX KW stem cell differentiation; organ regeneration; organ differentiation.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.

XX WO9901560-A1.
 XX 14-JAN-1999.
 XX 01-JUL-1998; 98WO-US013835.
 XX 01-JUL-1997; 97US-0051410P.
 PR 21-JUL-1997; 97US-0053018P.
 PR 21-JUL-1997; 97US-0053018P.
 PR 04-AUG-1997; 97US-0054642P.
 PR 09-SEP-1997; 97US-0058287P.
 XX (CAMP-) CAMBIA BIOSYSTEMS LLC.
 XX Kilian A, Bowtell D;
 XX WPI, 1999-106060/09.
 DR N-PSDB; AX18271.
 XX New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PT growth following injury or bone marrow transplantation.
 XX Claim 4; Fig 11r-s; 134pp; English.
 XX This sequence is a truncated human telomerase of the invention. Primers
 CC that amplify the telomerase coding sequence can be used in a method for
 CC diagnosing cancer in a patient. The telomerase can be used for detection,
 CC diagnosis and drug screening. Inhibitors of telomerase activity can be
 CC used to treat cancers such as melanomas, other skin cancers,
 CC neuroblastomas, breast carcinomas, colon carcinomas, leukemias,
 CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
 CC growths. Enhancers of telomerase may be used to stimulate stem cell
 CC proliferation and differentiation (expansion of haematopoietic stem cells
 CC could be administered in the bone marrow transplant context). As well,
 CC many tissues have stem cells. Proliferation of these cells may be useful
 CC in wound healing, hair growth, treatment of disease such as Wilms
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury. Note: The C-terminus of
 CC this sequence can be replaced by the sequence shown in AAY00654
 XX
 SQ Sequence 1041 AA;
 Query Match 91.7%; Score 5467; DB 2; Length 1041;
 Best Local Similarity 98.8%; Pred No. 0;
 Matches 1039; Conservative 0; Mismatches 1; Indels 12; Gaps 1;
 QY 1 MPAPRCRAVRSLLSHYREVLPATFVRRGPGQWRLVQRGDPAAPRALVAQCLVCPW 60
 DB 1 MPAPRCRAVRSLLSHYREVLPATFVRRGPGQWRLVQRGDPAAPRALVAQCLVCPW 60
 QY 61 DARPPAAPSPFQVSCLELVARVLQRLCERGAQNVLAFFGALLDAGGPGPEAFTTSVR 120
 DB 61 DARPPAAPSPFQVSCLELVARVLQRLCERGAQNVLAFFGALLDAGGPGPEAFTTSVR 120
 QY 121 SYLPTNTVDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 DB 121 SYLPTNTVDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 QY 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGASRSPLPKRPRR 240
 DB 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGASRSPLPKRPRR 240
 QY 241 GAAPPERTPVQGSWAHPGRTRGSDRGFCVWSPARPAEATSLEGALSGTRHSHPSVG 300
 DB 241 GAAPPERTPVQGSWAHPGRTRGSDRGFCVWSPARPAEATSLEGALSGTRHSHPSVG 300
 QY 301 ROHAGPSTSPRPPTDTPCPVVAETKHFLYSSGDKQOLRPSFLSLRPSLTGARRL 360
 DB 301 ROHAGPSTSPRPPTDTPCPVVAETKHFLYSSGDKQOLRPSFLSLRPSLTGARRL 360
 QY 361 VETIFLGRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

DB 361 VETIFLGRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
 QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRHSSPWQVYGFVRACLRRLVPPGLNGS 480
 DB 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRHSSPWQVYGFVRACLRRLVPPGLNGS 480
 QY 481 RHNERRPLRNTKCFISLGKHAQLSLQELTWKMSVRDCAWLRSPGVCVGAAPAEHLRBEI 540
 DB 481 RHNERRPLRNTKCFISLGKHAQLSLQELTWKMSVRDCAWLRSPGVCVGAAPAEHLRBEI 540
 QY 541 LAKFLHLMMSVYVVELLSRPFYVTTTQKRLFPYKSVMSKLSQISGIRQHLKRVQLRE 600
 DB 541 LAKFLHLMMSVYVVELLSRPFYVTTTQKRLFPYKSVMSKLSQISGIRQHLKRVQLRE 600
 QY 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREKRAERLTSRYKA 660
 DB 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREKRAERLTSRYKA 660
 QY 661 LFSVLNTERARRRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELYFVK----- 710
 DB 661 LFSVLNTERARRRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELYFVK----- 710
 QY 721 PODRLTEVIASIIKPONTYCVRRYAVVQKAAGHVRAKAFKSHVSTLTDLQPMRQFVAHL 780
 DB 721 PODRLTEVIASIIKPONTYCVRRYAVVQKAAGHVRAKAFKSHVSTLTDLQPMRQFVAHL 780
 QY 769 QETSPRLDVAIVIEOSSLSNEASSGLFDVFLRFMCHHVRIRGKSVQCGIPQGSILSTL 828
 DB 769 QETSPRLDVAIVIEOSSLSNEASSGLFDVFLRFMCHHVRIRGKSVQCGIPQGSILSTL 828
 QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGPEYGVVNL 900
 DB 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGPEYGVVNL 900
 QY 901 RKTVPVPEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSTRASLTF 960
 DB 901 RKTVPVPEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSTRASLTF 960
 QY 961 NRGFKAGNMRKLFVGLRLKCHSLFDLOVNSLQTVCTNLYKILLQAYRPHACVQLP 1020
 DB 961 NRGFKAGNMRKLFVGLRLKCHSLFDLOVNSLQTVCTNLYKILLQAYRPHACVQLP 1020
 QY 1021 FHQWKNPTFFLRVISDTASLCYSILKAKNA 1052
 DB 1009 FHQWKNPTFFLRVISDTASLCYSILKAKNA 1040
 RESULT 44
 AAY00639
 ID AAY00639 standard; protein; 948 AA.
 AC AAY00639;
 XX 26-JUL-1999 (first entry)
 XX N-terminal truncated telomerase protein sequence.
 KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 OS Homo sapiens.
 OS Synthetic.
 XX WO9901560-A1.
 XX 14-JAN-1999.
 XX 01-JUL-1998; 98WO-US013835.
 XX 01-JUL-1997; 97US-0051410P.

PR 21-JUL-1997; 97US-0053018P.
 PR 21-JUL-1997; 97US-0053323P.
 PR 04-AUG-1997; 97US-0054642P.
 PR 09-SEP-1997; 97US-0058287P.
 XX
 PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
 XX
 PI Kilian A, Bowtell D;
 XX
 XX WPI; 1999-106060/09.
 DR N-PSDB; AAY00648.
 XX
 XX New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PT growth following injury or bone marrow transplantation.
 XX
 XX Claim 4; Fig 11j-k; 134pp; English.
 XX
 CC This sequence is a truncated human telomerase of the invention. Primers
 CC that amplify the telomerase coding sequence can be used in a method for
 CC diagnosing cancer in a patient. The telomerase can be used for detection,
 CC diagnosis and drug screening. Inhibitors of telomerase activity can be
 CC used to treat cancers such as melanomas, other skin cancers,
 CC neuroblastomas, breast carcinomas, colon carcinomas, leukemias,
 CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
 CC growths. Enhancers of telomerase may be used to stimulate stem cell
 CC proliferation and differentiation (expansion of haematopoietic stem cells
 CC could be administered in the bone marrow transplant context). As well,
 CC many tissues have stem cells. Proliferation of these cells may be useful
 CC in wound healing, hair growth, treatment of disease such as Wilms' s
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury
 XX
 XX Sequence 948 AA;
 SQ
 Query Match 84.0%; Score 5008; DB 2; Length 948;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 946; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPRAPCRAVSLRLSHRYEVLPLATFVRRLLPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
 DB 1 MPRAPCRAVSLRLSHRYEVLPLATFVRRLLPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
 QY 61 DARPPAPSPROVSCLELVARVLORLCERGAKNVLAFGALLDGAAGGPPPEAFTTSVR 120
 DB 61 DARPPAPSPROVSCLELVARVLORLCERGAKNVLAFGALLDGAAGGPPPEAFTTSVR 120
 QY 121 SYLPTNTVTDALRGSGAWGLLRLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 DB 121 SYLPTNTVTDALRGSGAWGLLRLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 QY 181 ATQARPPHAGSPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRPRR 240
 DB 181 ATQARPPHAGSPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRPRR 240
 QY 241 GAAPERTPVQGSWAHPGTRGDSRGFCVSPAPAEATSLGALSSTRHSHSVG 300
 DB 241 GAAPERTPVQGSWAHPGTRGDSRGFCVSPAPAEATSLGALSSTRHSHSVG 300
 QY 301 RQHAGPSTSRPRPMDTPCPVVAETKHYLSGDKQLRPSFLSSLRPSLTGARRL 360
 DB 301 RQHAGPSTSRPRPMDTPCPVVAETKHYLSGDKQLRPSFLSSLRPSLTGARRL 360
 QY 361 VETIFLGRPMWPGTRRLPLRPQRYWQMRPLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
 DB 361 VETIFLGRPMWPGTRRLPLRPQRYWQMRPLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
 QY 421 PAAGVCAREKPGQSVAAPEEDTPRRLVOLLROHSSPWQYGVFRACLRPLVPGLWGS 480
 DB 421 PAAGVCAREKPGQSVAAPEEDTPRRLVOLLROHSSPWQYGVFRACLRPLVPGLWGS 480
 QY 481 RHNERRFLNRTKFTISLGKHAKLSQLTLTKWMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

DB 481 RHNERRFLNRTKFTISLGKHAKLSQLTLTKWMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
 QY 541 LAKFLHLMWSVYVVELLSRFFYYTETTFQKNRLFYRKSVMKLSQSIGIRQHLKRVQLRE 600
 DB 541 LAKFLHLMWSVYVVELLSRFFYYTETTFQKNRLFYRKSVMKLSQSIGIRQHLKRVQLRE 600
 QY 601 LSEAEVQHQREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFREKRAERLTSRYKA 660
 DB 601 LSEAEVQHQREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFREKRAERLTSRYKA 660
 QY 661 LFSVLNVERARRPGLLGASVLGLDDIHRWRTFVLVRADPPPELFFVKVDVTGAYDTI 720
 DB 661 LFSVLNVERARRPGLLGASVLGLDDIHRWRTFVLVRADPPPELFFVKVDVTGAYDTI 720
 QY 721 PQDLRTVEIASIIKPNQYTCVRRYAVVQKAAHGVKAFKSHVSTLTDLPYMQFVAHL 780
 DB 721 PQDLRTVEIASIIKPNQYTCVRRYAVVQKAAHGVKAFKSHVSTLTDLPYMQFVAHL 780
 QY 781 QETSPLRDADVIEQSSSLNEASSGLFDVFLRFPMCHHAVIRGKSYVOCGIPQGSILSTL 840
 DB 781 QETSPLRDADVIEQSSSLNEASSGLFDVFLRFPMCHHAVIRGKSYVOCGIPQGSILSTL 840
 QY 841 LCSLCYGDMMENKLPAGIRRRDGLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
 DB 841 LCSLCYGDMMENKLPAGIRRRDGLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
 QY 901 RKTVPNPPEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSDYS 947
 DB 901 RKTVPNPPEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSDYS 947
 RESULT 45
 AAY00648
 ID AAY00648 standard; protein; 948 AA.
 XX
 AC AAY00648;
 XX
 DT 26-JUL-1999 (first entry)
 XX
 DE Truncated telomerase 3 protein sequence.
 XX
 KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilms' s tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 OS Homo sapiens.
 OS Synthetic.
 XX W09901560-A1.
 XX
 XX 14-JAN-1999.
 XX
 XX 01-JUL-1998; 98WO-US013835.
 XX
 XX 01-JUL-1997; 97US-0051410P.
 PR 21-JUL-1997; 97US-0053018P.
 PR 21-JUL-1997; 97US-0053323P.
 PR 04-AUG-1997; 97US-0054642P.
 PR 09-SEP-1997; 97US-0058287P.
 XX
 XX (CAMB-) CAMBIA BIOSYSTEMS LLC.
 XX
 XX Kilian A, Bowtell D;
 PI
 XX WPI; 1999-106060/09.
 DR N-PSDB; AAX18276.
 DR
 XX New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PT growth following injury or bone marrow transplantation.
 XX
 XX Claim 4; Fig 11ad-ae; 134pp; English.
 PS

XX This sequence is a truncated human telomerase of the invention. Primers
CC that amplify the telomerase coding sequence can be used in a method for
CC diagnosing cancer in a patient. The telomerase can be used for detection,
CC diagnosis and drug screening. Inhibitors of telomerase activity can be
CC used to treat cancers such as melanomas, other skin cancers,
CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC growths. Enhancers of telomerase may be used to stimulate stem cell
CC proliferation and differentiation (expansion of haematopoietic stem cells
CC could be administered in the bone marrow transplant context). As well,
CC many tissues have stem cells. Proliferation of these cells may be useful
CC in wound healing, hair growth, treatment of disease such as Wilm's
CC tumour, organ regeneration or differentiation after injury or diseases,
CC nerve cell or brain cell growth following injury. Note: The N-terminus of
CC this sequence can be replaced by the sequences shown in AAY00656-Y00658
XX
SQ Sequence 948 AA;

Query Match 83.9%; Score 5004; DB 2; Length 948;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 946; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPCRVRSLLSHYREVLPATFVRRLLGQWRLVQRCDDPAAFRALVAQCLVCPW 60
DB 1 MPRAPCRVRSLLSHYREVLPATFVRRLLGQWRLVQRCDDPAAFRALVAQCLVCPW 60

QY 61 DARPPAAPSPQVSCLELVARLQRCERAKNVAFGFPALLDGARGGPEATTTSVR 120
DB 61 DARPPAAPSPQVSCLELVARLQRCERAKNVAFGFPALLDGARGGPEATTTSVR 120

QY 121 SYLPTNTVDALRGSGAWGLLRVDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPTNTVDALRGSGAWGLLRVDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPHASPRLRCERAWNSVREAGVPLGLPAPGARRRGSASRLPLPKRPR 240
DB 181 ATQARPPHASPRLRCERAWNSVREAGVPLGLPAPGARRRGSASRLPLPKRPR 240

QY 241 GAAPPERTPVQSGWAPHGRTRGSPDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300
DB 241 GAAPPERTPVQSGWAPHGRTRGSPDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300

QY 301 RQHAGPSTSRPPRPMDTPCPVYAEKTHFLYSSGDKQLRPSFLLSRLPSLTGARRL 360
DB 301 RQHAGPSTSRPPRPMDTPCPVYAEKTHFLYSSGDKQLRPSFLLSRLPSLTGARRL 360

QY 361 VETIFLGRPWMPGTFRRLPRLPQRYQWMLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420
DB 361 VETIFLGRPWMPGTFRRLPRLPQRYQWMLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420

QY 421 PAAGVCAREKPGSVAAPEEEDTPRRLVOLLROHSSPMQVYGFVRACLRRLVPPGLWS 480
DB 421 PAAGVCAREKPGSVAAPEEEDTPRRLVOLLROHSSPMQVYGFVRACLRRLVPPGLWS 480

QY 481 RHNERRFLRNTKFTISLKGAKLSLQELTKWMSVRDCAWLRSPGVGCPVAAEHLRBEI 540
DB 481 RHNERRFLRNTKFTISLKGAKLSLQELTKWMSVRDCAWLRSPGVGCPVAAEHLRBEI 540

QY 541 LAKFLHLMVSVVVELLSFFVYTTTQKNRLLFFYKRSVMSKLSQIGIRQHLKRVQRE 600
DB 541 LAKFLHLMVSVVVELLSFFVYTTTQKNRLLFFYKRSVMSKLSQIGIRQHLKRVQRE 600

QY 601 LSEAEVROHREARPAALLSRLRFPKPGDLRPIVNMDDVVGARTFRREKRAELTSRYKA 660
DB 601 LSEAEVROHREARPAALLSRLRFPKPGDLRPIVNMDDVVGARTFRREKRAELTSRYKA 660

QY 661 LFSVLNYERARPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFKVVDVTGAYDTI 720
DB 661 LFSVLNYERARPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFKVVDVTGAYDTI 720

QY 721 PODRLTEVIASIKPQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLQPMRFVAHL 780

DB 721 PODRLTEVIASIKPQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLQPMRFVAHL 780

QY 781 QETSPLRDVAVTEQSSSLNEASSGLFDVFLRFMCHHAVRIRKGSYVQCGIFQGSILSTL 840
DB 781 QETSPLRDVAVTEQSSSLNEASSGLFDVFLRFMCHHAVRIRKGSYVQCGIFQGSILSTL 840

QY 841 LCSLCYGDMEKLFAGIRRDGGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYCGVNL 900
DB 841 LCSLCYGDMEKLFAGIRRDGGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYCGVNL 900

QY 901 RKTVVNFVEDEALGGTAFAVQMPAHGLFPWCGLLDDTTLTLEVSQSDYS 947
DB 901 RKTVVNFVEDEALGGTAFAVQMPAHGLFPWCGLLDDTTLTLEVSQSDYS 947

RESULT 46
AAY00642
ID AAY00642 standard; protein; 936 AA.
XX
AC AAY00642;
XX
DT 26-JUL-1999 (first entry)
XX
DE Truncated telomerase protein sequence lacking motif A.
XX
KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW stem cell differentiation; organ regeneration; organ differentiation.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9901560-A1.
XX
PD 14-JAN-1999.
XX
PF 01-JUL-1998; 98WO-US013835.
XX
PR 01-JUL-1997; 97US-0051410P.
PR 21-JUL-1997; 97US-0053018P.
PR 21-JUL-1997; 97US-0053329P.
PR 04-AUG-1997; 97US-0054642P.
PR 09-SEP-1997; 97US-0058287P.
XX
PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI Kilian A, Bowtell D;
XX
DR WPI; 1999-106060/09.
DR N-PSDB; AAX18270.
XX
PT New isolated vertebrate telomerase genes - used to develop products for
PT treating cancers or for organ regeneration, nerve cell or brain cell
PT growth following injury or bone marrow transplantation.
XX
PS Claim 4; Fig 11p-q; 134pp; English.
XX
CC This sequence is a truncated human telomerase of the invention. Primers
CC that amplify the telomerase coding sequence can be used in a method for
CC diagnosing cancer in a patient. The telomerase can be used for detection,
CC diagnosis and drug screening. Inhibitors of telomerase activity can be
CC used to treat cancers such as melanomas, other skin cancers,
CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC growths. Enhancers of telomerase may be used to stimulate stem cell
CC proliferation and differentiation (expansion of haematopoietic stem cells
CC could be administered in the bone marrow transplant context). As well,
CC many tissues have stem cells. Proliferation of these cells may be useful
CC in wound healing, hair growth, treatment of disease such as Wilm's
CC tumour, organ regeneration or differentiation after injury or diseases,
CC nerve cell or brain cell growth following injury

SQ	Sequence 936 AA;	
	Query Match 82.7%; Score 4932; DB 2; Length 936;	
	Best Local Similarity 98.7%; Pred. No. 0;	
	Matches 935; Conservative 0; Mismatches 0; Indels 12; Gaps 1;	
Qy	1 MPRAPRCRAVRSLLRSHYREVLPVRRLLGPGQWRLVQRGDPAAPRALVAQCIVCPW 60	
Db	1 MPRAPRCRAVRSLLRSHYREVLPVRRLLGPGQWRLVQRGDPAAPRALVAQCIVCPW 60	
Qy	61 DARPPAAPSPROVSCLEKELVARVLQRLCERGAKNVLAFGFALLDARGGPEAFTTSVR 120	
Db	61 DARPPAAPSPROVSCLEKELVARVLQRLCERGAKNVLAFGFALLDARGGPEAFTTSVR 120	
Qy	121 SYLPTNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180	
Db	121 SYLPTNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180	
Qy	181 ATOARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGASRSLLPLPKPRR 240	
Db	181 ATOARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGASRSLLPLPKPRR 240	
Qy	241 GAAPERTPYQGSWAHPGRTGFSDRGFCVSPAPAEATSLGALSCTRHSHPVG 300	
Db	241 GAAPERTPYQGSWAHPGRTGFSDRGFCVSPAPAEATSLGALSCTRHSHPVG 300	
Qy	301 ROHAGPSTSRPPRWDTPCPVVAETKHFVLYSSGDKQLRPSFLSSLPSTTGARRL 360	
Db	301 ROHAGPSTSRPPRWDTPCPVVAETKHFVLYSSGDKQLRPSFLSSLPSTTGARRL 360	
Qy	361 VETIFLGSRPWMPGTPRPLRPLQRYWQMRPLFLELGNHAQCPVGLLTKHCPRAAVT 420	
Db	361 VETIFLGSRPWMPGTPRPLRPLQRYWQMRPLFLELGNHAQCPVGLLTKHCPRAAVT 420	
Qy	421 PAAGCAREKPGSVAAPPEEDTDPRRLVQLLRQHSSEPWQVYGFVRACLRRLVPPGLWGS 480	
Db	421 PAAGCAREKPGSVAAPPEEDTDPRRLVQLLRQHSSEPWQVYGFVRACLRRLVPPGLWGS 480	
Qy	481 RHNERFLRNTKFFISLGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREI 540	
Db	481 RHNERFLRNTKFFISLGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREI 540	
Qy	541 LAKFLHLMWSVVVVELLSFFVTETTFQKRLFFYKSVMSKLSQIGIROHLKRVQIRE 600	
Db	541 LAKFLHLMWSVVVVELLSFFVTETTFQKRLFFYKSVMSKLSQIGIROHLKRVQIRE 600	
Qy	601 LSEAFVROHREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRYKA 660	
Db	601 LSEAFVROHREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRYKA 660	
Qy	661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQPPPELIPVKVDVTGAYDTI 720	
Db	661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQPPPELIPVKVDVTGAYDTI 720	
Qy	721 PQDRLETVIASIIPONTYCVRRVAVQKAAHGHVRKAFKSHVSTLTLDQPYMQFVAHL 780	
Db	711 --DRUTEVIAIIPONTYCVRRVAVQKAAHGHVRKAFKSHVSTLTLDQPYMQFVAHL 768	
Qy	781 QETSPLRDAVIEQSSSINEASSGLFDVFLRFMCHAVIRKSVVQCOGIPQGSILSTL 840	
Db	769 QETSPLRDAVIEQSSSINEASSGLFDVFLRFMCHAVIRKSVVQCOGIPQGSILSTL 828	
Qy	841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFTLTVRGVPEYGCVVNL 900	
Db	829 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFTLTVRGVPEYGCVVNL 888	
Qy	901 RKTVVNFFVEALGGTAVQMPAHLFPWCGLLDTRTLEVSQSDYS 947	
Db	889 RKTVVNFFVEALGGTAVQMPAHLFPWCGLLDTRTLEVSQSDYS 935	

Truncated telomerase (ver. 2) protein sequence lacking motif A.

Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia; neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma; smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour; stem cell differentiation; organ regeneration; organ differentiation.

Homo sapiens.

Synthetic.

WO9901560-A1.

14-JAN-1999.

01-JUL-1998; 98WO-US013835.

01-JUL-1997; 97US-0051410P.

21-JUL-1997; 97US-0053018P.

21-JUL-1997; 97US-0053329P.

04-AUG-1997; 97US-0054642P.

09-SEP-1997; 97US-0058287P.

(CAMB-) CAMBIA BIOSYSTEMS LLC.

Kilian A, Bowtell D;

WPI; 1999-106060/09.

N-PSDB; AAX18279.

New isolated vertebrate telomerase genes - used to develop products for treating cancers or for organ regeneration, nerve cell or brain cell growth following injury or bone marrow transplantation.

Claim 4; Fig 11ak-al; 134pp; English.

This sequence is a truncated human telomerase of the invention. Primers that amplify the telomerase coding sequence can be used in a method for diagnosing cancer in a patient. The telomerase can be used for detection, diagnosis and drug screening. Inhibitors of telomerase activity can be used to treat cancers such as melanomas, other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas, leukaemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin growths. Enhancers of telomerase may be used to stimulate stem cell proliferation and differentiation (expansion of haematopoietic stem cells could be administered in the bone marrow transplant context). As well, many tissues have stem cells. Proliferation of these cells may be useful in wound healing, hair growth, treatment of disease such as Wilm's tumour, organ regeneration or differentiation after injury or diseases, nerve cell or brain cell growth following injury. Note: The N-terminus of this sequence can be replaced by the sequences shown in AAY00656-Y00658

Sequence 936 AA;

Query Match 82.6%; Score 4923; DB 2; Length 936;

Best Local Similarity 98.6%; Pred. No. 0;

Matches 934; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPVRRLLGPGQWRLVQRGDPAAPRALVAQCIVCPW 60

Db 1 MPRAPRCRAVRSLLRSHYREVLPVRRLLGPGQWRLVQRGDPAAPRALVAQCIVCPW 60

Qy 61 DARPPAAPSPROVSCLEKELVARVLQRLCERGAKNVLAFGFALLDARGGPEAFTTSVR 120

Db 61 DARPPAAPSPROVSCLEKELVARVLQRLCERGAKNVLAFGFALLDARGGPEAFTTSVR 120

Qy 121 SYLPTNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

RESULT 47

AAY00651

Db 121 SYLNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAVQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGRRRLRCERAWNHSVREAGVPLGLPAPGARRRGSGASRSLLPKRPRR 240
Db 181 ATQARPPPHASGRRRLRCERAWNHSVREAGVPLGLPAPGARRRGSGASRSLLPKRPRR 240
Qy 241 GAAPERTPVCGGWAHPGRTGSDRGFCVVSAPPAEATSLGALSGRHSPHVG 300
Db 241 GAAPERTPVCGGWAHPGRTGSDRGFCVVSAPPAEATSLGALSGRHSPHVG 300
Qy 301 RQHAGPSTSPRPPTDPCPPVVAETKHFYSSGDKQLPSFLLSLRSLTGARRL 360
Db 301 RQHAGPSTSPRPPTDPCPPVVAETKHFYSSGDKQLPSFLLSLRSLTGARRL 360
Qy 361 VETIFLGRPMWPGTFRRLPRLPQRYQWRPLFLELLGNHAQCXYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGRPMWPGTFRRLPRLPQRYQWRPLFLELLGNHAQCXYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVAREKPGQSVAAPEEDTDRRLVOLLROHSSPWQVYGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVAREKPGQSVAAPEEDTDRRLVOLLROHSSPWQVYGFVRACLRRLVPPGLWGS 480
Qy 481 RINERFLRNTKFTSLGKHAKLSLQELTWKMSVRDCAWLRSPGVCVPAAEHLRBEI 540
Db 481 RINERFLRNTKFTSLGKHAKLSLQELTWKMSVRDCAWLRSPGVCVPAAEHLRBEI 540
Qy 541 LAKFLHMLSVVVELLSFFVYTTTFOKNLFFYKSVMSKLSQIGIRQHLKRVQRE 600
Db 541 LAKFLHMLSVVVELLSFFVYTTTFOKNLFFYKSVMSKLSQIGIRQHLKRVQRE 600
Qy 601 LSEAEVROHREARPAALLTSRLRPIPKDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVROHREARPAALLTSRLRPIPKDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNTERARPPGLGASVLGLDDIHRARWTFVLVRVRAQDPPPELYFKVDVTGAYDTI 720
Db 661 LFSVLNTERARPPGLGASVLGLDDIHRARWTFVLVRVRAQDPPPELYFKVDVTGAYDTI 720
Qy 721 PODRLTEVIASIIKQNTYCVRYAVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
Db 711 --DLTEVIASIIKQNTYCVRYAVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 768
Qy 781 QTSPLRDVAVTEQSSSNEASGLFDVFLRPMCHAVRIRKSVYVCGQIPQGSILSTL 840
Db 769 QTSPLRDVAVTEQSSSNEASGLFDVFLRPMCHAVRIRKSVYVCGQIPQGSILSTL 828
Qy 841 LCSLCYGMENKLFAGIRDDGLLRVDDFLAVTTHLTHAKTFLRVLRGVPEYGVNVL 900
Db 829 LCSLCYGMENKLFAGIRDDGLLRVDDFLAVTTHLTHAKTFLRVLRGVPEYGVNVL 888
Qy 901 RKTVVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDDTRTLEVSQDYS 947
Db 889 RKTVVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDDTRTLEVSQDYS 935

RESULT 48

AAW61349

ID AAW61349 standard; protein; 949 AA.

XX AAW61349;

XX AAW61349;

DT 25-MAR-2003 (revised)

DT 12-OCT-1998 (first entry)

XX Human telomerase protein 2 (TP2) partial polypeptide.

XX TP2; human; telomerase protein 2; cancer; AIDS; ageing; therapy.

XX Homo sapiens.

XX Key

FH Location/Qualifiers

FT 1..640

FT /note= "Claim 24"

Protein 1..563
Region /note= "Claim 24"
Protein 582..587
Protein 640..940
Region /note= "Claim 22"
Protein 644..648
Protein 696..953
Protein /note= "Claim 24"
Protein 696..940
Protein /note= "Claim 24"
Region 852..857
Region 884..8894

WO9821343-A1.

22-MAY-1998.

13-NOV-1997; 97WO-US021248.

15-NOV-1996; 96US-00751189.

11-JUN-1997; 97US-00873039.

16-OCT-1997; 97US-00951733.

(AMGE-) AMGEN INC.

(AMGE-) AMGEN CANADA INC.

Harrington LA, Robinson MO;

WPI; 1998-297946/26.

N-PSDB; AAV27872.

New nucleic acid encoding human telomerase protein-2 - used for

regulating telomerase activity, e.g. for treating cancer or acquired

immune deficiency syndrome.

Claim 1d; Fig 6; 150pp; English.

This polypeptide comprises a large portion of human telomerase protein 2 (TP2), a novel protein of the telomerase complex. Its amino acid sequence was deduced from partial cDNA clone 32 (see AAV27872), obtained from a human colon tumour cell line LIM1863 CDNA. A full-length polypeptide sequence (see AAW61350) is also disclosed. Expressing TP2 in a cell is used to increase telomerase activity and thus proliferation for treatment of e.g. HIV infection, AIDS and ageing disorders, while expressing an inactive mutant of TP2 (or molecule antisense to the gene) is used to decrease telomerase activity, e.g. for treatment of cancer. TP2 polypeptides can also be used to screen for agents that inhibit TP2 activity or its binding to TRIP1 (see AAW61347) or telomerase RNA, potentially useful therapeutically, also to raise specific antibodies useful in immunoassays and therapeutically as inhibitors. Also contemplated are transgenic animals in which the TP2 gene has been inactivated or is overexpressed. TP2 polypeptides are administered i.v., s.c. or orally, or they are delivered from engineered cells or gene therapy vectors. (Updated on 25-MAR-2003 to correct PR field.)

Sequence 949 AA;

Query Match 82.2%; Score 4300; DB 2; Length 949;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRVLRGDPAAFRALVAQCILVCVPW 60

Db 23 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRVLRGDPAAFRALVAQCILVCVPW 82

Qy 61 DARPPPAAPSPQVSCSLKELVARVLRQRCERAGKXNVLAFFGALLDARGGPEAPTTSVR 120

Db 83 DARPPPAAPSPQVSCSLKELVARVLRQRCERAGKXNVLAFFGALLDARGGPEAPTTSVR 142

Qy 121 SYLNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAVQVCGPPLYQLGA 180

Db 143 SYLNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAVQVCGPPLYQLGA 202

QY 181 ATOARPPPHASGRRRLCERAWNHSVREAGVPLGLPAPGARRRGGASRSRLPLPKPRR 240
Db |||||
QY 203 ATOARPPPHASGRRRLCERAWNHSVREAGVPLGLPAPGARRRGGASRSRLPLPKPRR 262
Db |||||
QY 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAERATSLLEGALSGTRSHSPSVG 300
Db |||||
QY 263 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAERATSLLEGALSGTRSHSPSVG 322
Db |||||
QY 301 ROHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQELRPSFLLSSRLPSLTGARRL 360
Db |||||
QY 323 ROHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQELRPSFLLSSRLPSLTGARRL 382
Db |||||
QY 361 VETIFLGSPPMPGTPRRLPLRPLQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPIRAAT 420
Db |||||
QY 383 VETIFLGSPPMPGTPRRLPLRPLQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPIRAAT 442
Db |||||
QY 421 PAAGVCAREKQGSVAAPBEDTPRRLVQLLRHSSPWQVYGFVRACLRRLVPPGLWGS 480
Db |||||
QY 443 PAAGVCAREKQGSVAAPBEDTPRRLVQLLRHSSPWQVYGFVRACLRRLVPPGLWGS 502
Db |||||
QY 481 RHNERRFLRNTKFKISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
Db |||||
QY 503 RHNERRFLRNTKFKISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 562
Db |||||
QY 541 LAKFLHLMMSVYVVELLSRFFYVTTTQKRLFPYRKSVWSKLQSGIQRHQLKRVQIRE 600
Db |||||
QY 563 LAKFLHLMMSVYVVELLSRFFYVTTTQKRLFPYRKSVWSKLQSGIQRHQLKRVQIRE 622
Db |||||
QY 601 LSEAEVROHREARPALITSRLRFLPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Db |||||
QY 623 LSEAEVROHREARPALITSRLRFLPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 682
Db |||||
QY 661 LFSVLNERRARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELYPVKVDVTGAYDTI 720
Db |||||
QY 683 LFSVLNERRARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELYPVKVDVTGAYDTI 742
Db |||||
QY 721 PODRLTEVIASIIKPONTYCYRRYAVVQKAHGHVRKAFKSHVSTLTDLPYMQFVAHL 780
Db |||||
QY 743 PODRLTEVIASIIKPONTYCYRRYAVVQKAHGHVRKAFKSHVSTLTDLPYMQFVAHL 802
Db |||||
QY 781 QETSPRLDAVVEQSSSLEASSGLFDVPLRFMCHHVRIRKSVVOCQIPQSGSILSTL 840
Db |||||
QY 803 QETSPRLDAVVEQSSSLEASSGLFDVPLRFMCHHVRIRKSVVOCQIPQSGSILSTL 862
Db |||||
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
Db |||||
QY 863 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYGCVVNL 922
Db |||||
QY 901 RKTVVNFFVEALGGTAFVQMPAHL 927
Db |||||
QY 923 RKTVVNFFVEALGGTAFVQMPAHL 949
Db |||||

RESULT 49
ADG90609
ID ADG90609 standard; protein; 1152 AA.
XX
AC ADG90609;
XX
DT 25-MAR-2004 (first entry)
XX
DE TERT consensus sequence SEQ ID NO:12.
XX
KW immune response; telomerase reverse transcriptase; TERT; cytostatic;
KW immunostimulant; cancer; cytotoxic T cell response.
XX
OS Unidentified.
XX
FN WO2004002408-A2.
XX
PD 08-JAN-2004.
XX
PF 24-JUN-2003; 2003WO-US019844.

XX 27-JUN-2002; 2002US-0393295P.
PR (GERO-) GERON CORP.
XX
PA Majumdar A, Ferber IA, Frolkis M, Wang Z;
XX
PI WPI; 2004-071946/07.
XX
DR Eliciting an immune response in a mammal specific for its own telomerase
XX reverse transcriptase (TERT), useful for treating or preventing cancer,
XX comprises administering a composition containing TERT of another
XX mammalian species.
XX
PS Claim 10; SEQ ID NO 12; 44pp; English.
XX
CC The invention relates to a novel method for eliciting an immune response
CC in a mammalian subject that is specific for its own telomerase reverse
CC transcriptase (TERT), comprising administering an immunogenic composition
CC containing a protein with at least 20 consecutive amino acids of TERT of
CC another mammalian species, or a nucleic acid encoding the protein. A
CC composition of the invention has cytostatic, and immunostimulant
CC activity. The protein or the nucleic acid encoding the protein is useful
CC in the manufacture of a medicament for the treatment of cancer in a human
CC or for eliciting a cytotoxic T cell response in a human.
XX
SQ Sequence 1152 AA;
Query Match 75.7%; Score 4515; DB 8; Length 1152;
Best Local Similarity 76.4%; Pred. No. 0;
Matches 880; Conservative 87; Mismatches 165; Indels 20; Gaps 6;
QY 1 MPRAPRCRAVRLSHRYREVLPLATFVRLGQGWRLVQRGDPAAFRALVAQCLVCVPW 60
Db |||||
QY 1 MPRAPRCRAVRLSHRYREVLPLATFVRLGQGWRLVQRGDPAAFRALVAQCLVCVPW 60
Db |||||
QY 61 DARPPPPAAPSFRQVSCLELVARVLQRLCERGANVLAFGFALLDARGGPEPFTTSVR 120
Db |||||
QY 61 GARPPPPAAPSFRQVSCLELVARVLQRLCERGANVLAFGFALLDARGGPEPFTTSVR 120
Db |||||
QY 121 SYLPNTVTYDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYVCGPPLYQLGA 180
Db |||||
QY 121 SYLPNTVTYDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYVCGPPLYQLGA 180
Db |||||
QY 181 ATQARPPPHASG-PRRRLG-----CERAWNHSVREAGVPLGLPAPGARRRGGASRS 231
Db |||||
QY 181 TTQARPPPHASGRRPRPVGRNFTNLGFCERAWNHSVREAGVPLGLPSPGAKRRGGASRS 240
Db |||||
QY 232 LPLPKRPRRGAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAERATSLLEGALSG 291
Db |||||
QY 241 LPLPKRARRGAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAERATSLLEGALSG 300
Db |||||
QY 292 TRHSHPSVGRQHHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQELRPSFLLSSLR 351
Db |||||
QY 301 LSLSGSVCCCHKFSSPPSLSPRPNAFQRPVTAETKHFLYSSGGRRLRPSFLLSLQ 360
Db |||||
QY 352 PSLTGARRLVETIFLGSRRPMPGTPRRLPLRPLQRYWQMRPLFLELLGNHQAQCPYGVLLKT 411
Db |||||
QY 361 PSLTGARRLVETIFLGSRRPMTSGPLCTRHLRRLRYWQMRPLFQELLGNHARCPVYRLRS 420
Db |||||
QY 412 HCPRLAAATVPAAGVCAREKQGSVAAPEE-----EDTDPRRLVQLLRHSSPWQVYGFVR 466
Db |||||
QY 421 HCPRLAAATVPAAGVCAREKQGSVAAPEEVAAPOEQTDSTRLMOLLRSHSSPWQVYFLR 480
Db |||||
QY 467 ACLRLRLVPPGLWGSRRHRRFLRNTKFKISLGKHAQLSLOBLTWKMSVRDCAWLRSPGV 526
Db |||||
QY 481 ACLKLVPPGLWGSRRHRRFLRNTKFKISLGKHAQLSLOBLTWKMSVRDCAWLRSPGV 540
Db |||||
QY 527 GCVPAAEHRLRREILAK---FHLWMSVYVVELLSRFFYVTTTQKRLFPYRKSVWSKL 583
Db |||||
QY 541 ESVPAAEHRLRREILAKFHLWMSVYVVELLSRFFYVTTTQKRLFPYRKSVWSKL 600
Db |||||
QY 584 LQSIGIRQLKRVQLRELSEAEVROHREARPALITSRLRFLPKPDGLRPIVNMVYVVGAR 643
Db |||||

```
Db 601 LQSIGVQHLEVRRLRELSQEVROHQEAWPAMPICRLRFIPKPNGLRPIVNMVSMGTR 660
Qy 644 TFRREKRAELTSRVKALFSLVNLVYERRRPGILGASVLGLDDIHRATWTFVLVRQAQPP 703
Db 661 AFGRKQAHFTQRLUKTLFSLVNLVYERTKHPHLGLGASVLGMNDIYTRWTFVLVRALDPT 720
Qy 704 PELYFKVDVTGAYDTIPQDRLETVIASLIK-PONTYCVRRYAVVQKAAHGHVRKAFKSH 762
Db 721 PRMYFVKADVTGAYDAIPQDKLVEIVIANMIRHSBSTYCIQYAVVQVQDAQOGVHKSFRQ 780
Qy 763 VSTLTDLPQYMRQFVAHLOET--SPIRDVAVIEQSSSLNEASSGLFDVFLPMCHAVRI 820
Db 781 VSTLSDLPQYMGQFLKHLQDSASALRNSVVEIQSISLNEASSSLFDFFLRLHSVVVKI 840
Qy 821 RGKSVVQCGIPIQGSILSTLCLSCVGMENKLPAGIRRDGILLRLVDELLAVTPLHSHA 880
Db 841 GRCYVQCGIPIQGSLSLTLCLSCFCGMENKLPFAEVQVQDGLLRFVDDFLVTPHLDOA 900
Qy 881 KTFELTLVRGVPEYGVVNLRTVNVFPVEDEALGCTAFVQMPAHGLFPWCGLLMDTRTL 940
Db 901 KTFELTLVRGVPEYGVVNLRTVNVFPVEDEALGCTAFVQMPAHGLFPWCGLLMDTRTL 960
Qy 941 EVQDSYSYARTSIRASITFNRGFKAGNMRKLPGLVRLKCHSLFLLDQVNSLQTVCTN 1000
Db 961 EVFCDYSYARTSIRASITFNRGFKAGNMRKLPGLVRLKCHSLFLLDQVNSLQTVCTN 1020
Qy 1001 IYKILLQAYRFHACVLOLPHQOYQWKNPTFPLRVISDTASLCYSILKAKNAGSLGAG 1060
Db 1021 IYKIFLLQAYRFHACVLOLPHQOYQWKNPTFPLRVISDTASLCYSILKAKNAGSLGAG 1080
Qy 1061 AAGPLPSEAVOWLCHQAFLLKILTRHRVTVVPLLSLRTAQTLRSKLPCTLTALAEAA 1120
Db 1081 AAGSPPEAAHWLVCQAFLLKLAHSVYKCLLGLPLRTAQQLCKLPEATWLTLEAAD 1140
Qy 1121 PALPSDFKTLILD 1132
Db 1141 PALSTDFQTLILD 1152

RESULT 50
AAW46997
ID AAW46997 standard; protein; 807 AA.
XX AC AAW46997;
XX DT 13-AUG-1998 (first entry)
XX DE Human telomerase reverse transcriptase Delta182 variant.
XX KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
XX KW cell proliferation; cancer; ageing; ribonucleoprotein.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN GB2317891-A.
XX PD 08-APR-1998.
XX PF 01-OCT-1997; 97GB-00020890.
XX PR 01-OCT-1996; 96US-00724643.
XX PR 18-APR-1997; 97US-00844419.
XX PR 25-APR-1997; 97US-00846017.
XX PR 06-MAY-1997; 97US-00851843.
XX PR 09-MAY-1997; 97US-00854050.
XX PR 14-AUG-1997; 97US-00911312.
XX PR 14-AUG-1997; 97US-00912951.
XX PR 14-AUG-1997; 97US-00915503.
XX (GERO-) GERON CORP.
XX PA (UYTE-) UNIV TECHNOLOGY CORP.
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XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX WPI; 1998-171633/16.
DR N-PSDB; AAW22382.
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX Disclosure; Fig 20; 387pp; English.
PS The present sequence represents a human telomerase reverse transcriptase
CC (hTERT) variant from the present invention. The present invention also
CC describes the following methods: (A) determining whether a test compound
CC is a modulator of hTERT, by detecting the change in hTERT recombinant
CC protein or polynucleotide, on administration of the compound; (B)
CC preparation of a telomerase RNA component; (C) detection of the hTERT RNA or
CC of hTERT with a telomerase RNA component; (D) detection of the hTERT RNA or
CC protein in a sample by binding a relevant probe to the sample and
CC detecting the complex formed or in the case of RNA detection, amplifying
CC the product and correlating the presence of complex or amplification
CC product with presence of hTERT in the sample; and (D) increasing the
CC proliferation of a vertebrate cell by increasing hTERT expression; and (E)
CC the use of an agent that causes an increase in cell vertebrate cell
CC proliferation to create a medicament that inhibits ageing. A protein
CC preparation of hTERT and the polynucleotide encoding hTERT can be used in
CC the manufacture of medicaments for inhibiting the effect of ageing or
CC cancer. Inhibitors of telomerase activity can be used to treat conditions
CC that are associated with high telomerase activity. A protein preparation
CC of hTERT can also be used in the new methods
XX
XX Sequence 807 AA;
```

```
Query Match 68.0%; Score 4052; DB 2; Length 807;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPAPRCRAVRSILRSHYREVLPATFVRRLPGQWRVLRQDPAAPFALVAQCVCVWP 60
Db 1 MPAPRCRAVRSILRSHYREVLPATFVRRLPGQWRVLRQDPAAPFALVAQCVCVWP 60
Qy 61 DARPPAAPSPROVSCCLKELVARVLQRLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120
Db 61 DARPPAAPSPROVSCCLKELVARVLQRLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120
Qy 121 SYLPTNTVTDALRGSGAWGLLRVGGDDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVTDALRGSGAWGLLRVGGDDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPRRRRLGCERAWNHVSREAGVPLGAPAGARRRGGASRSILPLKPRRR 240
Db 181 ATQARPPPHASGPRRRRLGCERAWNHVSREAGVPLGAPAGARRRGGASRSILPLKPRRR 240
Qy 241 GAAPERTPVQGSWAHPGTRGFCVSPARPABEATSLGALSSTRHSHPSVG 300
Db 241 GAAPERTPVQGSWAHPGTRGFCVSPARPABEATSLGALSSTRHSHPSVG 300
Qy 301 RQHAGPSTSRPRPMDTTPCPVYAEKTHFLYSSGDEQLRPSFLSSLSRPSLTGARRL 360
Db 301 RQHAGPSTSRPRPMDTTPCPVYAEKTHFLYSSGDEQLRPSFLSSLSRPSLTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRLLPRLPORYQWRPLFLELGNHAQCYPVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRLLPRLPORYQWRPLFLELGNHAQCYPVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYVGFVACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYVGFVACLRRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKFTISLCKHAKLSIQELTWKMSVRDCAWLRRSPGVCPVAAEHLRBEI 540
Db 481 RHNERRFLRNTKFTISLCKHAKLSIQELTWKMSVRDCAWLRRSPGVCPVAAEHLRBEI 540
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Db	481	RHNRRLRNTKKTSLGKHAKLSLQELTWKMSVRDCAWLRSPGVCVPAEHLREEI	540
Qy	541	LAKFLHMLMSYVVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIROHLKRVOLRE	600
Db	541	LAKFLHMLMSYVVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIROHLKRVOLRE	600
Qy	601	LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA	660
Db	601	LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA	660
Qy	661	LFSVLNTERARRPGLGASVLGLDDIHRAWTFVLVRQAQDPPPELYFVKVDVTGAYDTI	720
Db	661	LFSVLNTERARRPGLGASVLGLDDIHRAWTFVLVRQAQDPPPELYFVKVDVTGAYDTI	720
Qy	721	PODLRTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHV	763
Db	721	PODLRTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHV	763

Search completed: August 5, 2005, 14:07:57
Job time : 197 secs

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OM protein - protein search, using sw model

Run on: August 5, 2005, 14:04:33 ; Search time 50 Seconds
(without alignments)
2178.348 Million cell updates/sec

Title: US-10-053-758-225
Perfect score: 5961
Sequence: 1 MPRAPRCRAVRSLLRSHYRE.....TALEAANPALPSPDKTILD 1132
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	5961	100.0	1132	2 T03844	telomerase catalyt
2	724.5	12.2	1123	2 T51517	telomerase reverse
3	594.5	10.0	989	2 T03838	telomerase catalyt
4	395	6.6	1132	2 T31107	telomerase reverse
5	363	6.1	1117	2 T14891	telomerase (EC 2.7
6	356.5	6.0	884	2 S53396	telomerase catalyt
7	176.5	3.0	3530	2 A59266	unconventional myo
8	172.5	2.9	560	1 Q0BE3	BHLF1 protein - hu
9	144	2.4	3511	2 A59295	unconventional myo
10	142.5	2.4	1560	2 T00080	hypothetical prote
11	140.5	2.4	1892	2 T18314	hypothetical prote
12	140	2.3	1460	1 ED8E1F	immediate-early pr
13	139.5	2.3	552	2 F75311	ABC transporter, A
14	138.5	2.3	924	2 S27923	gene LF3 protein -
15	135	2.3	1356	1 C45219	N-methyl-D-asparta
16	134.5	2.3	946	2 JC7810	inositol 1,4,5-tri
17	134	2.2	606	2 G75302	orotidine 5'-phosp
18	133	2.2	1106	2 J00405	hypothetical 119.5
19	132	2.2	860	2 S55543	RNA-directed DNA p
20	131.5	2.2	1184	2 G01763	atrophin-1 - human
21	131	2.2	1446	1 A45344	immediate-early pr
22	130.5	2.2	1184	2 S50832	atrophin-1 - human
23	130.5	2.2	2715	2 T13049	eyelid - fruit fly
24	129.5	2.2	383	2 S32975	gene BCRF2 protein
25	129	2.2	403	2 S52796	prpl2 protein - hu
26	129	2.2	1776	2 G86280	protein TSE2.13 [
27	128.5	2.2	628	2 S01955	hypothetical prote
28	128	2.1	376	2 C75580	adenine deaminase-
29	127.5	2.1	1048	2 T31425	C-terminal domain-

ALIGNMENTS

RESULT 1

T03844
telomerase catalytic chain - human
N:Alternate names: telomerase reverse transcriptase
C:Species: Homo sapiens (man)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T03844
R:Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.
Science 277, 955-959, 1997
A:Title: Telomerase catalytic subunit homologs from fission yeast and human.
A:Reference number: Z15111; MUID:97400623; PMID:9255227
A:Accession: T03844
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1132 <NAK>
A:Cross-references: UNIPROT:O14746; EMBL:AF015950; NID:g2330016; PIDN:AAC51672.1; PID:g-
A:Experimental source: kidney
C:Genetics:
A:Gene: TRT
A:Map position: 5p

Query Match	100.0%	Score 5961	DB 2	Length 1132
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1132	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MPRAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRVLVQRCDDPAAFRALVAQCLVCVPM	60	
DB	1	MPRAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRVLVQRCDDPAAFRALVAQCLVCVPM	60	
QY	61	DARPPAAPSPROVSKELVARVLQRLCERGAKNVLAFGFALLDGGAGGPEAFVTSVR	120	
DB	61	DARPPAAPSPROVSKELVARVLQRLCERGAKNVLAFGFALLDGGAGGPEAFVTSVR	120	
QY	121	SYLPTNTVDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPYQLGA	180	
DB	121	SYLPTNTVDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPYQLGA	180	
QY	181	ATQARPPHAGSPRRRLCERAWNHVSREAGVPLGLPAGARRRGGSASRSLPLPKRPRR	240	
DB	181	ATQARPPHAGSPRRRLCERAWNHVSREAGVPLGLPAGARRRGGSASRSLPLPKRPRR	240	
QY	241	GAAPPEPTPVQGSWAHPGTRGSDRGFCVVSAPDAEATSLGALSGRTHSHPSVG	300	
DB	241	GAAPPEPTPVQGSWAHPGTRGSDRGFCVVSAPDAEATSLGALSGRTHSHPSVG	300	
QY	301	RQHAGPSTSRPRPMDTPCPVVAETKFLYSSGDKQLRPSFLLSSLRPSLTGARRL	360	
DB	301	RQHAGPSTSRPRPMDTPCPVVAETKFLYSSGDKQLRPSFLLSSLRPSLTGARRL	360	
QY	361	VETIFLGSRPWMPGTTPRLPQRYQWMPRLFLELLGNHQAQCPYGVLLKTHCPRAAVT	420	
DB	361	VETIFLGSRPWMPGTTPRLPQRYQWMPRLFLELLGNHQAQCPYGVLLKTHCPRAAVT	420	

proline-rich prote
actin-depolymerizi
probable mucin DKF
mixed-lineage prot
hypothetical prote
hypothetical prote
probable nucleic a
transposase, uncha
pol protein - silk
Wiskott-Aldrich sy
wiskott-aldrich sy
viral proteinase -
tenascin Y precurs
immediate-early pr
N-methyl-D-asparta
hypothetical prote

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Qy 421 PAAGVCAREKPGQGSVAAPAEEDTDPRRLVQLLRQHSHPWYGVFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQGSVAAPAEEDTDPRRLVQLLRQHSHPWYGVFVRACLRRLVPPGLWGS 480
Qy 481 RHNERFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCPAAEHRLREEI 540
Db 481 RHNERFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCPAAEHRLREEI 540
Qy 541 LAKFLHLMWSVYVVELLSFFVYTTTFOKRLFFYRKSVMKLSQSGIRQHLKRVOLRE 600
Db 541 LAKFLHLMWSVYVVELLSFFVYTTTFOKRLFFYRKSVMKLSQSGIRQHLKRVOLRE 600
Qy 601 LSEAEVRQHRREARPAALLTSRLRFTPKPDGLRPIVNMVYVGARTFRREKRAERLTSRYKA 660
Db 601 LSEAEVRQHRREARPAALLTSRLRFTPKPDGLRPIVNMVYVGARTFRREKRAERLTSRYKA 660
Qy 661 LFSVLNVERARRPGLLGASVLGLDDIHRAMETFVLVRQAODPPPELYEVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRAMETFVLVRQAODPPPELYEVKVDVTGAYDTI 720
Qy 721 PQDRLTEVIASIIKPNQTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
Db 721 PQDRLTEVIASIIKPNQTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
Qy 781 QETSLRDAVIEQSSSNEASSGLFDVFLRPMCHHAVIRGKSYVQCGIPQGSII STL 840
Db 781 QETSLRDAVIEQSSSNEASSGLFDVFLRPMCHHAVIRGKSYVQCGIPQGSII STL 840
Qy 841 LCSLCYGMENKLFAGIRBDGLLRVDDLLVPHLTHTAKTFLRTLVRGPEYGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRBDGLLRVDDLLVPHLTHTAKTFLRTLVRGPEYGCVVNL 900
Qy 901 RKTVMNFFVEALGCTAFVOMPAGHLPFWCGLLDDTRTLEVQSDYSSYARTSIRASLTF 960
Db 901 RKTVMNFFVEALGCTAFVOMPAGHLPFWCGLLDDTRTLEVQSDYSSYARTSIRASLTF 960
Qy 961 NRGFKAGNRRKRLFGVLRKLSHSLFDLQVNSLTQVCTNIVKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNRRKRLFGVLRKLSHSLFDLQVNSLTQVCTNIVKILLQAYRFHACVLQLP 1020
Qy 1021 FHOQWKNTPTFLRVISTASICYSILKAKNAGSLGAKGAGPLPSEAVOMLCHOAELL 1080
Db 1021 FHOQWKNTPTFLRVISTASICYSILKAKNAGSLGAKGAGPLPSEAVOMLCHOAELL 1080
Qy 1081 KLTHRVTVVPLLSRLTAQTLQSLRKLPGTTLTALEAANPALPSDFKTILD 1132
Db 1081 KLTHRVTVVPLLSRLTAQTLQSLRKLPGTTLTALEAANPALPSDFKTILD 1132

RESULT 2
TS1517
telomerase reverse transcriptase - Arabidopsis thaliana
N:Alternate names: protein F5E19_190
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: TS1517
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
submitted to the Protein Sequence Database, August 2000.
A:Reference number: Z25394
A:Accession: TS1517
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1123 <SAT>
A:Cross-references: UNIPROT:Q9SPU7; EMBL:AL391147
A:Experimental source: cultivar Columbia; BAC clone F5E19
C:Genetics:
A:Map position: 5
A:Introns: 100/3; 125/3; 147/3; 185/1; 300/3; 325/1; 369/2; 414/3; 765/3; 942/2; 1033/2
A>Note: F5E19_190

Query Match 12.2%; Score 724.5; DB 2; Length 1123;
Best Local Similarity 23.8%; Pred. No. 3.2e-41;
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Matches 294; Conservative 199; Mismatches 511; Indels 233; Gaps 39;
Qy 1 MPRAPRCRAVRSLRSHYREVLPLATFV-----RRLGPGQGR-----L 38
Db 1 MPRKPRHRVPEILLWRLFGNRAARNLDAI VDLI PNRIQPEQCRGQGLCCSSDKKPAFL 60
Qy 39 VQRGDPAAFRALVAQCLVCPWDARPPPAAPSFRQVSLKELVARVLQRL---CERGAKN 95
Db 61 LRSDDPITHYRKLHRCFV-VLHEQTPLLDPSPTSMWSQREIIVERIITEMOSGCD--CON 117
Qy 96 VLAFGFALLGARGGPEAFPTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLIAR 155
Db 118 VICARYDKYDOS-----SPILSLLT-SSWFEFLKRGVGHVWVYLLOQ 159
Qy 156 CALFVLVAPSCAYQVCGPPPLYQLGAAT-----QARPPPHASGPPRRRLGGERAWNHSYRE 209
Db 160 TSIFLPLLGKKHQVSGPPLCIKHKRTLSVHENKRRDDNVQPTTKRQLWSSAVDDCPKD 219
Qy 210 AGVPLGLPAPG-----ARRRGSASRSLPLPKRPRGA-----APEPERTVGOQSWA 257
Db 220 DSATI-TPIVGEDVDHREKTKTKRSRIYLRKRRKQKRVNPKVKVDCNAPCITP----- 271
Qy 258 HPGRTGPSDRGFCVSPARPABEATSLEGALSGTRHSHPSVGRQHHAGPSTSRPPRPW 317
Db 272 ---STNGKVTG-----NDENMLHIGINGSLTDFVKQAKQ----- 303
Qy 318 DTPCPPVYAETKGFYLS-SGDKEQLRPSFLSSLRPSLTGARRLIVETIFLGSRRPMPGTP 376
Db 304 -----VKRNKNPKFGLSETYSVIPNHILKTLRPNCSDSKLLMNHIFGEVNVWSTTPS 356
Qy 377 RRLPRLPQ-----RYWQMRPLFLELLGNHAQCPYVLLKTHCP-----LRAAVTPAAG 424
Db 357 HGKNCPSGSGICLYHSLKSLKLNLIKTKSHLKMLLDKHCPVLLLOEDALSKGTTSSQSS 416
Qy 425 VCAREK---PQGSVAA-----PEEEDTDPRVLQLLRQHSHPWYGVFVRACLRRLVPPG 476
Db 417 --RQKADKPLHGSSSQTKPKCPSVEERKL-----YCTNDQVVSFIWACRIVIPES 468
Qy 477 LMGSRHNRERFLRNTKFPISLGHAKLSLOBLTWKMSVRDCAWLRRSPGVGCPAAEHRL 536
Db 469 LLGTTTHQMRVLKNIAMFVSRRNEKCTVNOQLHKVXPSDPPFPARKE--LCCMVNGHEL 526
Qy 537 REE-----ILAKFLHLMWSVYVVELLSFFVYTTTFOKRLFFYRKSVMKLSQSIG 588
Db 527 QSESIRSTQOQMLCTKWISLFWLEIVKLVHFNFTATESQGGRLNIYYTRKESWELISKE 586
Qy 589 IROHLKRVOLRELSAEVROHREARPAALLTSRLRFPFKPDGLRPIVNMVYVGARTFRRE 648
Db 587 ISKALDGYLVDDAEASSRKK-----LSKFRFLPKANGVRVLD-----FSSS 630
Qy 649 KRAERLTSRVKALFSVLNVERARRPGLLGASVLGLDDIHRAMRTFVLVRQAODPP-PELY 707
Db 631 SRSQSL---RDTHAVLKDIQLKEPDLVGGSVFDHDDFYRNLCPLYLHLRSQSGLPPLY 686
Qy 708 FVKVDVTGADYDTPQDRITEVIASIIKPNQTYCVRRYAVVQAAHGH-----YRKAPKS 761
Db 687 FVADVFKAQFSDVDQGLLHVLIQSLKDE--YILNCRCLVCCGKRKNVWVKILVSSDKNS 744
Qy 762 HVSTLTDLQPYMRQFVAHLQBSTPLRDAVIEQSSSNEASSGLFDVFLRPMCHHAVIR 821
Db 745 NFSRFTSTVPYNA-----LQ-----SIVVDKGENHRVRKDLMWVIGNMLKNNMLQILD 792
Qy 822 GKSYVQCGIPQGSII STLCSLCYGMENKLFAGI-----RRDGL----- 862
Db 793 KSFVYQIAGIPQGHRLSSLLCCFYVYGHLERTLIVPFLSEASKDVSSKCSREEELIPTS 852
Qy 863 --LLRLVDDLELLVTPHLTHTAKTFLRTLVRGPEYGCVVNLKTVVNFVPEDE----- 912
Db 853 YKLLRFIDDLVLFVTSRDQASSFYHRLKHGPKDYNCFMNETKFCINCFDKBEHRCSNRM 912
Qy 913 --ALGGTAFVOMPAHGLFPWCGLLDDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGNRM 970
Db 913 FVGDNQGVFFVR-----WTGILLINSRTFEVQVDYTYLSGHSLSSTSVAWQNKPVNL 964
```



```
Query Match          6.6%; Score 395; DB 2; Length 1132;
Best Local Similarity 22.2%; Pred. No. 1e-18;
Matches 136; Conservative 114; Mismatches 305; Indels 58; Gaps 15;

QY 450 QLLRHSSPQWQYGFVRAACRLRLVPPGLWGRHNRRLNTRKTFISLGHAKLSLQELT 509
DB 451 QLFVEQDQORQISNLFTEFVANVPKPLEGK-NKKIFNKQMLQPVKFNRESFTKISLL 509
QY 510 WMSVRDCAWLRSPGVCVPAAEH---RLREILAKFLHLMMSVYVVELLRSFFYVTE 566
DB 510 NKFRVNEVSWL-----SPKCKDENKFFMNEHVFVKLVKWFEDLAITLMRCYFST 565
QY 567 TFQKNRLFYKSVMSKLSQIGIROHLKRVOLRELSEAEVQHRARPALLTSRLRTPK 626
DB 566 AKEYQRIFYYRKNINWMIRLSIDLLKQ-NLKQVEKKEMRIFCESQ-NFAPGKLRLIPK 623
QY 627 PDGLRPIVNMVYVGARTFRRE-----KRAERLTSRVK---ALFSVLNYSRARRPGLLG 677
DB 624 GDTFRPIM-----TFNRKIPNOVGKFSQSRMTNNKLOTAMMLKXKMPKHSFG 674
QY 678 ASVLGLDTHRAWRTFVLVRQAQDPPPELYFVKVDVTGAYDTIPDRLTEVIAS----- 731
DB 675 FAVENYDDIMKRYENFVQWK-QINSPKLYFVAMDIKCYDNVDCERVVNFQKSDMLDK 733
QY 732 -----LIKPNQTYCVRRYAVVQAAHGHVRKAFKSHVSTLTLDQPYMQFVAHLQET 783
DB 734 EYFIINTFVLKRNKNIIVERSNFRKLPKQVRYFKQK-IGIDGSSYPTLFEILLEPND 792
QY 784 SPLRDAVIEOSSSLNEASSGLDFVFLRFMCHHAVIRGKSVVOCQIPQSGISLTLCS 843
DB 793 LNMKBTIIVEQBQRKFPKNDLLQVLVKICQNNYVTFNKQYKQMKGIPOGLCVSYILSS 852
QY 844 LCYGMENKLFAGIRRD-----GLLLRLVDDFLVTHLTHAKTFLRTLVRGVPEY 894
DB 853 FYIANLEENALQFLRKESMDPEKPEINLLMLRLTDDYLLMTTEKNAMLFIEKLYQLSLGN 912
QY 895 GCVNLRKTVNVPFVEDEALGTAFOV---NPAHGLFPMCGLLDTRTLEVSQDSSYAR 951
DB 913 FPKFHKMLKTNFALNQLKIGCTNTQDIDSINDDLFWIGISIDIKTLNIQNT-NIKK 971
QY 952 TSIRASLTFNRGFKAGRNMRKLFGLVRLKCHSLFLDLQVNSLQTVCTNVIKILLQAYR 1011
DB 972 EGILCTLVNMQTNSILWLKXKLSFLNMNISFYFKSTINTKQPANITLSKLYIAAEK 1031
QY 1012 FHACVLQLP-FHQ 1023
DB 1032 YVACCOEFPKRFHE 1044

RESULT 5
Tl4891
telomerase (BC 2.7.7.-) catalytic chain p133 - Tetrahymena thermophila
N:Alternate names: telomerase reverse transcriptase
C:Species: Tetrahymena thermophila
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: Tl4891
R:Collins, K.; Gandhi, L.
Proc. Natl. Acad. Sci. U.S.A. 95, 8485-8490, 1998
A:Title: The reverse transcriptase component of the Tetrahymena telomerase ribonucleoprotein complex
A:Reference number: Z18252; MUID:98337941; PMID:9671704
A:Accession: Tl4891
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1117 <COL>
A:Cross-References: UNIPROT:O77448; EMBL:AF061284; NID:g3335166; PID:g3335167; PIDN:AAC3
C:Genetics:
A:Gene: TERT
A:Genetic code: SGC5
C:Keywords: nucleotidyltransferase

Query Match          6.1%; Score 363; DB 2; Length 1117;
Best Local Similarity 20.2%; Pred. No. 1.6e-16;
Matches 193; Conservative 160; Mismatches 368; Indels 234; Gaps 35;

QY 322 PPVVAETHKFLYSGDKEQLRPSPLLSRLSPSTGARRLVETIIFLGSRPMPWPTERRLP 381
DB 239 PGVP-KSFFNYS-----EIKGQFKVIOEKLQGR-----FINSKIKPDHPOTIIK 286
QY 382 --LPORY-----WOMRPLFLE-----LLGNHAQCPYGVLLKTHCPLRAAAVTPAAGVCAR 428
DB 287 KTLKEVQSKNFSCQERDILFLEFTEKIVQNFHNFNFNLLKFKCL----- 333
QY 429 EKPGSVAAPBEEDTPRRLVQLLRHS-----SPQVYGFVRACL 469
DB 334 -----PENYQSLKSQVKQIVQSENKANOQSCENLNSLYDTEISYKQITNPLRQII 384
QY 470 RRLVPPGLWGRHNRRLNTRKTFISLGHAKLSLQELTWMQSVRDCAWLRSPGVCV 529
DB 385 QNCVPNQLLGGK-NFKVLEKLYEFVQMKRFENQKVDYICFMDVDFVEWF-----V 435
QY 530 PAAEHL-----REETILAKFLHLMMSVYVVELLRSFFYVTEFQKNLFFYKRSV 580
DB 436 DLKQKFTQKKYISDRKKILGDLIVFIINKIVIPVLRVNFYITEKHGSGQIFYYRKP 495
QY 581 W---SKLQSIGI-RQHLKRVQLRELSEAEVQHRARPALLTSRLRTPKDGRLPVM 636
DB 496 WKLVSKLTIKLBEELEKVEEKLIPEDSFOKYPQ-----GKLRIPKKSFRPIM-- 546
QY 637 DYVVGARTFRREKRAERLTSRVKALFS-----VLNERARRPGLLGASVLGLDDIHRWRT 692
DB 547 -----TFLRKQKQNIKLNLQILMDSQVLFRNLKMDLQKIGSYVFNKQISEKFAQ 599
QY 693 FVLVRQAQDPPPELYFVKVDVTGAYDTIPDRLTEVIASIIKPQNTYCVRRYAVVQAAH 752
DB 600 FIEKWKNG-RPQLYVYTLDIKKCYDSIDQWKLNFNQSDLIQDTYFINKYLLFQNRK 658
QY 753 GHVAKAPKSHVSTLTLDQ-----PYM-----ROFVAHLOE----- 782
DB 659 PLLQIQOTNNLNSAMEIEEEKINKKPFKMDNINFPYFNLKERQIAYSLYDDDDQILQKG 718
QY 783 -----TSPLRDAVIEOSSSLNEASSGLDFVFLRFMCHHAVIRGKSVVOCQIPQSGISL 838
DB 719 FKETQSDRRPFTVINQDKPRCITKDIHNLKHSIQYNVISFNKVPKPKRKGIPQGLNIS 778
QY 839 TLICSLCVGMENKLFAGIRRD-----GLLLRLVDDFLVTHLTHAKTFLRTLVRGV 891
DB 779 GVLCSFFFGKLEEBYTOFLKNAEQVNGSINLLMLRLTDDYLFISDSQNALMLIVQLNCA 838
QY 892 PEYGVVNLKRTVYN--FPVEDEALGTAFOVPAHGLFPMCGLLDTRTLEVSQDSSY 949
DB 839 NNNGFMFENDQKITTNFQFQEDYNL---EHPKISVQNECQWIGKSIDMNTLEIK---SIQ 892
QY 950 ARTSIRASLTFNRGFKAGRNMRKLFGLVRLKCHSLFLDL-----OVNSLQTVCTNII 1002
DB 893 KQTOQETINQITINVAISI-KNLKSQKKNLR-----SLFLNLQIDYFNPNNISFEGLCRLQY 947
QY 1003 ---KILLQAYRFHACVLQ-----PQQQVWK---NPTFFLRVISDTAS-----LCY- 1044
DB 948 HHSKATVWKFPFMTKLFQIDLKSKQYSQVQKENTNENFLKDIYYTVDEVCKILCYL 1007
QY 1045 -----SILKAKNAGMSLGAKGAGPLPSEAVQWLCHQA 1077
DB 1008 QFEDEINSNIKEIFKNLYSWIMWDIIVSYLKKKKQ-----FKGYLNKL----- 1050
QY 1078 PLLKLTHERVTVPL-LGSLRTAQTOLSRKLPGLTTLTALEAANPALPSDFKTL 1131
DB 1051 -LQIRKSRFFYLKGBGCKSLQILISQOQYQNLKKLEAIEFIDLNNLQDITKLI 1104

RESULT 6
S53396
telomerase catalytic chain EST2 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein L8543.12; protein YLR318W
C:Species: Saccharomyces cerevisiae
C>Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S53396
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R;Du, Z.
 submitted to the EMBL Data Library, February 1995
 A:Description: The sequence of *S. cerevisiae* cosmid 8543.
 A:Reference number: S53390
 A:Accession: S53396
 A:Molecule type: DNA
 A:Residues: 1-884 <DUZ>
 A:Cross-references: UNIPROT:Q06163; EMBL:U20618; NID:G2258165; PID:G662136; GSPDB:GN0001
 A:Experimental source: strain S288C (AB972)
 C:Genetics:
 A:Gene: SGD:EST2; MIPS:YLR318W
 A:Cross-references: SGD:S0004310; MIPS:YLR318W
 A:Map position: 12R

Query Match 6.0%; Score 356.5; DB 2; Length 884;
 Best Local Similarity 22.1%; Pred. No. 3.1e-16;
 Matches 167; Conservative 127; Mismatches 309; Indels 151; Gaps 28;
 QY 329 KHLVSSGDKQLRPS--FLLSRLPSLTGARRLV---ETIFLGSRPMPGTPRRLPLRP 383
 DB 185 KQFLH---KLNINSSFPFYSKILPSSSIKGLTDLREAIPTNLVKIP 230
 QY 384 QRYQWRPLFLE-LLGNHACQPGVLLKTHCPRAAVTAAAGVCAREKPGGVAAPED 442
 DB 231 QRLKVRINLTQKLLKRLKRLNYVSLNSICP-----PLEGTVL----- 269
 QY 443 TDPRLVLQRLHSSPQVYGFVRACLRLVPPGLWGRHNRRLNTKKFISLGKIAK 502
 DB 270 ----DLSHLSRO-SPKRVLKIIIVILQKLLQFMEFGSKNKGKIIKNLNLISLPLNGY 324
 QY 503 LSLQELTWKMSVRDCAWLRSPGVGCPAAEHLRL--EELAKFLHWSVYVVELLSRF 560
 DB 325 LFPDLSLLKRLKDFRWL---FSDIWTGKNFNENLQALCFISWLPQLIPKIIQTF 380
 QY 561 FYVTETFOKRLFFVRKSVMSKLSQIGIRQHLKRVQLRELSEAEV-ROHRRARPALLT- 618
 DB 381 FYCTEIS-STVTIVFRHDTWKNLITPFIYEFKTY----LVENNVCRNHNSYTLNFNH 435
 QY 619 SLRLFPKPDGLRPIVMDYV-----GARTFRREKRAELTSLRVKALFSLVNYERARR 672
 DB 436 SKMRIIPKKS-----NNEFRIIAPCRGADSEEFYIKENHKNALOPTOKILEYLRNKR 489
 QY 673 PGLGASVLGLDDIHRAMRTFVLV--RAQDPPELPYFKVDVTGAYDTIPQDRLTEVIA 730
 DB 490 PTFSP-TKIYSPQIADRIKEFKORLLKFNVLPELYFMKFDVSKYDSI PRMECWRLK 548
 QY 731 SIIPKONTVCVRYAVVQAAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQETSLPDAV 790
 DB 549 DALKNENGPFVRSQYFFN--TNTGVILKF-NVYNASRVPKPY-----EL 589
 QY 791 VLEQSSSLNEASSGLPDLFRMCHHVRIRKSVYQCOGIPQGSITLSTLLCSLCYGDW- 849
 DB 590 YIDNVRTVLSNQDVINVMEIFKTLWVEDKCIYREDGLFGQSSLSAPIVDLVYDDL 649
 QY 850 --ENKLFAGIRDGLLLRLVDLFLVTHLTHAKTFLRTLVRGVPYGCVMNLRTKV-VN 906
 DB 650 EYSEFKASPSQDTLILKLADFLIISTDQOQVINIKKLAMGGFQKYNKANEDKILAVS 709
 QY 907 FPVEDBALGGTAFVQMPAHGLFPWCGLLDTLTLEVOSSYSSYARTSIRASITFNKGFKA 966
 DB 710 SQSDDDT-----VIQFCAMHIFVKEVLEVKHSTWNPHIRS-----KS 748
 QY 967 GRNMRKLGVLRLKCHSLFLDLQVNSLOTVCNI-----YK-----ILLQA 1009
 DB 749 SRGIFRSLIALFNTRISYKTIPTDNLNSTNTVLMDIHHVKNISSECYSAFKOLSINVTQN 808
 QY 1010 YRFHACVLQLPFHQVQWKNPTFLRVISDTASLC 1043
 DB 809 MQFH-----SFLQRIENTVSCG 826

unconventional myosin-15 - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C:Accession: A59266
 R:Li, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; M.
 an, T.B.; Fridell, R.A.
 Genomics 61, 243-258, 1999
 A:Title: Characterization of the human and mouse unconventional myosin XV genes respons
 A:Reference number: A59266; MUID:20021762; PMID:10552926
 A:Accession: A59266
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-3530 <LIA>
 A:Cross-references: UNIPROT:Q9UKN7; GB:AF144094; NID:G6224682; PID:AAF05903.1; PID:G62
 F:1225-1887/Domain: myosin motor domain homology <MMO>
 Query Match 3.0%; Score 176.5; DB 2; Length 3530;
 Best Local Similarity 20.6%; Pred. No. 0.0041;
 Matches 263; Conservative 144; Mismatches 392; Indels 475; Gaps 68;
 QY 107 ARGGPPEAFTTS-----VRSYLP-----NTVTDALRSGGAWG 138
 DB 2313 SRGGKVVFGNSWDSDEDMSTRPQOEHPKVLDSGYSSHNDGTNGTEAQRGT-ATH 2371
 QY 139 LLLRRVDDVLVHLLARCALFVLVAP-----SCAYQVCGPPLYQLGAA--- 181
 DB 2372 QESDSLGEPAVPHKGLDCLVDSLPVLSYGDADLEKPTAIAYRMKGQGPQGGSSSGTE 2431
 QY 182 -TOARPP---PHASGPRRLGECERAWNHSVRAGV---PLGLPAPGARRGGSSAS-RSLP 233
 DB 2432 DTPRPPEPKPTPGLDASTALQQAIFH--KQAVLLARGMTIQTALQOQPLSAALRSLP 2489
 QY 234 LPKRRRGAAAPERTPVGGQSWAHPGRTRGPRSDRGFCVVSPARPAEATSLEGALSGTR 293
 DB 2490 AEKPP-----APAAQTSVGTGPPAKPVLRL-----ATPKPLAPA----- 2524
 QY 294 HSHPSVGRQHAGAPSTSPRPMDTPCPVYA-----ETKHFLYSSGDKQLRSPFLL 347
 DB 2525 -----PLAKAPRLPIKPAAPVLAQOQASPET-----TSPSELVRYSTLN 2565
 QY 348 SSLRPSLTGARLLETIFLGSRPMPGTPRRLPLRPQRYWQMRP-----LFLELLGNH 400
 DB 2566 SEHFFQPT--QQIKNIVRQYQPPFRGPEALRKDGKGVKMRPDPHEALMILKQOMTH 2623
 QY 401 AQCPYV-----VLKK--THCLRAAVTPAAGVCAREKPGGSAVAPEE-EDTDPRRLV 449
 DB 2624 LAAAGTQVSRRAVALVKVTSAP-RPSMAPTSAL-----PSSLEPPELTQTLRLRLI 2677
 QY 450 --QLLRHSSPQVYGFVR-----ACLR-----RL 472
 DB 2678 NENFYQYQDAPWKI--FLRKEVFPKDSYHPVQLDILLFRQILHDLTSLSEACLRISDERL 2735
 QY 473 VPPGLWGRHNRRLFNRTYKFIISLG-KHAKLSLOELTWKMSVRDCAWLRSPGVGCVPA 531
 DB 2736 RMKALFAQOQ-----LDTQKPLVTSVKRAVVSTARDTWEV-----YFSRIPTATGSVGT 2785
 QY 532 AEHLREBELTAKFLHWSVYVVELLR-----SFFVYVTEFTT-OKNR 572
 DB 2786 G-----VQLLA-----VSHVGIKLLRMVMVKGQAGQQLRVLRVAYSFADILFTVMPSONM 2834
 QY 573 LFFYRKSVMKLSQSIGIRQHLKRVQLRELSEAEVQRHREARPAALLTSRLRFLPKPDGLRP 632
 DB 2835 LEFNLAS--EKVILFSARAH---QVKTLDVDDFILELKK----- 2867
 QY 633 IVNMVYVVGARTFRREKRAELTSLRVKALFSLVNYERA-----RRPGLLGAS----- 679
 DB 2868 --DSDYVAVARNFLPEDPA-----LLAFHKGDIIHLQPLEPRPVGVSGACVVR 2913
 QY 680 --VLGLDDIHR-----AMRTFVLVRQAQDPPELPYFKVDVTGAYD-----TIP-QDRLT 726
 DB 2914 RKVYVLEELRRGPDGFWGRFGTIRHGRVGFPSSEL-----VQPAAPDFLOLPTPEPGRRAA 2969
 QY 727 EVIASIIRKPNQTCYVRRY-----AVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQ 781

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Db 2970 AVAAVAGAAAAQEVRRREGPPVARSADHGEDALALPPY-TMLEFAQKFRDPQRRPQ 3028
QY 782 E-----TSPRLDAVVIEQSSLINEASSGLFDFVFLRFMCHAVR 819
Db 3029 DGLRLKKEPRESRTLEDMLCTKTPLOESLIELSDSLSKWATDMFLAVRMFGDAPLK 3088
QY 820 IRGKSYVOQGIPOGSIILSLCSICYGD---MENKLPAGI-----RRDG 861
Db 3089 GQSDLDVLNC-----LLKLC-GDHEVMRDECYQVVKQITDNTSSKQDSCQGW 3136
QY 862 LLRLVDDF---LLVTPHLTHAKFLRLTLVR--GVPEYG---CVVNLKRTVNVFPVED 911
Db 3137 RLLYIVTAYHSCSEVHLHLTR---FLQVSRTPGLPFGQIAKACEQLQKTL----- 3186
QY 912 EALGGTAFVQMPAHGLFPWCGLLLDTRTEVQSDYSSYARTSIRASLTFRNGFKAGRNMR 971
Db 3187 -RFGG-----RLPSS-----TELRAWL-----AGRSK 3210
QY 972 RKLK---GV---LRLKCHSLFLDQVNSLQTVCT-----NIYKILLQAYRPHA 1014
Db 3211 RQLFLPGLGRLHLKIKTCTVALDV---VEEICAEMALTRPEAFNEYVIFVVTNRGQHV 3266
QY 1015 CVL-----QLPEHQVWKNTPEF-----LRLVSDTASLCY 1044
Db 3267 CPLSRAYILDVASEMEQVGGYMWFRVLDQPLKFENELYVTMHNQVLDPLYLKGLF 3326
QY 1045 SILKAKNAGMSGAKGAGPLPSEAVQMWLCHQAFLLKLTTRHVT---YVPLLGLSLRTAQ- 1100
Db 3327 SSVPASR-----PSEQ---LLQVSKLASIQHRAKDHFLP---SVREQVE 3366
QY 1101 ---TOLSKRLPOTT 1111
Db 3367 YIPAQLYRTTAGST 3380

RESULT 8
QBEB3
BHLF1 protein - human herpesvirus 4 (strain B95-8)
C:Species: human herpesvirus 4, Epstein-Barr virus
C>Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
C:Accession: A03742
R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
A:Reference number: A93065; MUID:85035713; PMID:6092825
A:Accession: A03742
A:Molecule type: DNA
A:Residues: 1-660 <BAN>
A:Cross-references: UNIPROT:P03181
R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
Nature 310, 207-211, 1984
A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A:Reference number: A03794; MUID:84270667; PMID:6087149
A:Contents: annotation; protein coding region
C:Comment: The sequence contains four perfect repeats (residues 149-273, 274-398, 399-52
C:Superfamily: human herpesvirus 4 BHLF1 protein

Query Match 2.9%; Score 172.5; DB 1; Length 660;
Best Local Similarity 26.1%; Pred. No. 0.00078;
Matches 94; Conservative 16; Mismatches 159; Indels 91; Gaps 16;
QY 167 AVQVC--GPPLYQLGAATQA--RPPPHASGPRRLGCRANWHSVREAGVPLGAPGAR 222
Db 244 AAQRCFAGPPPTTRSGAAQRTTHRRPPGCPRSARNPGCPRTWR---RRSGAQRGHPPGAG 300
QY 223 REGGSASRLP-LPKRPRGAPEP-ERTPGQGSMAHPGRTGRGSDRGFCV-VSPAR-- 277
Db 301 QRPSGPTGGRPAAGPAGTPAAGPGGAAVPSGATPHPERGSGPADPPAARLPPEQOE 360
QY 278 -----PAEATSLLEGAL-----SGTRHSH 297
Db 361 PRLPDALAAQRCFAGPPPTTRSGAAQRTTHRRPPGCPRSARNPGCPRTWRRRRSGAQRGHP 420
```

```
QY 298 SVGRQHAGPSTSRPRPW--DTFCPP-----VVAETKHFLLYSGDKX-----QLR 342
Db 421 PPGAGQPSGTGTPAAPGAGPTPAAPGPGGGAAPSGATPHPERGSGPADPPAARLP 480
QY 343 PSFLLSSRLSLTCARLIVETIFLGSRPWMPG-----TPRELRLPQ-----RYWQM 389
Db 481 PEREPLRPDLAAARCP-----AGPPPTTRSGAAQRTTHRRPPGCPRSARNPGCPRTWR 536
QY 390 RPLFLELLGNHAQCPYGVLLKTHCPL--RAAVTPAAGVCAREKPGQGSVAAPEEEDTPRR 447
Db 537 RS-----GAQRGHPPGAGQRPSTGTPAAPGAGPTPAAPGPGGGAAPSGATPHPER 591

RESULT 9
A59295
unconventional myosin-15 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C:Accession: A59295
R:Li, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; Mi
an, T.B.; Fridell, R.A.
Genomics 61, 243-258, 1999
A:Title: Characterization of the human and mouse unconventional myosin XV genes responsi
A:Reference number: A59266; MUID:20021762; PMID:10552926
A:Accession: A59295
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-3511 <LIA>
A:Cross-references: UNIPROT:Q9QZ4; GB:AF144095; NID:G6224684; PIDN:AAF05904.1; PID:G622
C:Genetics:
A:Gene: MGI:Myo15
A:Cross-references: MGI:1261811
A:Map position: 11:33.9
F:1209-1871/Domain: myosin motor domain homology <MMO>
```

```
Query Match 2.4%; Score 144; DB 2; Length 3511;
Best Local Similarity 17.6%; Pred. No. 0.68;
Matches 189; Conservative 117; Mismatches 385; Indels 380; Gaps 44;
QY 3 RAPRCRAVRSLLRSHYREVLPATFVRRLPGQWRVLVQGDPAAPRALVAQCLVCPV-- 59
Db 677 RPPLASPYSLRQH-----PPW-----AAAHVFPFPPQA 707
QY 60 --WDARPPPA-----PSFQVSCIKELVARVLQRLCERGAKNVLAFQFA 102
Db 708 NMGFAEPGPGTSPEVAPDLLAFPPVPSFR-----ASRSRRAAYGFP 751
QY 103 LLDGARGGPEAFITTSVRSYLPNTVTD--ALRGSGAWGLLLRRVGDVVLHLLARCALFV 160
Db 752 -----SPSLIGSRRRPHLPSPQPSLRSLPQQG----- 778
QY 161 LVAPSCAYQVCGPPLYQLGAATQAQAPPPHAGSPRRRLGCRANWHSVREAGVPLG----- 215
Db 779 -----YHSLGCLPSQLSLRGRFPQPPPPRRPQSLREAP--SLRASRGLGPPRSP 830
QY 216 -----LPAGARRRGGSASRSLPLPKR-----PRGAAPERT---PVGGS 255
Db 831 VLGSFRPPSPPLLLKHGPRHRSNLNLPGLRPLRTRRLSEPPTRAVKFWVHRAVPPPPSAGP 890
QY 256 WAHPQRTGSDRGFCVVSAPAPAEATSLLEGALSGTHSHPSVGRQHHAGPPSTSRPBR 315
Db 891 W---GASTGALE-----QENQREADESETPTWTFPLAPSVDVMPPTPQRPPS 935
QY 316 PWDTPC-----PPVVAETKHFLLYS-----GDKEQLRPSFLLS 348
Db 936 PWPBGISLGRFSPPPVPENPILLEHTSPSCPOSEDRVSNLTGIFLQHHDPGPGQLTK 995
QY 349 SLRPSLTGARRLVETIFLGSRPWMPGTPRRL-PRLPQRYWQMRPLFLLELGNH----- 400
Db 996 SADPSL---EKPEEVTLLGD--PQPAPBEALNTPPNKNVSVSRKVLRSASYPLVTCQK 1051
QY 401 --AQCP---YGVLLKTHCPLRAAVTPAAGVCAREKPGS----- 434
```

Db 1052 ARATPQWHRWKTSTPAPLAPTRAPGPLLKAGEQPAEGRFAVMPQVRGVSSFRPK 1111
QY 435 ----VAAPPEEDTDPR-----LVQLLRHSSPMOVYGVPRAC 468
Db 1112 GAPVQPPHPDDEQAPQACSLRWCLWPPTDAHCLWSRITYSSQSHLRHGDC 1171
QY 469 LRLR---VPPGLWGRHNRRLNTKFKISGKHAQLSLQBLTWKMSVRDCAWLRSPG 525
Db 1172 HKSLWKTRPOSW---QNKWHSIRNLPMSRSEQRHEDGVEDTQLEDLQETVLAN--- 1225
QY 526 VCVPAAEHLREELAKEL-----HMLMSVYVELLSRF-----FYTT 564
Db 1226 ----LKTRFRNLITYIGSILVSNPYRMFAIYGPQVOQYSGRALGENPHLFAITA 1279
QY 565 ETTFOK-----NRLFFYR-----KSVMSKL-----QSIGIRQHLKRVQLRELSE 603
Db 1280 NLAFKMLDAKQNCQVSIISGSGSKTEATKILIRCLAAMNQRDVMQIKILEATPLE 1339
QY 604 A-----EVQRHREAPALTSRLRFPKDPGLRPIVMNDYVVGARTFREKRAER----- 653
Db 1340 AFGNAKTVRNDSNR---PGKEVEIFEGGVICGAIITSQYLLKSKRIVFOAKNERNYHIF 1396
QY 654 ----LTSRVKALSVLNYE-----RARRPGILGASVLGLDDIHRAWRTFVLVRAQD 701
Db 1397 YELLAGLPAQLROAFSLQEAETYYILNQGNCEIAGKS--DADDPR----- 1441
QY 702 PPELFFVKVDVTGAYDTIPQRLTEVIASIIKPNQYCVRRYAVVQKAHGHVRKAFKS 761
Db 1442 ----LLAMEVLG-FTSEDDQSIIFRILASILHLGNVFEKHETDAQEA----- 1485
QY 762 HVTSLTDLQPMYRQFVAHLQETSP--LRDAVIEQSSLSNEASSGLFDVFLRMCHEAVR 819
Db 1486 SVVSAREIOA-----VAELLOVSPGLQKAITFKVTETIRE-----KIFTEPLTVESA 1534
QY 820 IRGKSYVQCGIPQSGSILSTLCSLCYGDMEKNLFAGI--RRDGLLLRLVD 868
Db 1535 AR-----DATAKVLVALLFGWLITRVNALVSPKQDTLSAILD 1572

RESULT 10
T00080
hypothetical protein KIAA0522 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C:Accession: T00080
R:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
DNA Res. 5, 31-39, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. IX. The complete
A:Reference number: Z14086; MUID:98290545; PMID:9628581
A:Accession: T00080
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1560 <NAG>
A:Cross-references: UNIPROT:060275; EMBL:AB011094; NID:g3043567; PIDN:BAA25448.1; PID:g3
A:Experimental source: brain; clone HG1393
C:Genetics:
A:Note: KIAA0522

Query Match 2.4%; Score 142.5; DB 2; Length 1560;
Best Local Similarity 29.5%; Pred. No. 0.28;
Matches 65; Conservative 15; Mismatches 89; Indels 51; Gaps 12;

QY 173 PPLYOLGAATQARPPPHASGRRRLCGECERAWNHSREAGVP-----LGLPAGARRGG 226
Db 1365 PPLPOLGSI-----PPPPASAP--PVGPHR---HFHAHGVPVGPQHYTLGRGCRARRGAG 1415
QY 227 SASRSLPLKRP-RKGAPEPERTVVGQSWAHGPKRTRGSDRGFCVSWSPARPAEATSL 285
Db 1416 GHPQAPGCRHPLHQPTSLPLYSAPQHPAH---KQPKKFIISHHPQMPMPAGAAGG 1472
QY 286 EGAL-SGTRHSHSPVGRQHAGGPPSTSR---PPREWDTPCPVYAEKTHF----- 331

Db 1473 PGSRPFGSGSYSHP-----HHQSPLSPHSPIPPHPSYPLPPSPHTSPHSPPLPTSPHGP 1527
QY 332 LYSSGDKQLRPSFLLSLRPSLTGARRLIVETIFLGSRW 371
Db 1528 LHASGPPAQPTP--VQTPRPSQA-----GSAFW 1554

RESULT 11
T18314
hypothetical protein L7610.4 - Leishmania major
C:Species: Leishmania major
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18314
R:Oliver, K.; Murphy, L.; Quail, M.; Lawson, D.; Harris, D.; Rajandream, M.; Ivens, A.;
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18876
A:Accession: T18314
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1892 <OLI>
A:Cross-references: UNIPROT:097007; EMBL:AL034356; NID:e1371878; PID:e1371559; PIDN:CAA
C:Genetics:
A:Note: L7610.4

Query Match 2.4%; Score 140.5; DB 2; Length 1892;
Best Local Similarity 23.4%; Pred. No. 0.51;
Matches 111; Conservative 47; Mismatches 195; Indels 121; Gaps 25;

QY 44 PAAPFALVAQCIVCPWDARPPAPSPROVSCLELVARVLQRLCERGAKNVLAFGPAL 103
Db 366 PSSLHPQOPQVILVLP---QPRAPPQOERLPYSSSTRPAGGSPRGAVQNNIYAGMAA 422
QY 104 LDGARGGPEAPTTSVRS-----YLPNTVTDALRGSGAWGLLRVDDVLVHLLARCAL 158
Db 423 EDTSGASEVTSRSTRQVFRAPVATSDIPTGS-PYGA-----PT 465
QY 159 FVLVAPSCAYQVCGPPLYQLGAATQARPPPHASG-----PRRRLG-----ERAWN 204
Db 466 YAVVMFQ--RSLPAPPKTGASAASAGLPPSPAEEAAQOQHNRCPPSSSRSPQESRD 523
QY 205 HSVREAGVPLGLPAPGAR-----RRGGSASRLP-----LPKRP--RRGAAPPERT 249
Db 524 HAAREQ--PLPQPPQKRPALPQRHQPORAETAKSQLPPRMFLPADFPFYSEELIPEQRR- 580
QY 250 PVGQSWAHGPKRTRGSDR-GFCVVSPARPA-----EEATSLGALSGTRHSHP-SVGRQ 302
Db 581 ---EGWNGNASTQSGHSGHVSVPQQQLSLSHEDLSAMLSSATVAAPISTKTD 637
QY 303 HHAGPPSTRPPRPMWDTCPVPVYAEKTHFLYSSGDKQLRPSFLLSLRPSLTGARRL-V 361
Db 638 PVAGHTAPDGEPRPLHVPMPPIIQRP--YAATEE-----GAPRFVS 678
QY 362 ETIFLGSRPWPGTTPRLPRLPQRYWQMRPLFLELLGNHQAQCPYG--VLLKTHCPLRAA- 418
Db 679 RKVTAPOQESDAPSRHSP-----PAEHTLLHSRGAADAGEAAAKETREQLSAAK 728
QY 419 ---VTPAAGVCAREKPO-----GSVAAPEEDTDPRILVQ---LLRQHSSP 458
Db 729 EAVTAMTTAGVQSSKKPQOLOHEPDGS---PNGDVD---ELLEADDLIMQPSRP 777

RESULT 12
EBE1F
immediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Funkhauser)
C:Species: suid herpesvirus 1
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C:Accession: S04713
R:Cheung, A.K.
Nucleic Acids Res. 17, 4637-4646, 1989
A:Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies v
A:Reference number: S04713; MUID:89315207; PMID:2546124
A:Accession: S04713
A:Molecule type: DNA

A;Residues: 1-1460 <CHE>
A;Cross-references: UNIPROT:P11675
C;Superfamily: herpesvirus immediate-early protein IE175
C;Keywords: DNA binding; early protein; transcription regulation

Query Match 2.3%; Score 140; DB 1; Length 1460;
Best Local Similarity 24.3%; Pred.No. 0.38;
Matches 114; Conservative 35; Mismatches 163; Indels 158; Gaps 27;

QY 46 AFRALVAQCILVCVPMWDARPPPAAPSPRQVCLKELVARVLQRLCERGAKNVLAFGFALLD 105
DB :
704 ACRGVIERLIPC-PLRLPAPARIPAALGPACLEEVTHALL- - - - -ALRD 746
QY 106 GARG-GEPPE-----AFTTSVRSYLPTNTVDALRGSGAWGLLLRRVGDDVLVHLLAR 155
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
747 AIFGAGPAERQQAADSVVALVARTVAPLVRYSDGARAREAAW-----TYA 791
QY 156 CALFLVIVAPSCAVQVCGPPIYQLGAATQARPPIPHASGRRLRCERAWN- - - - -S 206
DB ||| ||| :
792 AALF--APA--NVAGARL----AEAAARPGPAEPAP-----GLPLLWPQPGLVVVPAPA 837
QY 207 VREAGVPLGH-PAG- ---ARRRGSSARSILPKCPRRGPAEPERTPVCGGSWAHPGRT 262
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
838 PAAAGAPSGULPGSGPSPATKSGSTKSSTGSLGSS-----GYARLPFRRR 887
QY 263 RGPSDRGFCVVSP---ARP--ABEATSLSG-ALSCTRHSHPVSGRHAGAPPSTGRP-- 313
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
888 PGFSARAQAEEAPAGARRPDGDEEDGLSGSALRGDCHGRD--DEEDRGPRKRSLG 945
QY 314 --PRPWTPCPPVYAETKHFLYSGDKELQRPSFLJSSLRPSLTGARRLVETIFIGSRPW 371
DB :
946 LGPAP-DPAPALVYSSSSS--SSSEDDRLLR-----RP-----LGPMPE 980
QY 372 MPCTPRELPLRQRYWMRPLFLELLGNHAQCPYVLLKTHCP-----L 415
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
981 HPAPDGFRRVPAQ-----ETHTRPSAALAAYCPPEVARALVDQEVFPFLW 1028
QY 416 RAAVT--PA--AGVCAREKPQSVAAPDEEDTPRLVQLLRQHSSPQV 461
DB :
1029 RPALTDPDALAHIAAR--RGAGAP-----LRRRAWMRQIADPEDV 1069

RESULT 13
F75311
ABC transporter, ATP-binding protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: F75311
R;White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F75311
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-552 <WHI>
A;Cross-references: UNIPROT:Q9RSH9; GB:AB002048; GB:AB000513; NID:G6459929; PIDN:AAF116B
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2145
A;Map position: 1

Query Match 2.3%; Score 139.5; DB 2; Length 552;
Best Local Similarity 22.3%; Pred.No. 0.11;
Matches 134; Conservative 38; Mismatches 196; Indels 233; Gaps 27;

QY 132 RGSGAWGLLLRRVGDDVLVHLLARCALFVLVAP-----SCAYQVCGP 173
DB :
24 RGS---RLQFRVSGKSTRIRFTSGTLCUPLGLTIASGTCSFIHSSDVAAATRAPR 80
QY 174 P----LYQLGAATAQARPPPHASGRRLRG-----C 199

Db	81	PGTRHRRRAG--AA PRPPADGPAREGAAAGGARRRQNHAAAAARASCARERHPDVC	138
QY	200	ERAWNHSVRAGVPLGLPAPCARRRGSGASRSLPLKPRPRGAAPEPERTPVGQGSWAHP	259
Db	139	ARRTGSAPFRAGA--AYPERGGAGRGVLSHRLTGTDARRAAGRGGRTTAAVGSDA--	194
QY	260	GRTRGSDRGFCVVVSPARPAABEATSLLEGALSGTRHSHPSVGRQHHAGPSTSRPPRMDT	319
Db	195	-RTRRPVGRG-----DYTDRRGALAGARLSHPLA---RAAPFGDAGP-----	232
QY	320	PCPVPVATKHFLYSSGDKQLRPSFLLSSLRPSLTGARRLVETIFLGRPMPGTPRRL	379
Db	233	-----RPDARAA-----PAAARRI	246
QY	380	PLRPQRYWOMRPLFLEL---LGNH-----AOCYPGYLLKTHCPLRAAVTPA	422
Db	247	HRWPERSGPRPRRAAPGCGGHGVGAGDPPARGSPDAELAHGVRSGRRTERRAARLPI	306
QY	423	-----AGVCAREKPGQSVAAPEBEDTD-----PRRLVQLLRQHSSPQV---YGF	464
Db	307	RSRPSGGASTGPLCGTAAALVELTDAEVFRNGHRALGFLSWTAAAGQH---WLVTGENGS	363
QY	465	VRACLRLVP-----PGLWGRSHRERRFLRNTTKFISLGKHAKLSLOELTWKMSVDC-AW	519
Db	364	GKSTLARLIAGELHPALGGS--VARPFL-----ARDVQSE	396
QY	520	LRSPGVGCVPAAEHRLREILAKFLHLMSSVYVVELLRSPFYVTE-----TTFQKNRLF	574
Db	397	RRRTTG---LVSAEVGIQRSGVSGREWLG---DVIASAFAGTEGTGVDTAQ---	445
QY	575	FYRKSVMSKQSTGIR-----OHLKRVOLRELSEAEVQRHREARPALLTSLRLF	623
Db	446	-----WDAVGTTLAERLELGELLSRDQVQALSQGLRLLRLAARAAVHR-PRLLILDEGLDF	498
QY	624	I 624	
Db	499	V 499	
RESULT 14			
S27923			
gene Irf3 protein - human herpesvirus 4			
C;Species: human herpesvirus 4, Epstein-Barr virus			
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004			
C;Accession: S27923			
R;Parker, B.D.; Bankier, A.; Satchwell, S.; Barrell, B.; Farrell, P.J.			
submitted to the EMBL Data Library, August 1990			
A;Description: Sequence and transcription of Raji Epstein-Barr virus DNA spanning			
A;Reference number: S27923			
A;Accession: S27923			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-924 <PAR>			
A;Cross-references: UNIPROT:Q99307; EMBL:M35547; NID:G330420; PIDN:AAA45896.1;			
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal			
Query Match 2.3%; Score 138.5; DB 2; Length 924;			
Best Local Similarity 27.0%; Pred. No. 0.26;			
Matches 80; Conservative 25; Mismatches 136; Indels 55; Gaps 16			
QY	179	GAATQARP-----PPHAGSPRRRLGCGRRWNHVSREAGV-----PLGLPAPCARRRGGA	228
Db	26	GAADPADPVGHAPAAPRAGPPEPRTRLOQA---TPRRGAADPADPVGHGA---APRAPGE	80
QY	229	SRLSLPLPKRRGAAPEPERTPVGQGSWAHPGRTGRGSDRGFCVVVSPARPAABEATSL	288
Db	81	PRTELQAPATPRRGAADP-ADPVG-----HPAARAPGPEPRTRLOQATPRRGAADPAD	134
QY	289	LSGTRHSHPSVGRQHHAGP-----PSTSR-----PPRPWDTCPFPVATKHFLYSSGD	337
Db	135	PVG-----HPAAPRAPGPEPRTRLOQATPRRGAADPADPVGHGAAP-----RAPGP	181

A;Reference number: A75250; MUID:20036896; PMID:10567266	A;Residues: 1-924 <PAR>
A;Accession: F75311	A;Cross-references: UNIPROT:Q9307; EMBL:M35547; NID:G330420; PIDN:AAA45896.1; PID:G3304
A;Status: preliminary	C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology,

Query Match 2.2%; Score 134; DB 2; Length 606;
 Best Local Similarity 22.4%; Pred. No. 0.3;
 Matches 100; Conservative 45; Mismatches 137; Indels 164; Gaps 21;

QY 132 RGSAGKLLRRVGDVLLHLLARCALFVLVAPSCAYCGPPLVQLGAATQARPPPHAS 191
 DB 21 RRSEFVGALLQIGERRVHLTARHAPFLOV-----LGAVR----- 57

QY 192 GPRRLGCERAWNHSVREAGVPLGLPAPCARRRGSGASRLPLPKRRRGAPEP----- 246
 DB 58 -PSRRFG-----VGVFSGGQRRG-----VVLDEQR-----PQPFQFVF 91

QY 247 -ERTVPQGSWAHPGTRGSDRGFCVVSPPARPAEATSLGALSCTHSHSPVGRQHA 305
 DB 92 RQRT-----GVLRAAKQO-----VVKVQPPQFAAGV-GVVVGAQ-VHVPVQAAVA 136

QY 306 GPPSTSRPPRPMDTPCPPVYAEKFLYSSGDKQOLRPSFLSLRPSLTGARRLVETIF 365
 DB 137 A-----PRP-----RAQRRRLPPAPVAARLVP---GFQRRQOT--- 167

QY 366 LGSRPWMPGTPRRLPRLPQRYQWMPRLFLELLGNHAQCPYGVLLKTHCPLRAAVTPAAGV 425
 DB 168 AGERQLVFG-----LPRCHRV-----QARPGEDVALNRHVRPREAARP--GV 209

QY 426 CAR-----EKQGSVAAPBEEDTPRRLVQLLRQHSPPWQVYGFVYACLR 471
 DB 210 AARAGEGALPVRADQPELPLLDVGVLTGAGDGLRVEPLREOQPTFRTRIGVDIALRR 269

QY 472 LVPPGLGWSRHNERRFLNKKFISLGHAKLSLQELTWKMSVRDCAMLRSPGVG---- 527
 DB 270 YRPHAAHEGQ-----RPHRELARHRDAEVA-----GPGVAPHDR 306

QY 528 -----CVPAEHRLEIREILAKFLHW 547
 DB 307 KGHAQCTGPAQHPPFPVQLRPLHW 332

RESULT 18
 JQ0405
 N:Alternative names: ORF 1 protein
 C:Species: Micrococcus luteus
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 04-Feb-2000
 C:Accession: JQ0405
 R:Shiota, S.; Nakayama, H.
 M:Gen. Genet. 217, 332-340, 1989
 A:Title: Micrococcus luteus homolog of the Escherichia coli uvra gene: identification of
 A:Reference number: S04781; MUID:89364717; PMID:2549377
 A:Accession: JQ0405
 A:Molecule type: DNA
 A:Residues: 1-1106 <SHI>
 A:Cross-references: EMBL:X15867
 A:Note: this reading frame extends between two stop codons and does not begin with a sta
 A:Note: the gene encoding this protein overlaps uvra gene
 C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;

Query Match 2.2%; Score 133; DB 2; Length 1106;
 Best Local Similarity 23.9%; Pred. No. 0.79;
 Matches 129; Conservative 33; Mismatches 198; Indels 180; Gaps 25;

QY 185 RPPHASGPRRLGCE-----RAWNHSVREAGVPLGLPA--PGARRGGSGAS-----RSLP 233
 DB 516 RGPFPQHPGERARGVRHGRHPPAHARGHGVLLGAAADGPAADRGPAQGDGPGAGVP 575

QY 234 LPKRPRGAAPERTVPVQGSWAHPGTRGSDRGFCVVSPPARPAEATSLEGALSGTR 293
 DB 576 AGERPR---VPQ-----RAGRHPLRRG-----PAHPGHTDLR---AGRR 613

QY 294 HSHPSVGRQHHAGPSTSRPPRPMDTCPVVAETHKFLYSSGDKQOLRPSFLSLRPS 353
 DB 614 PLRP---RAVHRPAPAGPFPHPRRPPAPAGPQHPHRRRRRGRHD--RRGLDRGRPS 668

QY 354 LTGARRLVETIFL--GSRPMPGTPRRLPRLPQRYQWMPRLFLELLGNHAQCPYGVLLKT 411

Db 669 RGRVRRGRGLPGSGQGEHAVRRLPLRP-----PL----- 702
 QY 412 HCPLRAAAVTAAAGVCA-----REKQGSVA-----APEED-----TD 444

Db 703 HRGAGASRPEGARADGPRPGQPEGRLGPGARGPHGDRVLRVQVHADQDPLQG 762
 QY 445 PRLVQLLRQHSPPWQVYGFVVRACLRRLVPPGLMGSRHNRFLRNTKFKFISLGHAKLS 504

Db 763 PGQPAQRQARAPAPVRGGTRA-----PGQSGRGPPEH-----RAHATLQ 804

QY 505 LQELTWKMSVRDCAWLRSP---GVGCVPAEHRLEIREILAKFLHLWMSVVVVELLRFF 561
 Db 805 PRHLHVR-RDPQALRGDPRGEGG-LIPAGVLL----- 837

QY 562 YVTETTFQKRLFFYRKSVMSKLSIGIRQHLKRVQLRELSEAEVROHREARPALLTSL 621
 Db 838 -----OH-----QGRALGVRGRHRAEDRDELPAGR 864

QY 622 RPI-PKPDG-LRPIVNDYVVGARTFRREKRAER-----LTSRVKALFSLVLYERARRPGL 675
 Db 865 RAVRGVPRGPVQGDARGHLQGEHRRGRPRHADRGRLQVRHPLAVPGHARRRRSGL 924

RESULT 19
 S55543
 N:Alternative names: DNA polymerase (EC 2.7.7.49) - fruit fly (Drosophila melanogaster) transpos
 C:Species: Drosophila melanogaster
 C:Date: 27-Oct-1995 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: S55543; S55544
 R:Judomkit, A.; Forbes, S.; Dalgleish, G.; Finnegan, D.J.
 Nucleic Acids Res. 23, 1354-1358, 1995
 A:Title: BS a novel LINE-like element in Drosophila melanogaster.
 A:Reference number: S55543; MUID:95273172; PMID:7753626
 A:Accession: S55543
 A>Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-860 <UDO>
 A:Cross-references: UNIPROT:Q95SX7; EMBL:X77571
 A:Experimental source: strain Y Hw
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1994
 A:Note: the complete translation is not shown
 A:Accession: S55544
 A>Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 57-860 <UD2>
 A:Cross-references: EMBL:X77571
 A:Experimental source: strain Y Hw
 C:Genetics:
 A:Gene: FlyBase:BS
 A:Cross-references: FlyBase:FBgn0000224
 A:Mobile element: transposable element BS
 C:Keywords: nucleotidyltransferase

Query Match 2.2%; Score 132; DB 2; Length 860;
 Best Local Similarity 19.1%; Pred. No. 0.65;
 Matches 140; Conservative 100; Mismatches 250; Indels 244; Gaps 37;

QY 358 RRLVETIFL-GSRPMPGTPRRLPRLPQRYQWMPRLFLELLGNHAQCPYGV----- 407
 Db 110 RELALSVTGAKILATGSPTRYPVFVSH-----TPSCIDPAVYH-----GIPDHATITQ 160

QY 408 ---LLKTHCPRLAAVTPAAGVCAAREKPGQGSVAAPBEEDTPRRLVQLLRQHSPPWQVYGF 464
 Db 161 SWDLSDDLPLIISI-----ETDSTHV-----NPSP----- 186

QY 465 VRACLRRLVPPGLMGSRHNE-RRFLRNTKFKFISL-----GKHAKLSLQELTWKMSVRDC 517
 Db 187 -----RLV-----TKHTDLLAFSRQLESLSLNTLNSGEIEMAVDNLT--ESIHA 232

QY 518 AWRRSRPGVGCVP-----AAEHLREEI-----L 541

```
Db 233 AAVTSP-----VPRIGTVGIVLTREARELLTKRRLRRRAIRASQDPWDRLLWNRAKQL 288
QY 542 AKFLHLMVYVVELLSFFYVTTTFQKNRLFYFRKSVMSKLSQSIGRHLKRVOLR-- 599
Db 289 RNVLRNLFNFPEQLASWDYTDAGY-----SLWKCTYSLK-RQPFQVPIRCP 337
QY 600 --ELSE-----AEVROHREARPAALLTSRURFIPKPDGLRPIYN 635
Db 338 GGELAKNEBEQANCFANHLETRFTHQFATTEQYQETLDSLETPLQMSLP-----IKPI-R 392
QY 636 MDVVVGARTFRREKRAERLTSRVKALFSLVNYERARRPGLGASVLGLDDIHRWR-TFV 694
Db 393 VBEIVAIKSLPKSGIDNVNATLKALPVRTILYLALITYNALIRUVQFFQKMWKAAI 452
QY 695 LRVRAODPP---PELY---FVKVDVTGAYDTIPQDRLTEVIAS-IIPQNTYCVRYAYV 747
Db 453 LMIHKPKPEESPESYRPISSLSSLSKLWERLIANLNDIMTERRILPDHQCFRQ---- 508
QY 748 QXAAHGHVKAFK--SHVSTLTDLPYMQFVAHLOET--SPLRDAVITEQSSSLNEASS 803
Db 509 --GHSTVQVHRLTKHILQAFDDKEYCNAVFIDMQQAFDRVWHDGLISKVKLFPAPYY 565
QY 804 GLFDVPL---RWMCHHAVIRKSY----VQCGIPIQSGISLTLSCVGDW--ENKLF 854
Db 566 GVLKSYLEDRREM----VRVR-NSYSIPRVMRAGVPGSGVLGGLYSVFTADLPCCNAYH 620
QY 855 AGIRRDGLLRVDDPLLVTPHLTHAKTELRTLVRGVPEY-----GCVNLRKT 903
Db 621 MADPRKALLATYADDIALI-----YSSNCCNEARGLQBYLITTLAACKRWNLKYNPQT 675
QY 904 V-----VNFVPEDEALGGTAFVQMPAHGLFPWCGLLDTRTLVBQSDYSYART 952
Db 676 INPCTFLTKLSPVTABIELE-----GVILD-----QPSQAKYLGI 710
QY 953 SIRASITFNRGKA 966
Db 711 TLDKRLTFGPHLKA 724

RESULT 20
G01763
atrophin-1 - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: G01763
R:Margolis, R.L.
submitted to the EMBL Data Library, March 1995
A:Reference number: G08343
A:Accession: G01763
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1184 <MAP>
A:Cross-references: UNIPROT:P54259; EMBL:U23851; NID:g915325; PID:g915326
C:Genetics:
A:Gene: GDB:DRPLA; B37
A:Cross-references: GDB:270336; OMIM:125370
A:Map position: 12p-12p

Query Match 2.2%; Score 131.5; DB 2; Length 1184;
Best Local Similarity 22.8%; Pred. No. 1.1;
Matches 89; Conservative 23; Mismatches 153; Indels 125; Gaps 17;

QY 162 VAPSCAYQVCGPLYOLGAATQARPPH-----ASGPRRLGGERAWNSVREA 210
Db 188 VFTGTHAMWEPSTSRMFQAPGAPPPHPOLYFGTGGVLSG----- 230
QY 211 GVPLGLPAPCARRR--GGASRSRLPLKRP-----RRGAAP-EPERTPVQGSWAHPG 260
Db 231 --PMGPKGGAASSVCGPNKGKHPPPTTPISSVSSGASGAPTKPTTPVGGN----- 283
QY 261 RTRGSPDRGFCVVSPPARAEATSLGALSGTRHSHPSVGRQ-----HHAG----- 306
Db 284 LPSAPPANFPHVTNLPPLPPALR---PLNNASAPPLGQAQPLPGLHPSHAMGGIGG 340
```

RESULT 21

A45344

immediate-early protein - suid herpesvirus 1 (strain Kaplan)

C:Species: suid herpesvirus 1

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: A45344

R:Vicek, C.; Kozmik, Z.; Paces, V.; Schirm, S.; Schwyzler, M.

Virology 179, 365-377, 1990

A:Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented o

A:Reference number: A45344; MUID:91021039; PMID:2171211

A:Accession: A45344

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-1446 <VLC>

C:Cross-references: UNIPROT:P33479; GB:M34651; NID:g334070; PIDN:AAA47470.1; PID:g33407

C:Superfamily: herpesvirus immediate-early protein IS175

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 2.2%; Score 131; DB 1; Length 1446;

Best Local Similarity 21.4%; Pred. No. 1.6;

Matches 105; Conservative 37; Mismatches 156; Indels 192; Gaps 25;

```
QY 46 AFRLVAQCLVCVPWDARPPPAAPSRQVSCUKELVARVLQRCERGAKNVLAFGALLD 105
Db 693 ACRGYLERLLPC-PLRLPAPAPAPALGPAFLCEVTAALL-----ALRD 735
QY 106 GARG-GPPEAFTTSVRSYLPNTVTDALRGSGAWGLLRVGGDDVLVHLARCALFVLVAP 164
Db 736 AIPGAGPAER-----RONADSA--LVAR-----TVAP 761
QY 165 SCAYQVCGPLYQLG-----AATQARPPPHASGPRRLGGERAWNH- 205
Db 762 LVRYSDGARAREAAWTYAAALFAPANVAARLAEEAARPGPAEPAP---GLPPLWPQ 817
QY 206 -----SVREAGVPLGLPAPG-----ARRGGASRSRLPLK-----RPRGA 242
Db 818 PGLVVVPAPAPAAAGAPSGLPGSPSPASTKSSSTKSSSTKSGSGSYASSPAAGP 877
QY 243 APEPERTPVQGSWAHPGRTGPGSRGFCVVSPPAR--ABEATSLG-ALCSTRSHSPV 299
Db 878 DPAPER-----RKKRRRAPGAR-----RPGGEEDEGLSGAALRGDGHGRD- 919
QY 300 CRQHAGAGPSTSRP-----PRPMDTPCPVYAEKTHFLYSSGDKQLRPSFLLSLRPSLT 355
Db 920 -DEEDRGPRRKERSLGLGPAP--DPAPALLSSSS-----SSSEDDLRL-----RP--- 961
QY 356 GARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELIGNHAQCPYGVLLKTHCPL 415
Db 962 -----LCPMPHEHPADCGFRVPAG-----ETHTPRPSSEALAAAYCP- 998
QY 416 RAAVTPAAGVCAREKPGQSVAAPEEE-----DTPRELVLQLLRHSHSPWQYGVF 465
Db 999 -----PEVARALVDQEVFPELWRPALTFDPAALAHIAARRGAPLRRRA--- 1041
QY 466 RACLRLRVPP 475
```


237	Db	-----APQPSPHPPQLL-----ASPQPPQPEG-PPQPGV	268
387	Qy	WQNRPLFELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPGQGSVAAP	438
269	Db	APFLPEWPLLP-----ASHPSPLSLPPHVRHQ-----GRDPGPGFVSVP	307

Query Match	2.2%	Score 129;	DB 2;	Length 1776;
Best Local Similarity	21.8%	Pred. No. 2.8;		
Matches 131;	Conservative 63;	Mismatches 204;	Indels 204;	Gaps 33
Qy	252	GQGSWAHPGTRGSDRGFCVVS	PARPAEEATSLEGALSGTRHSHPSVGRQHH-	-----G 306
Db	664	GDGVYGDPSFGPA	-----AFPPRP	-----GVPTVRPLPPQNLA
Qy	307	PPSTSRP--PRPDWTP--CPPIYATKHF	LYSSGDKQLRPFLLSLSPSLTGARRLVET	363
Db	707	PPSVQYEGAPRLGLGVMQPMYQQ--	HQLSMGSPHG--HPSMMMSR--EPQMPQVMRV	--- 758
Qy	364	IFLGRSRRMWTGTPRRLPRLPORYWQMRPL	FLFLELGNHAQCFYGVLLKTHCP	LRAAVTAA 423
Db	759	-----PPPGQFSHMQVPQYQLPPLSGMM	-----	-----QPPMAEMPP-- 796
Qy	424	GVCAREKPGQSVAAPESEDTPRR	-----LV--QLLRHSSPWQYGVFVRC	LCRLRV 473
Db	797	-----PPPPGEAPPLPEEPKPKQKDES	ALVPEDQFLAQHPG	-----ATIRVSK 843
Qy	474	PPGLWSRRHNERFLRNTKKFIS--LG	-----	-----KHAKLSIQELTWKSV 514

[illegible]

RESULT 27
S01955
hypothetical protein, 69K - turnip yellow mosaic virus
C:Species: turnip yellow mosaic virus, TYMV
C:date: 21-Nov-1993 #sequence revision 26-May-1995 #text_change 09-Jul-2000
C:Accession: S01955
R:Worrich, M.D.; Boyer, J.C.; Haenni, A.L.
Nucleic Acids Res. 16, 6157-6173, 1988
A:title: Overlapping open reading frames revealed by complete nucleotide sequencing of the genome of turnip yellow mosaic virus
A:reference number: S01955; PMID:86289359; PMID:3399388
A:Accession: S01955

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: A53800; 158395
 R/Gallo, K.A.; Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Godowski, P.J.
 J. Biol. Chem. 269, 15092-15100, 1994
 A>Title: Identification and characterization of SPRK, a novel src-homology 3 domain-cont
 A/Reference number: A53800; MUID:94253068; PMID:8195146
 A/Accession: A53800
 A>Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-847 <GAL>
 A/Cross-references: UNIPROT:Q16584; GB:U07747; NID:9464027; PIDN:AAA19647.1; PID:9464028
 R/ing, Y.L.; Leung, I.W.; Heng, H.H.; Tsui, L.C.; Lassam, N.J.
 Oncogene 9, 1745-1750, 1994
 A>Title: MLK-3: identification of a widely-expressed protein kinase bearing an SH3 domain
 A/Reference number: 158395; MUID:94239754; PMID:8183572
 A/Accession: 158395
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-847 <RES>
 A/Cross-references: GB:L32976; NID:9488295; PIDN:AAA59859.1; PID:9488296
 C/Genetics:
 A/Gene: GDB:MLK3; PTKJ; SPRK
 A/Cross-references: GDB:134755; OMIM:600050
 A/Map position: 11q13.1-11q13.3
 C/Superfamily: mixed-lineage protein kinase 3; protein kinase homology; SH3 homology
 C/Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein k
 F:48-100/Domain: SH3 homology <SH32>
 F:115-383/Domain: protein kinase homology <KIN>
 F:123-131/Region: protein kinase ATP-binding motif
 F:403-424/Region: leucine zipper motif
 F:438-459/Region: leucine zipper motif
 F:468-482/Region: basic

Query Match 2.1%; Score 127; DB 1; Length 847;
 Best Local Similarity 23.1%; Pred. No. 1.4;
 Matches 122; Conservative 49; Mismatches 179; Indels 178; Gaps 34;

Qy 44 PAAFRALVAQCLVCPWDARPPAPSPROV-SCUKELVARVLQRL-----CERGAKN 95
 Db 348 PEPFALMADC-----W-AQDPHRRPDPFASLIQQLALEAQVLEMRDPSFHSMQEGWKR 401
 Qy 96 VLAQFALLDGARG-----GPPEAFTTSVRSYLTNTVTDALRGS-----GAW----- 137
 Db 402 EIQ-----GLFDELRAKEKELLSEBELTRAAR-ORSAEQURRREHLLAQWELVFERE 456
 Qy 138 -GLLRRV-----GDDVLVHLLARCAFLVIVAPSC-----A 167
 Db 457 LTLQLQVDRERPHVRRRRTGFKSKLRARDGGERISMPLODKHRTTVOASPGLDLRRNV 516
 Qy 168 YQVCGP---PLYQLGAANTQARP---PPHAG---PRR-----RLGCERAWNHSVREAG 211
 Db 517 FEV-GFGDSPTFRFRATQLEPAEPGQAWGRSPRLRDSNGERRAC-WAWGPS----- 569
 Qy 212 VPLGLPAPGARRRGGSASR-----SLPL-----PKPRRGAAPPEPRT 249
 Db 570 ----SPKFGEAQNGRRSRSMDEATWYLDSDSSPLGSGSTPPALNGNPPRSLSEPEEPR 625
 Qy 250 PVQGQSWAHGTRGSDRGFCVWSP---ARPAEATSLGALSCTRHSHPVSGRQHAG 306
 Db 626 PV-----PAERGSSSGTKPLIQALLRGTTALLASGLGLGRDLQPPGGPGRERG 672
 Qy 307 PPSTSRPPRPWDTPCP--PVYAEATKHFYSSGDKQLRPSFLSSL-----RPSLTGARR 359
 Db 673 ESPTT-PTPTTAPCTPEPPPSPLICFSLKTPDSPP-TPAPLLDLGLFVQGRSAKSPRR 730
 Qy 360 LVE-----TIFLGSRRPMPGTPRLRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTH-CP 414
 Db 731 EEPREGTIV---SPP--FGTSRSAGTP-----GTPRSPLGLISRPSP 771
 Qy 415 LRAAVTPAAGVCAREKPGQSVNAPEEDTPRRLVOLLRQHSSPQVY 462
 Db 772 LRSRIDPWSFVSAGPRP-SPLPSQPA---PRR-----APWTLF 806

RESULT 34

T46289
 hypothetical protein DKFZp434A1010.1 - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
 C/Accession: T46289
 R/Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, January 2000
 A/Reference number: Z23035
 A/Accession: T46289
 A>Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-862 <AAA>
 A/Cross-references: UNIPROT:Q9NT23; EMBL:AL137579
 A/Experimental source: adult testis; clone DKFZp434A1010
 C/Genetics:
 A/Note: DKFZp434A1010.1

Query Match 2.1%; Score 127; DB 2; Length 862;
 Best Local Similarity 21.8%; Pred. No. 1.4;
 Matches 102; Conservative 28; Mismatches 147; Indels 130; Gaps 23;

Qy 43 DPAAFRALVAQCLVCPWDARPP-----PAAAPSPROV 74
 Db 316 DPLTFR-----CSPTPGDPAPPASPAPPAPAPPRVTPQAISPRGTPSPASPAALDI 370
 Qy 75 SCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEAFTTSV---RSYLPNTVTDA 130
 Db 371 S--EPLAVSVPPAVLE-----LLGAGAPASATPTPALSFGRSIRPHILPLL 415
 Qy 131 LRSGAWGLLLRRVGGDVLVHLLARCAFLVIVAPSCAYQVCG----- 172
 Db 416 LRGAEA-----PLTDACQOEMCSKLRGAQGLPGDMESPLP 451
 Qy 173 -PPLYQL--GAATOARPPPHASGPRRLG---CERAWNHSVREA-----GVPLGLPAPGA 221
 Db 452 PPPUSLRPGA-----PPPPKPNPARLMALALARAQVAEQSQOQECGGTPPASQSPFH 507
 Qy 222 RRRGGSASRSLPLPKRP--RRGAAPERTPVGGGSAHPG----- 260
 Db 508 R-----SLSLVGGEPGLTSGSGPPP-----NSLAHPGAWVPGPPPLPQQSGSL 554
 Qy 261 ---RTGPSDRGFCVWSPAPPAEATSLGALSCTRHSHPVSGRQHAGPPSTRPP-- 314
 Db 555 LRSQRPMTGTSRRGL-----RGPAQVSAQLRA--GGGGRDAPEAAQAQSPCVSPQVPTGPF 607
 Qy 315 -RPWDTPC-PPVYAEATKHFYSSGDKQLRPSFLSSLRPSLTGARRLVETIFLGSRRPM 372
 Db 608 FSPAPRCLPFLGVPRGLYPLGP-----PSFQSPSPAP-----VWR 645
 Qy 373 P--GTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPURA 417
 Db 646 SSLGPPAPLDRGENLYYE-----ICASEGSPYSGLTRSWSPFRS 684

RESULT 35

T35878
 hypothetical protein SC9B10.09 - Streptomyces coelicolor
 C/Species: Streptomyces coelicolor
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T35878
 R/Oliver, K.; Harris, D.; Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, November 1997
 A/Reference number: Z21592
 A/Accession: T35878
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1039 <OLI>
 A/Cross-references: UNIPROT:O50516; EMBL:AL009204; PIDN:CAA15799.1; GSPDB:GN00070; SGOED
 A/Experimental source: strain A3(2)
 C/Genetics:
 A/Gene: SGOEDB:SC9B10.09

Query Match 2.1%; Score 127; DB 2; Length 1039;
Best Local Similarity 26.1%; Pred. No. 1.9;
Matches 89; Conservative 26; Mismatches 146; Indels 80; Gaps 16;

QY 4 APRCAVSRLLSHRYEVLLPLATFVRRLGQWHLVORGDPAFRAVAQCLVCVPPWDAR 63
DB 462 AQCGHVAVRATR-----LPHATVSALLRQAG---VIRVD--TITDLVDAGLLA---RQ 506
QY 64 PPPAAPSPRQVSKLKVRLQRLCERGAKNVLAFAFGFALLDGCARGPPEAFITTSVRS-- 121
DB 507 PLPAGPRVAILGNSESL-----GLTTYDACLSGLRQPPLDITTAASADD 552
QY 122 -----YLPNTVTDAL-----RSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCA 167
DB 553 FHAALARALADTCDVAVVTAIPTLGEA-----AGDAALAEALRSAAAAVPTKPVLV 605
QY 168 YVCGPPLVQLGAATOARPPPHASGPRRLG-----CERAWNHSVREAGVPLGLPA--PGAR 222
DB 606 VHV-----ELGGLAEALSAASTAPQTAGTGTAGTAAAGTASRAASAALPAPDPAV 659
QY 223 RRGGSASRLPLPKPRRRGAAPERTPVQGSWAHPGRTGRPSDRGFCVWSPAPAEBA 282
DB 660 RRG-----TPSGPASGAASGNTP--GTAPHAAP-----GPADQ---LPSGASGSPGF 703
QY 283 TSLEGALSCTRHSHPVSGRQHAGPPSTSRPPRPMDTPCPP 323
DB 704 SGPSGSPGSPGSPGS--GPSGSPGSPGSPGSPGSPGSAAPGRP 743

RESULT 36
H75272
probable nucleic acid-binding protein, HRDC family - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: H75272
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vanathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: H75272
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-603 <WHI>
A:Cross-references: UNIPROT:Q9RRP4; GB:AE002074; GB:AE000513; NID:G6460257; PIDN:JAF1198
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2444
A:Map position: 1

Query Match 2.1%; Score 126.5; DB 2; Length 603;
Best Local Similarity 25.0%; Pred. No. 0.96;
Matches 131; Conservative 39; Mismatches 184; Indels 171; Gaps 32;

QY 37 RLVO-----RGDPAAPRALVAQCLVCVPPWDARPPPAAPSPROVSC-LKELVARVLORLCER 91
DB 12 RLVLQHAERGDHPHGLAALAALEDTDWGLLAGEAALRQAALLGPGLRVDGLR-DV 70
QY 92 GARNVLAFGALLD-----GARG-----GPPFAFTTSVRSYLPNTVTDAL-LRSGAWGLL 140
DB 71 GRAALAEAGLAVADLHGLDLAGARAVWLLEPDRAAVERARRAGRVIVDTATLAPGGW--- 127
QY 141 LRRVGDVLLHLLARCALFVLVAPSCAYVCGPPLVQLGAA--TOARPPH----- 189
DB 128 -PROGADYVYVRNATLTGHADAPLAA-----LFGSGTAPTAPPPPSDLAVALALRD 179
QY 190 -ASGPR-----RLGCERAWNHSVREAGVPLGLPAPGA-----RRRG--SA 228
DB 180 VATLPLRLARFARTATQLTDRIGA-----SVRQAGPTALLAPDSAADTPAQGGVLA 233
QY 229 SRSLLP-----LPKRPRRGAAPERTPVQGSWAHPGRTGRPSDRGF 270

DB 234 ARHVPDGLLLTPGLEDPQVLLGLLRDQBE---ARRQDORASQGEASQ--REQQORDER- 287
QY 271 CVVSPARPAEATSLGALSQGRHSHPSVGRQHAGPPSTSRPPRPMDTPCPPVVAETKH 330
DB 288 -ORNEDRFDNA---EGRAPADREPRPERSQVRSPERSREDRPRD---FRDDR 339
QY 331 FLYSGDKQLRPSFLLSRLSLTGCARLVTETIFLGSRPWMPGTPRRLLPRL-----PQRY 386
DB 340 ---REGRRDRFRPS--PGPDRPTRTGER-----RDDAPARPAELERFTFEAPQQA 384
QY 387 -----WQRPPLFLELLGNHAQCPYGVLLKTHC-----PL----- 415
DB 385 PAPSDELPEPEIVF---SDHA---PQNVPL--THTVSSGPDAPPLTPTPLADTLSEADA 437
QY 416 ---RAAVTPAAGVCARE-----KQGSVAAPPEEDTDPR 446
DB 438 GDAAAQVTPAELFVHAHAAPVSSEAAQTPEQ--VEAPEEAEPQ 480

RESULT 37
E98119
transposase, uncharacterized, truncation [imported] - Streptococcus pneumoniae (strain
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: E98119
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: E98119
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-330 <KUR>
A:Cross-references: UNIPROT:Q8DN10; GB:AE007317; PIDN:AAL00786.1; PID:G15459687; GSPDB:
C:Genetics:
A:Gene: transposase H

Query Match 2.1%; Score 126; DB 2; Length 330;
Best Local Similarity 21.8%; Pred. No. 0.45;
Matches 46; Conservative 29; Mismatches 62; Indels 74; Gaps 4;

QY 707 YFVKDVTGAVDTIPQDRLTEVIASIIKPONTYCVRRVAVVQKAAHGHVKAFKSHVSTL 766
DB 39 MIVDIDLEKFFDTVPQDRLMSLVHNIIDGDT----- 70
QY 767 TDLQPMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYV 826
DB 71 -----ESLIRKYLHSGVLIINGQRYK 90
QY 827 OCGPIQSGSIISLTLCSLCYGDMEKNLFGAIRRDGL-LRLVDDFLVTPHPTHAKTFUR 885
DB 91 TLVGTPOGGLSPLLSNI---MLNELDKELEKGLRFRVRYADDCVITVVSAAAKRMV 146
QY 886 TLVRGVPE-YGCVNLRKTVVNFVDEALG 915
DB 147 SVSRFIEKRLGLKVNMTKTITRPRELYLG 177

RESULT 38
T18196
pol protein - silkworm
C:Species: Bombyx mori (silkworm)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18196
R:Takahashi, H.; Okazaki, S.; Fujiwara, H.
Nucleic Acids Res. 25, 1578-1584, 1997
A:Title: A new family of site-specific retrotransposons SART1, is inserted into telomeric
A:Reference number: Z18809; MUID:97248614; PMID:9092665
A:Accession: T18196

A:Map position: 1

A:Introns: 72/3; 519/3; 564/1

Query Match 2.1%; Score 125.5; DB 2; Length 574;

Best Local Similarity 25.7%; Pred. No. 1;

Matches 72; Conservative 16; Mismatches 107; Indels 85; Gaps 12;

QY 173 PLYQLGAATQ-----RPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAPGARRGGSA 228

DB 294 PSSRSVAALAAANKRPPPPPPSRNRGKPIGNSSNSLPP---PPPPR---SNA 347

QY 229 SRSLLPKPRGAAPERTPVGGQSWAHGRTGPRGRCVGVSPAPABEATSLEGA 288

DB 348 AGSILPPOGRSAPPPPR-----SAPSTGRQPPFLSSRAVSNPPAPP----- 392

QY 289 LSGTRHSPSV-GRQHHAGP-----STSRPRPWDTCPVPVVAETHKFLYSSGDKQLR 342

DB 393 -----PAIFGRSAPALPPLGNARTSTPVPPTPSLPP-----SA 427

QY 343 PSFLSSLRPSLTGARRLVETIFLGSRPWMPGTTPRLPRLPQRYWQMPLFLELLGNHAQ 402

DB 428 PPSLPSAPSLP-----MGA-PAAPLPPSAPIAP-----PL----- 459

QY 403 CPGVLLKTHCPRLRAAVTPAAGVCAREKPKQGSVAAPPEED 442

DB 460 -PAGMPAAPPLPPAAPAPAPAPAPAPVASTAELPQOD 498

RESULT 41

S52216

viral proteinase - rabies virus

C:Species: rabies virus

C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Aug-1998

C:Accession: S52216

R:Camacho, A.; Tabaro, E.

submitted to the EMBL Data Library, June 1994

A:Reference number: S52215

A:Accession: S52216

A>Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-522 <CAM>

A:Cross-references: EMBL:X79983

A>Note: the source is designated as pseudorabies virus

C:Superfamily: varicella-zoster virus gene 33 protein

Query Match 2.1%; Score 125; DB 2; Length 522;

Best Local Similarity 23.5%; Pred. No. 0.99;

Matches 112; Conservative 47; Mismatches 192; Indels 126; Gaps 25;

QY 14 LRSHYREVLPATFVRRLLGPGQWRVLQVGDPAARALVAQCLV-----CVPWDARPPPA 67

DB 100 LLSNY---LPSASLSR-----RLPGDAPDETFLFAHVALCVIGRRVGTIVVYDASPERA 150

QY 68 APSFRQVSC-LKELVARVLQRCERAKNVLAFFGALLDARGGPPPEAFTTSVRSYLPNT 126

DB 151 VGFPELSAGRESELLARAE---SPDAERVHMS-----EDALT---RALLSTA 193

QY 127 VTDALRGSGAWGILL-RRVGGDVLVHLLARCALFVLVAPSC-----AYVCGPPPLYQLGA 180

DB 194 VNNMLL-RDRWELVAERREAGVRAHTYLOATWAGLLPKSGASPGARACQGH-----GS 247

QY 181 ATQARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAPGARRGGSASRSLPKPRR 240

DB 248 PAERTPGDVFYFAAQ-----INQLVNVQ-----RPAPLSLSQLG-AIVSAAMDORRRH 295

QY 241 GAAPERTPV-----GGQSWAHGRTGPRGRCVGVSPAR----- 277

DB 296 SPSEEP-RPPARKRRYDDYAQDNAYYPGEAPPTRATSRVAVSLQREISHLRAQHVRYPT 354

QY 278 -----PAEATSLEGALSGTRHSHPSVGRQHHAG-----PPSTRPRPPWMTPTCPVVAETK 329

DB 355 PYYAPAPQLLPFGAVVGHPPHP-----HHAAGALYPPMYPAPQGLHAPPPSPV----- 404

QY 330 HELYSGDKQLRPSFLSSLRPSLTGARRLVETIFLGSRPWMPGTTPRLPRLPQRYWQM 389

DB 405 -----AHAVPAL-PGLPASRRCCGPAHVPAQV-VPQOPVVVQAPVAVPAA 448

QY 390 RPLFLELLGNHAQCPYGVLLKTHCPRLRAAVTPAAGVCAREKP-QGSVAAPPEEDTDP 445

DB 449 APPPLRLQORHAPA-----APVQAA-APRAPASAPQPPVQASVASPRPTESP 495

RESULT 42

T42635

tenascin Y precursor, variant 206.5K - chicken

C:Species: Gallus gallus (chicken)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T42635

R:Hagios, C.; Koch, M.; Chiquet, M.; Spring, J.; Chiquet-Ehrismann, R.

J. Cell Biol. 134, 1499-1512, 1996

A:Title: Tenascin-Y: a protein of novel domain structure is secreted by differentiated f

A:Reference number: Z22222; MUID:96427453; PMID:8830777

A:Accession: T42635

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1914 <HAG>

A:Cross-references: UNIPROT:Q91008; EMBL:X99062; NID:gl1419545; PIDN:CAA67509.1; PID:gl1

C:Genetics:

A:Gene: tn-Y

C:Keywords: extracellular matrix; heparin binding; heptad repeat

F:1-19/Domain: signal sequence #status predicted <Sig>

F:20-1914/Product: tenascin Y, variant 206.5K #status predicted <MAT>

Query Match

2.1%; Score 125; DB 2; Length 1914;

Best Local Similarity 20.8%; Pred. No. 5.9;

Matches 130; Conservative 42; Mismatches 212; Indels 240; Gaps 28;

QY 64 PPPAAPSPQVSCLEKELVARVLQRCERAKNVLAFFGALLDARGGP--PBAFTTSVRS 121

DB 27 PPPVPP---ELSCGAEVLEAVLGR-----RALEGEVRALQCGDLSLGPQAGTGSTAA 77

QY 122 YLPNTVTDALRGSGAWGILLRRVGGDVLVHL-----LARCALFV-LVAPSC 166

DB 78 ---RRLCDTPGAGGCCGRCGLSGDGLPCAPRCPDLCSDQRCRAGRCHCEFTGTPFC 134

QY 167 AYQVCGPPPLYQLGAATQARPPPHAS-----GPRRLGRCERAMNHSVRE-----A 210

DB 135 ATPVCPP-----GRGGPHCTLETPSVTLRLAARNOTSFRTVTPPAKPDVGYEVA 184

QY 211 GVPLGLP-----APGARRRGSASRS 231

DB 185 VIPMDEPAALATHELPGSAVTPEVTGLTPGQAFEIFQAQREQLHLCAPGTLRVTLTAQS 244

QY 232 LP-----LPKPRRGAAPERTPVGGQSWAHGRTGPRGRCVGVSP 275

DB 245 LPNHGGPGRTPTFLASPVAPASPSARQSPASPSVSLGSLGSPASLSRP-----VSP 297

QY 276 ARPAAEATSLLEGALSGTRHSHPSVGRQHHAGPSTSRPRPW-----TPCPPV 324

DB 298 ESSAAPA-SLSPWSPASPRSP-----ESPASVSPSRPTSPWSPASPOSPLSPASFISPV 352

QY 325 YAEKHFLYSSGDKQLRPSFLSSLRPSLTGAR---RLVETIFLGSRPWMPGTTPRLR 381

DB 353 LPNVPS-LHELGVKLSSYNGSLQRLSHLRATNPLRGNQTVPAVARAILSYLLRRSPA 411

QY 382 LPQ-----RYQWRP-----LFLELLGNHAQ-----PYG----- 406

DB 412 SLRYQFLHLOONPHKPVQLFGAAGEALVDLGLRHAETVIRYIRLLEEGEGEVR 471

QY 407 -----VLKTHCHPLRAAVTPA-----AGV-----CA 427

DB 472 VPGDTTVARVGLVPGATYRVEVGVGRVSKYSTSLVLTGLDGTSEPPPEWENLYDME 531

QY 428 REKPGQSV--AAPEEEDTDP--RLVQLLRQHSPP-----MQV-----YG 463

DB 532 VTEPQGANAKAAPSSEPPQPRGLGMLTVSHVTPSSIQLEMSVLSGTFDSFTVQYRDAQS 591

```
QY 464 FVRACL-----RRLVPPGLWGSRRH 482
Db 592 QPQALAVDGGSGRTVTVPGLSPSRH 615

RESULT 43
EBDE75
Immediate-early protein IE175 - human herpesvirus 1
C:Species: human herpesvirus 1
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C:Accession: A23510
R:McGeoch, D.J.; Dolan, A.; Donald, S.; Brauer, D.H.K.
Nucleic Acids Res. 14, 1727-1745, 1986
A:Title: Complete DNA sequence of the short repeat region in the genome of herpes simplex
A:Reference number: A23510; MUID:86148504; PMID:3005980
A:Accession: A23510
A:Molecule type: DNA
A:Residues: 1-1298 <MCG>
A:CROSS-references: UNIPROT:P08392; GB:X14112; GB:D00317; GB:D00374; GB:S40593; NID:gl94
C:Comment: This protein acts at the transcriptional regulatory level and is required for
C:Genetics:
A:Gene: IE3
A:Map position: short repeat region (IR-s)
C:Superfamily: herpesvirus immediate-early protein IE175
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 2.1%; Score 124; DB 1; Length 1298;
Best Local Similarity 21.2%; Pred. No. 4.1;
Matches 126; Conservative 34; Mismatches 207; Indels 226; Gaps 26;

QY 12 SLLRSHYREVLPPLATFVRRLGPGWRLVQGDPAAPRALVAQCLVCVPWDARPPPAAPSF 71
Db 419 SPITGSVARVPHLGYMAAGRFMGWL-----AHAAAVAMSRDYRAQKGF 465

QY 72 RQVSCLEKELVARVQLRCERGAKNVLAQFALLDGCAGSP---PEAFTTSVRSVLPNTV 127
Db 466 LLTS-LRRAYAPLLAR-----EN-----AALTGAAGSPGAGADDEGVAVAAPAAAGE- 511

QY 128 TDALRGSAWGLL--LRRV-----GDD-----VLVHLIAR 155
Db 512 RAVPAGYGAAGILAAALGRLSAAPSPAGGDDPDAAHADDADDDAGRAQAQGRVAECLEA 571

QY 156 C-----AL-----FVLVASCAYQVCGPPLYQLGAATQARPPPHAGSPRRRLGCERAW 203
Db 572 CRGILEALAEQDGLAAVPLGAGAPASPRPEGPAGPASPAPPPPHADAPRL-----RAW 626

QY 204 NHS-----VREAGVPLGLPAGARRRGG-----ASRL-----PLPKRPR----- 239
Db 627 LRELFRVDALVIMRLRG-DLKVAGGSEAAVAVRAVSLVAGALGPALPRDRLPSSAAA 685

QY 240 -----RGAAPERTPVQGSWA-----HPGKTRGPSDRGFCV 272
Db 686 AAADLLFDNQSLRPLAAASAPDAADALAAAAAASAPREGKRKSPGPAPPPGGG--- 742

QY 273 VSPARPAAEATSLGALSGTRHSHPSVGRQHAGPSPSPRPWDTPCPVPVYATKHFL 332
Db 743 --PRPPKTKSGADAPGSDARAPLPA-----PAPFST--PPGPAPAPAAAPRAA--- 789

QY 333 YSSGDKQLRPSFLSLSLRPSLTGARRLVETIFLGRPMWCTPRRLPRLPQRYQMWRPL 392
Db 790 -----AAQARPRVAVSRRA-----EGDPLGGWRRQPPGP----- 821

QY 393 FLELGNHAQCYPVLLKTHCKPLRA-----AVTPAAGVCARE 429
Db 822 -----SHTAAPAAALAEAYCSPRAVAELTDHPLFPVWPWRPALMFPDPRALASIAACAGP 875

QY 430 KQGSVAAPAEEDTDP-----RLVOLLRQHSPPQV 461
Db 876 APAAQAACGGGDDDDNPHPHGAAGGLRFGPLRASGFLRRMAWMRQIPDPEDV 928

RESULT 44
```

S27224

N-methyl-D-aspartate receptor epsilon-4 chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Feb-1994 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C:Accession: S27224

R:Ikeda, K.; Nagasawa, M.; Mori, H.; Araki, K.; Sakimura, K.; Watanabe, M.; Inoue, Y.; N.
FEBS Lett. 313, 34-38, 1992
A:Title: Cloning and expression of the epsilon-4 subunit of the NMDA receptor channel.
A:Reference number: S27224; MUID:93050214; PMID:1385220
A:Accession: S27224
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1323 <IKE>
A:CROSS-references: EMBL:D12822
C:Superfamily: N-methyl-D-aspartate receptor 2D; glutamate receptor homology
C:Keywords: transmembrane protein
F:451-879/Domain: glutamate receptor homology <GRH>

Query Match 2.1%; Score 124; DB 2; Length 1323;

Best Local Similarity 23.4%; Pred. No. 4.2;

Matches 92; Conservative 17; Mismatches 106; Indels 178; Gaps 21;

QY 2 PRAPRC-----RAVRSLLRSHYREVLPPLATFVRRLGPGWRLVQGDPAAPRALVAQCLV 56

Db 1061 PRASRCWVGARAAALGPRPHRRV-----RTAPP-----P 1091

QY 57 CVPWDARPPPAAPSFQVSCLEKELVARVQLRCERGAKNVLAQFALLDGC----- 106

Db 1092 CAYLDLESPS-----DSEDSLSLGASLGLEPPWFAFP 1127

QY 107 ----ARGGPEAFTTSVRSVLPNTVTDALRG--SGANGLLLRRVDDDLVHLLARCALFV 160

Db 1128 YPYAERLGPFGRYWSV-----DKLGWRAGSDYLPFRGCP---AWHCRHCASLE 1175

QY 161 LVAP-----SCAYQVC-----GPLYQLGAATQARPPPHASGP-----RRRLGCERAWNSHV 207

Db 1176 LLPPRHLSCSHDGLDGGWAPP-----PPWAAAGFPAPRRARCCGPR----- 1218

QY 208 REAGVPLGLPAGARRRGGSSASRLPLPKRPR-----GAAPEPERTPVQGSWAHPGRT 262

Db 1219 -----PHPHRPRASHAPAPAAAPHHHRRAAGGWDLP--- 1250

QY 263 RPSDRGFCVSPARPAAEATSLGALSGTRHSHPS---VGRQHAGPSPSPRP---W 317

Db 1251 -----PPAPTSKSLD-LSSCCRAAPTRRLTGPSRHA-----RRCPHAAHW 1290

QY 318 DTPCPPVVAETKHFYSSGDKQLRPSFLISSL 350

Db 1291 GPPLP-----TASHRRHGGDLGTRGSAHFSSL 1319

RESULT 45

S16506

hypothetical protein - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Nov-1994

C:Accession: S16506

R:Mariman, E.C.M.; Schepens, J.T.G.; Wieringa, B.

Nucleic Acids Res. 17, 6385, 1989

A:Title: Complete nucleotide sequence of the human creatine kinase B gene.

A:Reference number: S15935; MUID:8936665; PMID:2771648

A:Accession: S16506

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-381 <NUC>

A:CROSS-references: EMBL:X15334

Query Match

Best Local Similarity 2.1%; Score 123.5; DB 2; Length 381;

Matches 88; Conservative 23; Mismatches 117; Indels 123; Gaps 18;

QY 137 WGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGAATQ-ARPPPHASGPRR 195

Db 137 WGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGAATQ-ARPPPHASGPRR 195

Db 29 WLLWALRSNSSAGKRSFSAW-LLEKMAAAGCGETRGQGPARRGSRAPAYHSGRR 87
QY 196 RLGCEAWNHSVREAGVPLGLPAPGARRRGSGASRLP-LPKRRRGAPEPPTPVGO- 253
Db 88 R-----APRRPGRGQGRGQPGARCAPSSPTGSGARSRRAPFARS 132
QY 254 -----GSAH-PGRTRGSDRGFCVVSAPAEATSLGAL-----SGTRHSH-- 296
Db 133 AFSQADAPGPRHSPG---GRAGAGALRPSAAGATQANSGRSALPRLRGTTTAAHWR 189
QY 297 -----PSVGR-----QHAGPPSTS---RPPRPDTECPVVAETKFLY 333
Db 190 LFIANSFWPARGGAALSAARSQHPGRPELSPRPDPAQSPADLEAET----- 244
QY 334 SSGDKQLRPSFLLSRLSLTGARRLVETIFLGRPMWPTPR-LP---RLPOR-YWQ 388
Db 245 -----SGPMISGSPRTPLPLGGKLRASGH 270
QY 389 MRPL-FLELLGNHAQPYGLVLTHTCPLR-AAVTAAAGVCAREKPGGVAA 437
Db 271 SRTLGFIRILE-----PARLVOPAPAAAARGAKAFGASAA 306
RESULT 46
A30411
synapsin Ia - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 09-Jul-2004
C:Accession: A30411; B30411
R.Suedhof, T.C.; Czernik, A.J.; Kao, H.T.; Takei, K.; Johnston, P.A.; Horiuchi, A.; Kana
Science 245, 1474-1480, 1989
A:Title: Synapsins: mosaics of shared and individual domains in a family of synaptic ves
A:Reference number: A30411; MUID:89388265; PMID:2506642
A:Accession: A30411
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-704 <SUE>
A:Cross-references: UNIPROT:P09951; GB:M27812; NID:G206920; PIDN:AAA42145.1; PID:G206921
A:Accession: B30411
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-659, 'KA', 662, 'PAQAP' <SU2>
A:Cross-references: GB:M27924; NID:G206932; PIDN:AAA42148.1; PID:G206933
C:Keywords: actin binding; alternative splicing; phosphoprotein
Query Match 2.1%; Score 123.5; DB 2; Length 704;
Best Local Similarity 25.8%; Pred. No. 1.9;
Matches 69; Conservative 18; Mismatches 67; Indels 113; Gaps 15;
QY 172 GPPLYQLGAATQARPPP-----HASGPRRLRGCEAWNHSVREAGVPL--GLPAPGARRRG 225
Db 476 GPPL-----QORPPQOQHLG-----LG-----PPAGSPLPQLRPSPTAAPQ- 514
QY 226 GSASRLPL-----PKRRRGAPEPER----- 248
Db 515 QSASQATPMTQCGQRSPVAGGCGAPPAAARPASPSFORAGPQATQASISGPAPPK 574
QY 249 ----TPVCGSWAHFGRTRGSDRGFCVVSAPAEATSLGALSGTRHSHPSVGRQH 304
Db 575 VSGASPGGQGRGPPKPGPA-----GPTRQASQAG-----PGPRTGPTTQOQPRP 621
QY 305 AGPPSTSRPPR-----WDTFCPPVVAETKFLYSSGDKQLRPSFLLSRLSLTGA 357
Db 622 SCGPAGRTKQLAQKSDQVP-PPITAAAGPPHPQLNKSQ-----SLTNA 668
QY 358 RRLVETIFLGRPMWPTPRRLPLPQ 384
Db 669 FNLPE-----PAPPR--PSLSQ 683

RESULT 47
T42214
otogelin - mouse

N:Alternate names: mucin-like extracellular matrix protein
C:Species: Mus musculus (house mouse)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
C:Accession: T42214
R.Cohen-Salmon, M.; El-Anraoui, A.; Leibovici, M.; Petit, C.
Proc. Natl. Acad. Sci. U.S.A. 94, 14450-14455, 1997
A:Title: Otogelin: A glycoprotein specific to the acellular membranes of the inner ear.
A:Reference number: 222079; MUID:98070772; PMID:9405633
A:Accession: T42214
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2910 <COH>
A:Cross-references: UNIPROT:O55225; EMBL:U96411; NID:G2760883; PID:G2760884; PIDN:AAB965
A:Experimental source: strain BALB/c
A>Note: Component of all the acellular membranes of the inner ear
C:Superfamily: von Willebrand factor type A repeat homology; von Willebrand factor type

Query Match 2.1%; Score 123.5; DB 2; Length 2910;
Best Local Similarity 18.8%; Pred. No. 13;
Matches 236; Conservative 115; Mismatches 393; Indels 513; Gaps 60;
QY 111 PPEAFTTSVRSVLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAVQV 170
Db 1473 PP---TTSAEQQLP-----QGLPGASAYS-----PAPVPVAPPTS--A 1505
QY 171 CGPLYQLGAATQAR-PPPHASGP--RRRLGCERA-----WNHSVREAG----- 211
Db 1506 PNPPM---AATEGAQPSPGSTQPLQPLGLTNNFPAGTTEATAREGAASLLTTSHP 1561
QY 212 -----VPLGLPAPGARRRG-----ASRSLPLPKRP---RRGAAP 244
Db 1562 PGFSSSLPSSQLMPTSGIVSGATETTKVITFTGSPNTTVASRSPPIPRFPLMTRAVTVP 1621
QY 245 EPERTPVG---QGSWAHPGRTGRGSDRGFCVVSARP----- 278
Db 1622 SHDSFPVKTTPLOQSWLWSLSRPMWLSGATSWPTSPGSHLSTAVTKVANKTWSLSVL 1681

QY 279 ABEATSLGALSG--TRHSHP-----SVGRQHAG-----PPSTSRPPRPW 317
Db 1682 AOSTSSSQPLAAVTAHRAFPASPLVTKGLVSVATEKEAGHSQLTLPVSPSPAPPI 1741
QY 318 DTPCPPVVAETKFLYSSGDKQLRPSFLLSRLSPSLTGARRLVETIFLGRPMWPTPR 377
Db 1742 DLHPAQHTTT-----APGPSALSPG-ILAAAGSPS-TGAHRPGATALASLEPTRP--PH 1791
QY 378 RLPLPQRYWQMRPLFLELLGNHAQ-----CPYGVLL 409
Db 1792 LLSGLPLD-----TSLPLAKVGTSPVATPGSKGYIPTPPPOHQAATLTAMTVSPLTOSL 1847
QY 410 KTHCPRLAAVTPAAGVCAREKPGQSVAAPEBEDTDPRLVQLLRQHSSFWOVYGFVRACL 469
Db 1848 SLTVPLMSAVEQAHSPPSPKPPQGTGMAPDQ-----MLGATLPSFGASSVIAG----- 1895
QY 470 RRLVPPGLWGRHNRRLRNKTKFISLGKHAULS-----LOELTWKMS--VR 515
Db 1896 ---VPPTVSAAPRKS-----TTQRAAILSK-KVSPPTLISDSVQGGTELTPIVSHVT 1945
QY 516 DCAMLRSPGVGCVPAAEHRLREILAKFLHLMWSVYVVELLSRFFYVTEFTFQKRLFF 575
Db 1946 PLATEAGFRAGTVP-----LVPTTYS----- 1967
QY 576 YRKSVMWSKLQIGIRQHLLKRVQLRELSEAEVRQREARPALITSRLRIPKPDGLRPIVN 635
Db 1968 -----LSRVSAITAS-----REGPLVLLPOLAEAYGTPAGLQP--Q 2001
QY 636 MDYVVGARTPRREKRAERLTSRVKALFSVLNY----- 667
Db 2002 EDLMRQATTEQSGRSAPASPAQSIAEESMEAEVNTSATCPVIAEQDCVHHICLEGQLIRVNOT 2061
QY 668 -----ERARRP--GLLGASV-LGLDDIHRW-----RTFVLVRQAODPPPELVKVDVTGA 716
Db 2062 QHCPQGAVRPRCGVLGLAVRVGGDRCCPQWECACRCSIF-----PDLFSVTFD--GS 2111

```
QY 717 YDTPQDRLTEVIASIIKQNTYCYVRRYAVVQKAH-CHVR-----KAFKSHVS 764
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2112 HAALFKEAIYYLSQS---PDETISV--HVLDCKSANLGHANWPPCLVILNVTHLAHVS 2166
QY 765 -----TLTDLQ---PYMRQFVAHLQSTPLRDADVIEQSSSLNEASSGLFDVFLRMC 814
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2167 IDRFNKRKTVDSQVWPMPMSRYGFRIEDTG----- 2196
QY 815 HHAIVRKSVYVQCGIPOGSI-----STLCSLCYGMENKLFAGIRRDGLL 863
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2197 -HMYMVRTPSHIQIQLHSSGLMILEASKVSKTQGHGCGICDGDAAIDL---TLKDGSV 2252
QY 864 LRLVDLFLVPHLTHAKTFLTLVRGVPYVCCVNLKTVNPFVEALGCTAFVOMP 923
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2253 LGEABD-----P 2259
QY 924 AHGLFPWCGLLLDRTLTEVQSDYSSYARTSIRAS-----LTFNRGFKAGRNMR 971
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2260 APFLDSW-----QVPSLTSEGQTRFPDSCATADCSPLRMVSNRTFSA----- 2304
QY 972 RKLFGVRLKCHSL-----FLDLQNS---LQVCTNTYKILLQAYRPHACVILQLPFPQ 1023
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2305 -----CHSFVSPESFCBLWIRDTKYVQPCVAL-TVVVAMCHKFHCI----- 2346
QY 1024 QVWKNPTF--FLRVISDTSILCYSLKXKNAGMSLGAGAPLPSEAVQWL-----CHQ 1076
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2347 -EWRGSDYCPFLCSSDSTYQACVAAACEPPDTCQD-----GVLGPLDPEQCQVLGSGVCCTE 2401
QY 1077 AFLKLKLRHVTVVPLLGSLRTAQLSKLPGTTLTALEA-----AANPALPSD 1126
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2402 GTILH-RRHSALCIPEDKCACTDSTGVPRALGETWNSLSGCCQCCQCAPDTIIPVD 2457

RESULT 48
WZBEC8
68.6K capsid protein - equine herpesvirus 1 (strain Ab4p)
C:Species: equine herpesvirus 1
A:Note: host Equus caballus (domestic horse)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: I36798
R:Teiford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
submitted to GenBank, March 1992
A:Description: The DNA sequence of equine herpesvirus-1.
A:Reference number: A36805
A:Accession: I36798
A:Molecule type: DNA
A:Residues: 1-646 <TEL>
A:Cross-references: UNIPROT:P28936; GB:M86664; NID:g330791; PIDN:AAB02470.1; PID:g330827
R:Teiford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Virology 189, 304-316, 1992
A:Title: The DNA sequence of equine herpesvirus-1.
A:Reference number: A41831; MUID:92295566; PMID:1318606
A:Contents: annotation; possible protein-coding frames
A:Note: neither amino acid nor nucleotide sequence is given
C:Genetics:
A:Gene: 35
C:Superfamily: varicella-zoster virus gene 33 protein
C:Keywords: capsid protein

Query Match 2.1%; Score 123; DB 1; Length 646;
Best Local Similarity 22.9%; Pred. No. 1.8;
Matches 121; Conservative 72; Mismatches 190; Indels 146; Gaps 30;

QY 14 LRSHREVLPLATF-VRRILGPGQMRVLQVGPAAFRALVAQCLV-----CVPMDARPPP 66
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
114 LVSNY---LPSASLSSRLGPD-----EEDPDTLF-AHVSCLVIGRRVGTIVTDATEN 164
QY 67 AAPSPRQV--SCLKELVAVLQRLCERGAKNVLAFGFALLDGCAGGPPPEATTTSVRSVLP 124
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
165 AVAPFKRLSPSSRELL-----ITAREAQRLG-----DAAATHWLSEDTLTRY---LL 209
QY 125 NTVTDALRGSAWGLLLRR---VGGDVLVHLARCALFVL-----VAPSCAY- 168
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Db 210 STAVNNMLLRNWNLVARRRREAGIEGHTYLOASASFGITNGCNKADPCGAEIVDTCGYK 269
QY 169 ---QVCGPPLYQ--LGAA--TOARPP--PHASGPRRLGCERAWNH-SVREAGVPLGLPA 218
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
270 SGEKVHGAPYSRVTLGAKAFTSSSPNALPSSDNDKGIG-ERTQKHISAMASSNPQTLSA 328
QY 219 PGARRRGCSASRSLPLKPRPRRGAPEPERTPVCGGSWAHPGRTGRGSDRGFCVVSARP 278
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
329 AGAPLVSGD---YILVP-----AAQYNQLVWGQHT-SHPPINAGPAPVTHVPSQYIP 377
QY 279 -----AEEATSLGALS-----GTRHGHPVSGRQHAGPP 308
Db 378 PAYNSLMPPSMYQAPPYWSVPHSNALEAQITLVGALAADRKAATKGGDPHVIQSQCSPP 437
QY 309 STSRPPR-----PMDTPCPVYVYAEKHFYS-----SGDKEQLRPSFLSSL 350
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
438 LSPQERRRYARKRHWD-----ATTRDDLEGIYYPGERSPRPGERRAGRPSTTIADL 490
QY 351 RPSLTGAR-----RLVETIFLGSRPWMPGTTPRLPLPQRYWQ---MRP-----LFL 394
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
491 MGAVSSLLQEVSQLRAIQTVTAQPQAAPAGLYKPIPAVPPQYQYQIQPHAVSAIVAP 550
QY 395 ELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPGQSV---AAPEE 440
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
551 QLPQIPSQ-FTQAVLAPQVPAPEAGSAKVVAASTAFQAQAEQARAAPQ 598

RESULT 49
JT0396
reverse transcriptase homolog - fruit fly (Drosophila melanogaster) transposon jockey
C:Species: Drosophila melanogaster
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JT0396
R:Primaegi, A.F.; Mizrokhi, L.J.; Ilyin, Y.V.
Gene 70, 253-262, 1988
A:Title: The Drosophila mobile element jockey belongs to LINEs and contains coding sequences
A:Reference number: JT0395; MUID:89108009; PMID:2463954
A:Accession: JT0396
A:Molecule type: DNA
A:Residues: 1-916 <PRI>
A:Cross-references: UNIPROT:P21328; GB:M22874; NID:g157823; PID:g157825
C:Genetics:
A:Gene: FlyBase:jockey
A:Cross-references: FlyBase:FBgn0001283

Query Match 2.1%; Score 123; DB 2; Length 916;
Best Local Similarity 21.8%; Pred. No. 2.9;
Matches 155; Conservative 73; Mismatches 230; Indels 254; Gaps 36;

QY 339 EQLRPSFLSLSLRPSLTGARRLVETIFLGSRPWMPGTTPRLPR-----LPORYWQMRPLP 393
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
291 EAFRPLQPSILALLRLKRRVRKEYARTGDPRMQOIHSRLANLHLKALARRKQAQIDTF 350
QY 394 LELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPGQSVAAPEEDTTPRLVQLLR 453
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
351 LDNLGADASTNYS-LWRITRFRKAQPTPKSAI---KNPSGGWCRTSLEKTEV--FANNLE 404
QY 454 QHSSPQWQYGFVRACLRRLVPPGLWGRSHNERRF-----LRNTKFIISLGKAKL 503
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
405 QRFTP---YNYAPESLCRQV-----EYLESPPQMSIPLSAVTLSEEVKNI-----AKL 450
QY 504 SLQELTWMSVRDCAMWLRRSPGVCVPAABHRLREETILAKPLHWM-SVYVVELL----- 557
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
451 P-----LKKAPGEDLLDNRTIRLLPDQALQFALIFNSVLVDVGFPPKAWK 495
QY 558 -RSFFVYTTTFQKNRLFYVRKSVWSKLSQSIGIQHLKRVOLRELSEAEVQHREARPAL 616
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
496 SASIIMHKTKTPTDVSIRPT--SLDPSLG--KIMERLLINR-----L 536
QY 617 LTSR--LRFTPK-----PDGLRPIVNM-----DYVVGARTFRREKRAERLT 655
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
537 LTCKDVTKAIPKQFGFRFLQHGTEQLHRVNVFALEAMENKEYAVGA--FLDIQQA----- 590
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 5, 2005, 14:04:33 ; Search time 189 Seconds
(without alignments)
3067.056 Million cell updates/sec

Title: US-10-053-758-225

Perfect score: 5961

Sequence: 1 MPRAPRCRAVRSLLRSHRYE.....TALEAAANPALPSPFKTILD 1132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5961	100.0	1132	1 TERT HUMAN	O14746 homo sapien
2	5583.5	93.7	1069	2 Q8NG46	Q8NG46 homo sapien
3	4089.5	68.6	1123	1 TERT CANFA	Q6A548 canis fami
4	4052	68.0	807	2 Q8NGC3	Q8A6C3 homo sapien
5	3973	66.6	795	2 Q8NG38	Q8NG38 homo sapien
6	3628	60.9	1128	2 Q9QX24	Q9QX24 mesocricetu
7	3529.5	59.2	1125	2 Q673L6	Q673L6 rattus norv
8	3514.5	59.0	1119	2 Q673L5	Q673L5 rattus norv
9	3505	58.8	1122	1 TERT MOUSE	O70372 mus musculu
10	2825	47.4	524	2 Q9UBR6	Q9UBR6 homo sapien
11	2250	43.4	1346	2 Q6RD80	Q6RD80 gallus gall
12	2316.5	38.9	1191	2 Q9DE32	Q9DE32 xenopus lae
13	2207.5	37.0	523	2 Q9A4807	Q9A4807 homo sapien
14	2016	33.8	575	2 Q9JK99	Q9JK99 rattus norv
15	1408	23.6	615	2 Q673L3	Q673L3 rattus norv
16	1373	23.0	514	2 Q9R266	Q9R266 mus musculu
17	724.5	12.2	1123	2 Q9SE99	Q9SE99 arabidopsis
18	724.5	12.2	1123	2 Q9SPU7	Q9SPU7 arabidopsis
19	688	11.5	1259	2 Q9AU13	Q9AU13 oryza sativ
20	654.5	11.0	1261	2 Q8LKW0	Q8LKW0 oryza sativ
21	594	10.0	988	1 TERT SCHPO	O13339 schizosacch
22	478	8.0	1032	2 Q7Z1L1	Q7Z1L1 euploetes cr
23	474	8.0	1032	2 Q8MUB3	Q8MUB3 euploetes cr
24	469.5	7.9	939	2 Q7SD71	Q7SD71 neurospora
25	450	7.5	85	2 Q9UN56	Q9UN56 homo sapien
26	450	7.5	940	2 Q6C9D0	Q6C9D0 varrowia li
27	449	7.5	116	2 Q8OSU5	Q8OSU5 rattus norv
28	448.5	7.5	1031	1 TERT_EUPAE	O09339 euploetes ae
29	441	7.4	1032	2 Q7Z1L0	Q7Z1L0 euploetes cr
30	408	6.8	823	2 Q8SQQ0	Q8SQQ0 encephalito
31	397	6.7	104	2 Q9J1M1	Q9J1M1 mus musculu

32	395.5	6.6	1135	2 Q818Z7	Q818Z7 sterkiella
33	395	6.6	1132	1 TERT OXYTR	Q76332 oxytricha t
34	394	6.6	73	2 Q9UNR4	Q9UNR4 homo sapien
35	392	6.6	1108	2 Q818Z6	Q818Z6 sterkiella
36	389.5	6.5	861	2 Q8CS80	Q8CS80 kluyvaromyc
37	365	6.1	867	2 Q9P8T3	Q9P8T3 candida alb
38	364	6.1	895	2 Q9GRCS	Q9GRCS paramecium
39	363	6.1	1117	1 TERT TETTH	Q77448 tetrahymena
40	361	6.1	867	2 Q9P8T2	Q9P8T2 candida alb
41	356.5	6.0	884	1 TERT YEAST	Q06163 saccharomyc
42	355.5	6.0	894	2 Q8BU66	Q8BU66 debaromyce
43	342	5.7	896	2 Q8MUQ8	Q8MUQ8 paramecium
44	339	5.7	79	2 Q7YR69	Q7YR69 felis silve
45	338	5.7	79	2 Q76K45	Q76K45 canis fami

ALIGNMENTS

RESULT 1	ID	TERT HUMAN	STANDARD	PRT	1132 AA
AC	O14746	O14783			
DT	30-MAY-2000	(Rel. 39, Created)			
DT	30-MAY-2000	(Rel. 39, Last sequence update)			
DT	25-OCT-2004	(Rel. 45, Last annotation update)			
DE	Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit) (HES2) (Telomerase-associated protein 2) (TP2).				
DE	subunit (HES2) (Telomerase-associated protein 2) (TP2).				
GN	Name=TERT; Synonyms=EST2, TCS1, TRT;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Kidney;				
RX	MEDLINE=97400623; PubMed=9252327; DOI=10.1126/science.277.5328.955;				
RA	Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H.,				
RA	Lingner J., Harley C.B., Cech T.R.;				
RT	"Telomerase catalytic subunit homologs from fission yeast and human.";				
RL	Science 277:955-959 (1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97433088; PubMed=9288757; DOI=10.1016/S0092-8674(00)80538-3;				
RA	Meyerson M., Counter C.M., Eaton E.N., Ellisen L.W., Steiner P.,				
RA	Caddie S.D., Ziaugra L., Beijersbergen R.L., Davidoff M.J., Liu Q.,				
RA	Bacchetti S., Haber D.A., Weinberg R.A.;				
RT	"hEST2, the putative human telomerase catalytic subunit gene, is up-				
RL	regulated in tumor cells and during immortalization.";				
RN	Cell 90:785-795 (1997).				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=9267414; PubMed=10333526; DOI=10.1016/S0378-1119(99)00108-0;				
RA	Wick M., Zubov D., Hagen G.,				
RT	"Genomic organization and promoter characterization of the gene				
RL	encoding the human telomerase reverse transcriptase (hTERT).";				
RN	Gene 232:97-106 (1999).				
RP	SEQUENCE FROM N.A.				
RA	Londono-Vallejo J.A.;				
RT	"Sequence of a BAC carrying the entire hTERT gene.";				
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.				
RN	[5]				
RP	FUNCTION IN TELOMERASE ACTIVITY, TISSUE SPECIFICITY, ASSOCIATION WITH				
RA	TEPI, AND MUTAGENESIS OF ASP-868; ASP-869 AND ASP-712.				
RX	PubMed=9389643;				
RA	Harrington L., Zhou W., McPhail J., Oulton R., Yeung D.S., Mar V.,				
RA	Bass M.B., Robinson M.O.;				
RT	"Human telomerase contains evolutionarily conserved catalytic and				
RL	structural subunits.";				
RN	Genes Dev. 11:3109-3115 (1997).				
RP	ASSOCIATION WITH TEPI.				

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RX PubMed-11029039;
RA Beattie T.L.; Zhou W., Robinson M.O., Harrington L.;
RT "Polymerization defects within human telomerase are distinct from
RL Mol. Biol. Cell 11:3329-3340(2000).
CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
CC the replication of chromosome termini in most eukaryotes. It
CC elongates telomeres. It is a reverse transcriptase that adds
CC simple sequence repeats to chromosome ends by copying a template
CC sequence within the RNA component of the enzyme.
CC -!- SUBUNIT: Component of the telomerase ribonucleoprotein complex at
CC least composed of TEP1, EST1A, POT1 and a telomerase RNA template
CC component (TER). Interacts with PINK1.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: Activation of telomerase has been implicated in cell
CC immortalization and cancer cell pathogenesis.
CC -!- SIMILARITY: Belongs to the reverse transcriptase family.
CC Telomerase subfamily.
CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF015950; AAC51672.1; -.
DR EMBL; AF018167; AAC51724.1; -.
DR EMBL; AF128894; AAD30037.1; -.
DR EMBL; AF128893; AAD30037.1; JOINED.
DR EMBL; AY007685; AAG23289.1; -.
DR PIR; T03844; T03844.
DR GenBank; HGNC:11730; TERT.
DR MIM; 187270; -.
DR GO; GO:0000781; C:chromosome, telomeric region; TAS.
DR GO; GO:0042162; F:telomeric DNA binding; TAS.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. . .; TAS.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF000078; RVT; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR PROSITE; PS50878; RT_POL; 1.
KW DNA-binding; Nuclear protein; Ribonucleoprotein;
KW RNA-directed DNA polymerase; Telomere; Reverse transcriptase.
FT DOMAIN 605 935
FT MUTAGEN 868 868 D->A: Loss of telomerase activity.
FT MUTAGEN 868 869 DD->AA: Loss of telomerase activity.
FT MUTAGEN 869 869 D->A: Loss of telomerase activity.
FT MUTAGEN 712 712 D->A: Loss of telomerase activity.
FT CONFLICT 516 516 D -> G (in Ref. 2).
SQ SEQUENCE 1132 AA; 126996 MW; 94E35469C4CA33A0 CRC64;

Query Match 100.0%; Score 5961; DB 1; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVSLRSHREVLPVRRVLPQGRVLRVQGRDPAARFALVAQCILVCPW 60
DB 1 MPRAPRCRAVSLRSHREVLPVRRVLPQGRVLRVQGRDPAARFALVAQCILVCPW 60

QY 61 DARPPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
DB 61 DARPPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120

QY 121 SYLPTNTVTDALRGSGAWGLLRVGGDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPTNTVTDALRGSGAWGLLRVGGDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASPRRLRCERAWNHSVREAGVPLGPAPGARRRGGSASRSILPKRPRR 240
DB 181 ATQARPPPHASPRRLRCERAWNHSVREAGVPLGPAPGARRRGGSASRSILPKRPRR 240

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QY 241 GAAPEPERTVPGQSWAHPPGRTGPRGFCVSPARPAEATSLGALSSTRHSPSVG 300
DB 241 GAAPEPERTVPGQSWAHPPGRTGPRGFCVSPARPAEATSLGALSSTRHSPSVG 300

QY 301 ROHHAGPSTSRPRPMDTTCPPVYASTKHPYSSGDEQRLRPSFLSSLPSTLGARRL 360
DB 301 ROHHAGPSTSRPRPMDTTCPPVYASTKHPYSSGDEQRLRPSFLSSLPSTLGARRL 360

QY 361 VETIFLGSRRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCYPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCYPYGVLLKTHCPLRAAVT 420

QY 421 PAAGVCAREXPQGSVAAPSEEDTDPRLVLQRLLOHSSPWQYVGVFVACLRRLVPPGLMGS 480
DB 421 PAAGVCAREXPQGSVAAPSEEDTDPRLVLQRLLOHSSPWQYVGVFVACLRRLVPPGLMGS 480

QY 481 RHNERFLRNTKKEISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
DB 481 RHNERFLRNTKKEISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540

QY 541 LAKEFLHLMSSVYVELLRSFPYVTTTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVOLRE 600
DB 541 LAKEFLHLMSSVYVELLRSFPYVTTTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVOLRE 600

QY 601 LSEAEVQHRREARPAALLTSRLRFLPKDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVQHRREARPAALLTSRLRFLPKDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660

QY 720 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRADQPPPELVKVDVTGAYDTI 720
DB 720 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRADQPPPELVKVDVTGAYDTI 720

QY 780 PODRLTEVIASIIKPONTYCVRRYAVVQKAAGHVRKAFKSHVSTLTLDLOPYMQFVAHL 780
DB 780 PODRLTEVIASIIKPONTYCVRRYAVVQKAAGHVRKAFKSHVSTLTLDLOPYMQFVAHL 780

QY 781 QETSPLRDADVIEOSSSLNEASSGLFDVFLRFMCHHAVIRNGKSYVQCQGIPOQSILSTL 840
DB 781 QETSPLRDADVIEOSSSLNEASSGLFDVFLRFMCHHAVIRNGKSYVQCQGIPOQSILSTL 840

QY 841 LCSLCYGDMEKULFAGIRRDGLLRLVDDLLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
DB 841 LCSLCYGDMEKULFAGIRRDGLLRLVDDLLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900

QY 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRASLTF 960
DB 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRASLTF 960

QY 961 NRGPKAGRNMRKLFGLVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLOLP 1020
DB 961 NRGPKAGRNMRKLFGLVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLOLP 1020

QY 1021 PHQOVWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOMLCHOAFLL 1080
DB 1021 PHQOVWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOMLCHOAFLL 1080

QY 1081 KLTRHRYVYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTIIL 1132
DB 1081 KLTRHRYVYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTIIL 1132

RESULT 2
Q8NG46
ID Q8NG46 PRELIMINARY; PRT; 1069 AA.
AC Q8NG46;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Telomerase reverse transcriptase.
GN Name=hTERT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hisatomi H., Ohyaishiki K., Ohyaishiki J.H., Nagao K., Kanamaru T.,
 RA Hisatomi H., Hibi N., Tsukada Y.,
 RT "Expression profile of a gamma-deletion variant of the human
 RT telomerase reverse transcriptase gene.";
 RL Neoplasia 5:193-197(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Nagao K., Katsumata K., Aizawa Y., Saito N., Hirata H., Sasaki H.,
 RA Yamamoto S., Hikiji K., Koita T., Hisatomi H.;
 RT "Differential alternative splicing expressions of telomerase reverse
 RT transcriptase in gastrointestinal cell lines.";
 RL Oncol. Rep. 11:127-131(2004).
 DR EMBL; AB085628; BAC11010.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase...; IEA.
 DR InterPro; IPR003545; Telomerase_RT.
 DR PRINTS; PR01365; TELOMERASERT.
 DR RNA-directed DNA polymerase.
 SQ SEQUENCE 1069 AA; 120046 MW; BE1E77A653B1C666 CRC64;
 Query Match 93.7%; Score 5583.5; DB 2; Length 1069;
 Best Local Similarity 94.4%; Pred. No. 0;
 Matches 1069; Conservative 0; Mismatches 0; Indels 63; Gaps 1;
 OY. 1 MPAPRCRAVRSLRSHREVLPVPLATFVRRLLPQGWRLVQRGDPAAFRALVAQCLVCPW 60
 DB 1 MPAPRCRAVRSLRSHREVLPVPLATFVRRLLPQGWRLVQRGDPAAFRALVAQCLVCPW 60
 OY 61 DARPPAPSPROVCLKELVARLQRCERAKNVLAAGFALLDGCARGPPEATTSVR 120
 DB 61 DARPPAPSPROVCLKELVARLQRCERAKNVLAAGFALLDGCARGPPEATTSVR 120
 OY 121 SYLPTNTVDALGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAVQCGPPLYQLGA 180
 DB 121 SYLPTNTVDALGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAVQCGPPLYQLGA 180
 OY 181 ATQARPPPHASGRRRLGRCERAWNHSVREAGVPLGLPAPGARRRGGASRSPLPKRRR 240
 DB 181 ATQARPPPHASGRRRLGRCERAWNHSVREAGVPLGLPAPGARRRGGASRSPLPKRRR 240
 OY 241 GAAPERTPVQGSWAHPGRTGSDRGFCVSPAPAEATSLGALSGLTRHSHPSVG 300
 DB 241 GAAPERTPVQGSWAHPGRTGSDRGFCVSPAPAEATSLGALSGLTRHSHPSVG 300
 OY 301 ROHAGPSTSPRPDPWTPCPVVAETKHFYSSGDKQLRPSFLLSRLSLTGARRL 360
 DB 301 ROHAGPSTSPRPDPWTPCPVVAETKHFYSSGDKQLRPSFLLSRLSLTGARRL 360
 OY 361 VETIFLGRPMWPGTFRRLPLRPLQRYWQMRPLFLELLGNHACQPGVLLKTHCPLRAAVT 420
 DB 361 VETIFLGRPMWPGTFRRLPLRPLQRYWQMRPLFLELLGNHACQPGVLLKTHCPLRAAVT 420
 OY 421 PAAGVCAREKPGSVAAPPEEDTPRRLVQLLRQHSHPQVYGFVRACLRLVPPGLWGS 480
 DB 421 PAAGVCAREKPGSVAAPPEEDTPRRLVQLLRQHSHPQVYGFVRACLRLVPPGLWGS 480
 OY 481 RNERERFLNKKFISLGHAKLSLOELTWKNSVRDCAWLRSRPGVCPVPAEHLRBEI 540
 DB 481 RNERERFLNKKFISLGHAKLSLOELTWKNSVRDCAWLRSRPGVCPVPAEHLRBEI 540
 OY 541 LAKFLHLMVSVVILLRFFVYTTTFOKNRLFYFRKSVMSKQSIGIRQHLKRVQRE 600
 DB 541 LAKFLHLMVSVVILLRFFVYTTTFOKNRLFYFRKSVMSKQSIGIRQHLKRVQRE 600
 OY 601 LSEAEVQHQREARPAALLSRILFIPKPDGLRPIVNMVYVGARTFRREKRAERLTSRYKA 660
 DB 601 LSEAEVQHQREARPAALLSRILFIPKPDGLRPIVNMVYVGARTFRREKRAERLTSRYKA 660

661 LFSVLNTERARRPGLLGASVLGLDDIHRARWTFVLVRVRAQDPPPPPELYFVKVDVTGAYDTI 720
 DB 661 LFSVLNTERARRPGLLGASVLGLDDIHRARWTFVLVRVRAQDPPPPPELYFVKVDVTGAYDTI 720
 OY 721 PODRLTEVIASIIKPNQYTCVRRYAVVQAAHGHVVKAFKSHVSTLTDLQPMRQFVAHL 780
 DB 721 PODRLTEVIASIIKPNQYTCVRRYAVVQAAHGHVVKAFKSHVSTLTDLQPMRQFVAHL 780
 OY 781 QETSPLRDVAVTEQSSSINEASSGLFVFLRPMCHHVRIRKSVVQCGIPQGSITLSTL 840
 DB 781 QETSPLRDVAVTEQSSSINEASSGLFVFLRPMCHHVRIRKSVVQCGIPQGSITLSTL 840
 OY 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLTRLVGRVPEYGCWNL 900
 DB 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFL----- 884
 OY 901 RKTVVNPFVEALGGTAFVQMPAHGLFPWCGLLDDTLTLEVSQSYSSVARTSIRASLTFF 960
 DB 885 -----SYARTSIRASLTFF 897
 OY 961 NRGKAGNRMRKLPGLVLRKCHSLFLDLQVNSLOTCTNIYKILLQAYRHACVQLQ 1020
 DB 961 NRGKAGNRMRKLPGLVLRKCHSLFLDLQVNSLOTCTNIYKILLQAYRHACVQLQ 1020
 OY 1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
 DB 958 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1017
 OY 1081 KLTHRVTVYVPLLSLRTAQTQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
 DB 1018 KLTHRVTVYVPLLSLRTAQTQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1069

RESULT 3
 ID TEST CANFA STANDARD; PRT; 1123 AA.
 AC Q6A548;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit).
 GN Name=TERT;
 OC Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15225880; DOI=10.1016/j.gene.2004.03.032;
 RA Nasir L., Gault E., Campbell S., Veeramalai M., Gilbert D.,
 RA McFarlane R., Munro A., Argyle D.J.;
 RT "Isolation and expression of the reverse transcriptase component of
 RT the Canis familiaris telomerase ribonucleoprotein (dogTERT).";
 RL Gene 336:105-113(2004).
 CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
 CC the replication of chromosome termini in most eukaryotes. It
 CC elongates telomeres. It is a reverse transcriptase that adds
 CC simple sequence repeats to chromosome ends by copying a template
 CC sequence within the RNA component of the enzyme.
 CC -!- SUBUNIT: Component of the telomerase ribonucleoprotein complex at
 CC least composed of TEP1, EST1A, POT1 and a telomerase RNA template
 CC component (TER). Interacts with PIN1 (by similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the reverse transcriptase family.
 CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

Qy 61 DARPPAAPSFRQVSCLEKELVARVLQRLCERGAKNVLAFGFAALLDGGARGGPPPEAFTTSVR 120

Qy 61 DARPPAAPSFRQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGGARGGPPPEAFTTSVR 120

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Db 61 DARPPAAPSPROVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
QY 121 SYLNTVNTDALTGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
    |||||
Db 121 SYLNTVNTDALTGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLGCERAWNHISVRAGVPLGLPAPGARRRGGASRSILPLKPRPR 240
    |||||
Db 181 ATQARPPPHASGPRRLGCERAWNHISVRAGVPLGLPAPGARRRGGASRSILPLKPRPR 240
QY 241 GAAPPERTPVQGSWAHPGRTGRGSDRGFCVVSPPARPAEATSLGALSGTRHSHPSVG 300
    |||||
Db 241 GAAPPERTPVQGSWAHPGRTGRGSDRGFCVVSPPARPAEATSLGALSGTRHSHPSVG 300
QY 301 ROHAGPPSTSRPPRPMWTPCPVPVYAEKTHFLYSSGDKQLRPSFLLSLRSLTGARL 360
    |||||
Db 301 ROHAGPPSTSRPPRPMWTPCPVPVYAEKTHFLYSSGDKQLRPSFLLSLRSLTGARL 360
QY 361 VETIFLGSRPMPGTPRRLPRLPQRYQWQMRPLFLELLGNHQAOCPIGVLLKTHCPLRAAVT 420
    |||||
Db 361 VETIFLGSRPMPGTPRRLPRLPQRYQWQMRPLFLELLGNHQAOCPIGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRHSSPMQVYGFVRACLRRLVPPGLMGS 480
    |||||
Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRHSSPMQVYGFVRACLRRLVPPGLMGS 480
QY 481 RHNERFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREBI 540
    |||||
Db 481 RHNERFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREBI 540
QY 541 LAKFLHLMSSVTVVVELLSRFFVTETTFQKNRLFYRKSVWSKLSQSIGIRQHLKRVQURE 600
    |||||
Db 541 LAKFLHLMSSVTVVVELLSRFFVTETTFQKNRLFYRKSVWSKLSQSIGIRQHLKRVQURE 600
QY 601 LSEAEVROHREARPAALLTSRLRPIPKDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
    |||||
Db 601 LSEAEVROHREARPAALLTSRLRPIPKDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
    |||||
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763
    |||||
Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763

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RESULT 5

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Q8NG38 PRELIMINARY; PRT; 795 AA.
AC Q8NG38;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE ABG-deleted variant of telomerase reverse transcriptase.
GN Name=TER1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Hisatomi H., Ohyaashiki K., Ohyaashiki J.H., Nagao K., Kanamaru T.,
RA Hirata H., Hibi N., Tsukada Y.;
RT "Expression profile of a gamma-deletion variant of the human
RT telomerase reverse transcriptase gene.";
RL Neoplasia 5:193-197(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RA Nagao K., Katsumata K., Aizawa Y., Saito N., Hirata H., Sasaki H.,
RA Yamamoto S., Hikiji K., Koia T., Hisatomi H.;

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RT "Differential alternative splicing expressions of telomerase reverse
RT transcriptase in gastrointestinal cell lines.";
RL Oncol. Rep. 11:127-131(2004).
DR EMBL: AB086950; BAC11015.1;
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO: GO:0003721; F:telomeric template RNA reverse transcriptase.; IEA.
DR InterPro: IPR003545; Telomerase_RT.
DR PRINTS: PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 795 AA; 88964 MW; 6BEAC8A6D1A2E8CB CRC64;

Query Match 66.6%; Score 3973; DB 2; Length 795;
Best Local Similarity 98.4%; Pred. No. 2.6e-236;
Matches 751; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

QY 1 MPAPRCRAVNSLLRSHYREVLPATFVRRLLGPOQWRLVQRGDPAAFRALVAQCLVCPW 60
Db 1 MPAPRCRAVNSLLRSHYREVLPATFVRRLLGPOQWRLVQRGDPAAFRALVAQCLVCPW 60
QY 61 DARPPAAPSPROVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
Db 61 DARPPAAPSPROVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
QY 121 SYLNTVNTDALTGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
Db 121 SYLNTVNTDALTGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLGCERAWNHISVRAGVPLGLPAPGARRRGGASRSILPLKPRPR 240
Db 181 ATQARPPPHASGPRRLGCERAWNHISVRAGVPLGLPAPGARRRGGASRSILPLKPRPR 240
QY 241 GAAPPERTPVQGSWAHPGRTGRGSDRGFCVVSPPARPAEATSLGALSGTRHSHPSVG 300
Db 241 GAAPPERTPVQGSWAHPGRTGRGSDRGFCVVSPPARPAEATSLGALSGTRHSHPSVG 300
QY 301 ROHAGPPSTSRPPRPMWTPCPVPVYAEKTHFLYSSGDKQLRPSFLLSLRSLTGARL 360
Db 301 ROHAGPPSTSRPPRPMWTPCPVPVYAEKTHFLYSSGDKQLRPSFLLSLRSLTGARL 360
QY 361 VETIFLGSRPMPGTPRRLPRLPQRYQWQMRPLFLELLGNHQAOCPIGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRPMPGTPRRLPRLPQRYQWQMRPLFLELLGNHQAOCPIGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRHSSPMQVYGFVRACLRRLVPPGLMGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRHSSPMQVYGFVRACLRRLVPPGLMGS 480
QY 481 RHNERFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREBI 540
Db 481 RHNERFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREBI 540
QY 541 LAKFLHLMSSVTVVVELLSRFFVTETTFQKNRLFYRKSVWSKLSQSIGIRQHLKRVQURE 600
Db 541 LAKFLHLMSSVTVVVELLSRFFVTETTFQKNRLFYRKSVWSKLSQSIGIRQHLKRVQURE 600
QY 601 LSEAEVROHREARPAALLTSRLRPIPKDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVROHREARPAALLTSRLRPIPKDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763
Db 721 --DRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 751

RESULT 6
Q9QX24
ID Q9QX24 PRELIMINARY; PRT; 1128 AA.

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AC Q0X24;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Telomerase catalytic subunit.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21240330; PubMed=11342218; DOI=10.1016/S0167-4781(00)00306-7;
RA Guo W., Okamoto M., Lee Y.M., Baluda M.A., Park N.H.;
RT "Enhanced activity of cloned hamster TERT gene promoter in transformed
RT cells.";
RL Biochim. Biophys. Acta 1517:398-409 (2001).
DR EMBL; AF149012; AAF17334.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT.1; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1128 AA; 128393 MW; 1D4F81249012174E CRC64;

Query Match 60.9%; Score 3628; DB 2; Length 1128;
Best Local Similarity 63.3%; Pred. No. 7.4e-215;
Matches 736; Conservative 124; Mismatches 238; Indels 64; Gaps 16;

QY 1 MPRAECRAVRSLLSHREVLPVPLATFVRRILGPGQWRLVQVGDPAAPFALVAQCLVCPW 60
DB 1 MPRAECRAVRSLLSHREVLPVPLATFVRRILGPGQWRLVQVGDPAAPFALVAQCLVCPW 60
QY 61 DARPPPAAPSROVCKELVARVLQRLCERGAKNVLAFFGALLDARGGPEPFAFTTSVR 120
DB 61 DSQPPADLSFHQVSSSLKELVARVQRLCERGERNVLTFFGALLNGAOGGPPWFTTSVR 120
QY 121 SYLPNTVTDALRGSGAWGLLRRVGDVLLVHLARCALFVLVAPSCAYQVCGPPLYLGA 180
DB 121 SYLPNSVTESLRVSGAWMLLRVGDVLLVLLARCALYLLVPPSCAYQVCGSPLYQICA 180
QY 181 ATQARPP- PHASGPRRLG-----CERAWNSVREAGVPLGLPAGCARRRGSASRS 231
DB 181 TAETWPSVSRIRYRTPVGRNPTHLGSTRVNSHQBAWKPPPLPSREAKRSLSTNRS 240
QY 232 LPLPKRRRGAPEPRTPVGQGSWAHPGRTGRGFCVVSAPAR-----PAEBAATSLG 287
DB 241 VPPSKKARCIDLAPLEKGPYRQA-----VPTPSDKTW-VNPAKSHAVISRITK-ED 291
QY 288 ALSGTRGSHSPVGRQ-----HHAGPSTS-RPP-----RPWDTCPVVAETHFLYS 334
DB 292 LSSGVK--APGLSRGSGVCYKHKPSSTLSQSLQCNAPQLRP-----YTETKRFYS 341
QY 335 -SGDKEQLRPSLLSSLSPLTGARELVETITFLGSRPMPGTTPRLPLPORYQWRPLF 393
DB 342 REGGRRLNPSFLNLPNLSLTGAERLVEILFLGMRPRTSGPLCGRRRLSKRYQWRPLF 401
QY 394 LELLGNAHQCPGVLLKTHCPRLAAVTPAAGCAREKPGQSVAAPEEEDTPRLVLQLLR 453
DB 402 QQLLVNHARCPVLLLRSHCRFTAAHQVAGL-----NTTSFQRLMNLRL 447
QY 454 QHSSPWQVYGFVACLRILVPLPGLMGSRHNERFLRNTKFTSLGKHAKLSLQELTWQMS 513
DB 448 LHSSPWQVYGFVACVGLVPLPGLMGSRHNRQRRFPKRVKRTSLGKYDKLSLQELTWQK 507
QY 514 VRDCAWLRRSPGVGCVPAAEHRLREILAKFLHLMSVVVVVLLRSFFVVTETTFQKNRL 573

508 VQDCRWURSSPGNVCNVAEHRTRERILAVFLWMDAYVVELLRSFFVVTETTFQKNRL 567
574 FFYRKSVMSLQSIGIRQHLKRVQLRELSAEVQRHREARPALTSRLRFPKPDGLRPI 633
568 FFYRKSMWRRLQSIGVREHLLERVLQELSQEEVQRQEAAMPAMPICRLRFPKPSGLRPI 627
634 VMDYVVGARTFRREKKAERLTSRVKALFVSLNYERARRPGLIGASVLGDDIHARWTF 693
628 VNMSY-NGTRAFDQKQACHFTQCLKTLFSLNYELTKHTNLLGASVLGDLNIDYRTWTF 686
694 VLRVRAODPPPELYFVKVDVTGAVDTIPQDLRTVEIASIILK-PONTYCVRYAVVQAAH 752
687 VLRVRLDPPAPRVFVKADVTGAYDALPQDKLVEIANMRHPNSYICIQYAVVQDRQ 746
753 GHVRKAFKSHVSTLTDLPYMRQFVAHLQ--ETSPLRDVAVIEOSSLSNEASSGLFDVFL 810
747 GQIHKSFRQVSTLSDLPQPHMQPLKHLQSDTSALRNSVVIEQSLSNEASSSLDFDL 806
811 RFMCHAVIRGKSYVQCQIGIPQGSILSTLCSLCYGDMMENKLPAGIRRGDGLLRLVDDP 870
807 RFVRNSVVKIGRGYVQCQIGIPQGSILSTLCSLCYGDMMENKLPABVQDGLLRFVDDF 866
871 LLVTPHLTHAKTFLRTLVRGVEYGVVNLKRTVVPVEDEALGGTAFVQMPAHGLFPW 930
867 LLVTPHLVQAEAFURLVRGIVEYGMNINLQKTVVNFVDAGTUDGTAPQLPAHCLFPW 926
931 CGLLDTRTILEVQSDYSYARTSIRASLTFRNRFKAGRNMRRLFGVLRLLKCHSLFLDLQ 990
927 CGLLDLTQTLEVLCDYTGARTSIKASLTQRTFKAGRNMRQKLLAVLRLLKCHSLFLDLQ 986
991 VNSLQTVCTNIYKILLQAYRFHACVQLPFPHQVQWKNPTFFFLAVISDTASLCYSILKAK 1050
987 MNSLQTVCTNIYKILLQAYRFHACVQLPFPHQVQWKNPTFFFLAVISDTASLCYSILKAK 1046
1051 NAGSLGAKGAGPLPSEAVQWLCHOAFLKLKLTHTRYVTVPLGLSLTAQTOLSRKLPGT 1110
1047 NAGMTLAKAGASGFPPEAAWLCYQAFLLKLAGHSVYKCLLGPLRTAQLCKLPRA 1106
1111 TLTALEAAANPALPSDFKTILD 1132
1107 TMALETAADPALSTDFTQILD 1128

RESULT 7
Q67316 ID Q673L6 PRELIMINARY; PRT; 1125 AA.
AC Q673L6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Telomerase reverse transcriptase catalytic subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BN;
RA Kaneko R., Hirabayashi T., Yagi T.;
RT "Predominant expression of rTERB, an inactive splicing variant of
RT telomerase reverse transcriptase, in the adult rat brain and heart.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY539717; AAT09124.1; -.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
DR RNA-directed DNA polymerase.
SQ SEQUENCE 1125 AA; 126933 MW; B8B2A11C914372DF CRC64;

Query Match 59.2%; Score 3529.5; DB 2; Length 1125;
Best Local Similarity 62.3%; Pred. No. 8.6e-209;
Matches 722; Conservative 115; Mismatches 262; Indels 59; Gaps 12;
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QY 1055 SLGAKGAGPLPSEAVOMLCHQAFLLKLTTRHRTVTVPLLSRLTAQTSRLKPLPGLTTTLTA 1114
 Db 1048 SLRAGKPGSPPEATRWLCYQAFLLKLAHSTVYKCLLGLPLRTAQKQKCRKLPEATWTL 1107
 QY 1115 LEAANPALPSPDFKTLTD 1132
 Db 1108 LKTAADPALSTDFQTLTD 1125

RESULT 8
 Q673L5 PRELIMINARY; PRT; 1119 AA.
 AC Q673L5;
 DT 25-OCT-2004 (TremBLrel. 28, Created)
 DT 25-OCT-2004 (TremBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TremBLrel. 28, Last annotation update)
 DE Telomerase reverse transcriptase catalytic subunit splice variant
 DE a.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BN;
 RA Kaneko R., Hirabayashi T., Yagi T.;
 RT "Predominant expression of rTERB, an inactive splicing variant of
 RT telomerase reverse transcriptase, in the adult rat brain and heart.";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY539718; AAT09125.1; -
 DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR InterPro; IPR003545; Telomerase_RT.
 DR PRINTS; PR01365; TELOMERASRT.
 DR KWRNA-directed DNA polymerase.
 SQ SEQUENCE 1119 AA; 126224 MM; 4CABB74D64E3F972 CRC64;

Query Match 59.0%; Score 3514.5; DB 2; Length 1119;
 Best Local Similarity 62.3%; Pred. No. 7.2e-208;
 Matches 721; Conservative 115; Mismatches 257; Indels 65; Gaps 13;

QY 1 MPRAPRCRAVSLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCPW 60
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 Db 61 DARPPAAPSPFQVSCLEKELVARLQRCERGAKNVLAFFGALLDGAAGGPPPEATTSTVR 120
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 Db 61 GSQPPADLSFHQVSLKELVSRVQKLCERGERNVLAFFGALLDGAAGGPPPEATTSTVR 120
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 Db 121 SYLPTNTVDALRGSGAWGLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
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 Db 121 SYLPTNSVTESLCVSGAWMLLSRVGDDLLVLLSHCALYLLVPPSCAYQVCGPPLYQICA 180
 QY 181 ATQA-----RPPPHASGPRRLIG-CERAWNHSVREAGVPLGLPAPGARRGSGAS 231
 Db 181 TTDWSSVPAAGVPRTPVCGNFTNLGSAHQIKNSHQEAPKQALPSPGRTKLLSILTSTN 240
 QY 232 LPLKPRPRGAAPERTPVCGGWAHPCRTGSDRGFCVVP-ARPAEATSLEG--- 287
 Db 232 LPLKPRPRGAAPERTPVCGGWAHPCRTGSDRGFCVVP-ARPAEATSLEG--- 287
 QY 241 VPSAKKARFEPALRVDKGPHRQVVPPTSGKTWAPSP-----AASPVPAAKNLSLKGKAS 296
 Db 241 VPSAKKARFEPALRVDKGPHRQVVPPTSGKTWAPSP-----AASPVPAAKNLSLKGKAS 296
 QY 288 --ALSGTRHSHPSVGRQHH-----AGPSTSRPRPMDTPCPVYAEKHLFLYS-SGD 337
 Db 288 --ALSGTRHSHPSVGRQHH-----AGPSTSRPRPMDTPCPVYAEKHLFLYS-SGD 337
 QY 297 DPLSLG-----SVCKKHKPSSSLLSPPODAEKLRP-----FTETRHFLYSRGCG 342
 Db 297 DPLSLG-----SVCKKHKPSSSLLSPPODAEKLRP-----FTETRHFLYSRGCG 342
 QY 338 KEQLRPSFLLSLRPSLTGARRLVETIFLGSRPMPGTPRRLPRLPQRYQWQMRPLFLELL 397
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 QY 343 QEELNPSFLLNSLPSLTGARRLVETIFLGSRPMPGTPRRLPRLPQRYQWQMRPLFLELL 402
 Db 343 QEELNPSFLLNSLPSLTGARRLVETIFLGSRPMPGTPRRLPRLPQRYQWQMRPLFLELL 402
 QY 398 GNHAQCPGYVLKTHCPKRAAVTPAAGVCAREKPGSGVAABEEDTDPRRLVQLLRQSHS 457
 Db 398 GNHAQCPGYVLKTHCPKRAAVTPAAGVCAREKPGSGVAABEEDTDPRRLVQLLRQSHS 457
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 Db 398 GNHAQCPGYVLKTHCPKRAAVTPAAGVCAREKPGSGVAABEEDTDPRRLVQLLRQSHS 457
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Db 448 PQWYGFURACURELUPAGLWTRINERRFLKQVKKFISLQYAKLSQELMRWVQEDC 507
QY 518 AWRSSPGVGCVPAAAEHLRLREILAKFLHMLSVVVVLLRSFFVYTTTQKRLFFYR 577
Db 508 HWRSSPEKQTVPAAEHLRLREILAKFLHMLSVVVVLLRSFFVYTTTQKRLFFYR 567
QY 578 KSVWSKLOSIGIRHQLKRVQLRELSAEVROHREARPALLSRLRFPKPGDGLRPIVMD 637
Db 568 KSVWSKLOSIGIRHQLKRVQLRELSAEVROHREARPALLSRLRFPKPGDGLRPIVMD 627
QY 638 YVVGARTFRERREKRAERLTSRVKALPSVNLVNERARRPGLGASVLGLDDIHRARFTFLVR 697
Db 628 YGMDTRAFGKKQS-----UKLFSVNLVNERARRPGLGASVLGLDDIHRARFTFLVR 681
QY 698 RAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASII-KPQNTYCVRRYAVVQKAAHGHR 756
Db 682 RALDQTPRMVFKADVTGAYDAIPQDKLVEIVANIIRSESMYCIQYAVVQKDSQGQVH 741
QY 757 KAFKSHVSTLTLQPMYQFVAHQET--SPURDAVWTEQSSSLNEASGLFDVFLRPMC 814
Db 742 KSFRRQVSTSLDQPMYQFVAHQET--SPURDAVWTEQSSSLNEASGLFDVFLRPMC 801
QY 815 HHAVERIGKSVYQCGIIPQGSSTLTLCLSCYGDMMENKLFAGIRDDGLLRLVDDFLVLT 874
Db 802 HSVKIDGRFYVQCGIIPQGSSTLTLCLSCYGDMMENKLFAGIRDDGLLRLVDDFLVLT 861
QY 875 PHLTHAKTFLRLTVRGVPEYGCNVNLRKTVNVPFVEDEALGATFVQMPAHGLFPWCGLL 934
Db 862 PHLAHAKAFLSLTVHGVPEYGCNVNLRKTVNVPFVEDEALGATFVQMPAHGLFPWCGLL 921
QY 935 LDTRTLVEQSDSVYVARTSIRASLTFRNGFKAGNRNRKLGVLRLKCHSLFLDLQVNSL 994
Db 922 LDTRTLVEQSDSVYVARTSIRASLTFRNGFKAGNRNRKLGVLRLKCHSLFLDLQVNSL 981
QY 995 QTVCTNVIKILLQAYRFHACVQLQPFHQYVWKNPTFPLRFLVSTFASLCYSLTKAKNAGM 1054
Db 982 QTVCTNVIKILLQAYRFHACVQLQPFHQYVWKNPTFPLRFLVSTFASLCYSLTKAKNAGM 1041
QY 1055 SIGAKGAAGPLPSEAVOMLCHQAFLLKLTLRHRTVYVPLLSGLRTAQTLSRLKPLFTTLTA 1114
Db 1042 SLRAGKAGFSPPEATRWLCYQAFLLKLAHSTVYKLLGLPLRTAQKQLCRKLPEATWTL 1101
QY 1115 LEAANPALPSPDKTILD 1132
Db 1102 LKTAADPALSTDFQILD 1119

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RESULT 9

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TERT_MOUSE
ID TERT_MOUSE STANDARD; PRT; 1122 AA.
AC 070372; O35432;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit).
DE subunit).
GN Name=Tert;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98241176; PubMed=95802020; DOI=10.1038/sj.onc.1201933;
RA Greenberg R.A., Allsopp R.C., Chin L., Morin G.B., DePinho R.A.;
RT "Expression of mouse telomerase reverse transcriptase during development, differentiation and proliferation."
RL Oncogene 16:1723-1730(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98393668; PubMed=9724727; DOI=10.1073/pnas.95.18.10471;
RA Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;

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RT "Expression of mouse telomerase catalytic subunit in embryos and adult tissues.";
RN Proc. Natl. Acad. Sci. U.S.A. 95:10471-10476(1998).
(3)
SEQUENCE OF 550-616 FROM N.A.
RA Drissi R., Cleveland J.L.;
RT "Partial sequence of Mus musculus telomerase catalytic subunit homolog.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for the replication of chromosome termini in most eukaryotes. It elongates telomeres. It is a reverse transcriptase that adds simple sequence repeats to chromosome ends by copying a template sequence within the RNA component of the enzyme.
CC -!- SUBUNIT: Component of the telomerase ribonucleoprotein complex at least composed of TEP1, EST1A, POT1 and a telomerase RNA template component (TER). Interacts with PINK1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the reverse transcriptase family. Telomerase subfamily.
CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
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EMBL; AF051911; AAC09323.1; -
EMBL; AF073311; AAC34821.1; -
EMBL; AF029235; AAB84200.1; -
MGD; MGI:1202709; Tert.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT; 1
DR PRINTS; PR01365; TELOMERASERT.
DR PROSITE; PS50878; RT_POL; 1.
KW DNA-binding; Nuclear protein; Ribonucleoprotein;
KW RNA-directed DNA polymerase; Telomere; Transiferase.
FT DOMAIN 595 928 Reverse transcriptase.
FT CONFLICT 553 553 I -> V (in Ref. 3).
SQ SEQUENCE 1122 AA; 127977 MW; F85266905DD6558C CRC64;
Query Match 58.8%; Score 3505; DB 1; Length 1122;
Best Local Similarity 62.4%; Pred. No. 2.8e-207;
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;

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QY 1 MPAPRCRAVRSLRLSHYREVLPATFVRLRGLPGWRLVQGRDPAAPRALVAOCLVCPW 60
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QY 61 DAREPPAAPGFRQVSLKELVARLQRLCERGAKNVLAFFGALLDARGGPPFAFTTSVR 120
Db 61 GSQPPADLGFHQVSSKELVARVQRLCERNERNVLAFFGALLDARGGPPFAFTTSVR 120
QY 121 SYLENTVTDALRGSGAWGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQGA 180
Db 121 SYLENTVTETLRVSGAWMLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQGA 180
QY 181 ATQARPPPHAS-GPRRLG-----CERAWNHVREAGVPLGLPAGCARRRGGSAGRS 231
Db 181 TTDTPWSVSAVSYRTPFVGRNFTNLRFLQIKSSRQEAPEKPLALPSRGTGKHLSTSTS 240
QY 232 LPLPKRPRGAAPERTPVQGSWAHPGRTRGSDRGFCVVSAPAR-----PAEATSLE 286
Db 241 VPSAKKARCVPVPRVEGP-----HRQVLPTSGKSW-VPSPARSEVTAEDKLSK 292
QY 287 GALSGRHSHPSVGRQHAGPSTSRPRPMDTFCPPVYAEKFLYSSGD-KGOLRPSF 345
Db 293 GKVDLSLS-GSVCKHKPSSTLSLLSPRQNAFLRP-FIETRFYLSRGDQERLNPFS 350

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Db 573 KQISGVRGHLKRVOLRELSAEVQHRERAPALLTSRLRFTPKDGLRPIVMNDYVGA 632
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Db 693 TPMTFVKAADVTCAYDAIPQKLVVAVNMIRHSESTYCIROYAVVRDSQGVHKSFR 752
QY 762 HVTSLTDLPYMRQFVAHLOET--SPLRDVAVIEQSSSINEASSGLFDVFLRFMCHAVR 819
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QY 820 IRGKSYVOCQIPQGSISLTLCSLCYGDMEKLPAGIRRDGLLRLVDDFLVTPHLTH 879
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Db 873 AKTFRLTVRGVPYGCVVNLRKTVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRT 932
QY 940 LEVQSDYSYARTSIRASITFNRGKAGNMRKLPGLVLRKCHSLFDLQVNSLOTVCT 999
Db 933 LEVFCDSYGYAQTISLTSFOSVFKAGTKMKNLLSVLRKCHSLFDLQVNSLOTVCT 992
QY 1000 NIYKILLQAYRFHACVLPQHQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGA 1059
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QY 1120 NPALPSDFKTLID 1132
Db 1110 DPALSTDFQTLID 1122

RESULT 10
QY 99B6 PRELIMINARY; PRT; 524 AA.
AC Q99B6;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Telomerase reverse transcriptase (fragment).
GN Name=TERT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=99144726; PubMed=10022128; DOI=10.1038/sj.onc.1202669;
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```
RA Greenberg R.A., O'Hagan R.C., Deng H., Xiao Q., Hann S.R., Adams R.R.,
RA Lichtsteiner S., Chin L., Morin G.B., Depinho R.A.;
RT "Telomerase reverse transcriptase gene is a direct target of c-Myc but
RT is not functionally equivalent in cellular transformation.";
RN Oncogene 18:1219-1226 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99140777; PubMed=9988278; DOI=10.1038/6010;
RA Wu K.J., Grandori C., Anacker M., Simon-Vermot N., Polack A.,
RA Lingner J., Dalla-Favera R.;
RT "Direct activation of TERT transcription by c-MYC.";
RN Nat. Genet. 21:220-224 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Ducrest A.-L., Anacker M., Reichenbach P., Nabholz M., Lingner J.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Szutorisz H., Palmquist R., Roos G., Stenling R., Schorderet D.,
RA Reddel R., Lingner J., Nabholz M.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF121948; AAD24464.1; -
DR EMBL: AF114847; AAD17210.1; -
DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON TER 524
SQ SEQUENCE 524 AA; 57932 MW; 5F47DEFD01832B1B CRC64;

Query Match 47.4%; Score 2825; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 8.4e-166;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPPLATFVRRLGPGQWRVLRQGDPAAPRALVAQCLVCPW 60
Db 1 MPAPRCRAVRSLLRSHYREVLPPLATFVRRLGPGQWRVLRQGDPAAPRALVAQCLVCPW 60
QY 61 DARPPAAPSPRQVSCSLKELVARVLRQRCERGAKNVLAFFGALLDGAAGGPPFAFTTSVR 120
Db 61 DARPPAAPSPRQVSCSLKELVARVLRQRCERGAKNVLAFFGALLDGAAGGPPFAFTTSVR 120
QY 121 SYLNTVTDALRGSGANGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLNTVTDALRGSGANGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASPPRRRLCERAWNHSVREAGVPLGLPAPGARRRGSSASRLPLKRRPR 240
Db 181 ATQARPPPHASPPRRRLCERAWNHSVREAGVPLGLPAPGARRRGSSASRLPLKRRPR 240
QY 241 GAAPEPERTVPGQSWAHPTGTRGSDRGFCVSPARPAEATSLEGALSGTRHSHPSVG 300
Db 241 GAAPEPERTVPGQSWAHPTGTRGSDRGFCVSPARPAEATSLEGALSGTRHSHPSVG 300
QY 301 RQHAGPSTSRPRPMDTPCPVVAETKHFYLSGDKQLRPSFLLSRLPSLTGARRL 360
Db 301 RQHAGPSTSRPRPMDTPCPVVAETKHFYLSGDKQLRPSFLLSRLPSLTGARRL 360
QY 361 VETIFLGSRRPMPGTRELPRLPORYQWMPRLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRRPMPGTRELPRLPORYQWMPRLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSVAPAEEDTDPRLVOLLRHSSPWQYVGFVRACLRRLVPPGLMGS 480
Db 421 PAAGVCAREKPGQSVAPAEEDTDPRLVOLLRHSSPWQYVGFVRACLRRLVPPGLMGS 480
QY 481 RHNERFLRNTKFKISLGKHAQLSLQELTWKQSVRDCAWLRSP 524
Db 481 RHNERFLRNTKFKISLGKHAQLSLQELTWKQSVRDCAWLRSP 524

RESULT 11
QY 96RD80
ID Q6RD80
AC Q6RD80;
PRELIMINARY; PRT; 1346 AA.
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RL Gene 277:101-110(2001).
DR EMBL; AF212299; AAG43537.1; --
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF000078; RVT_1_2.
DR PRINTS; PRO1365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferrase.
SQ SEQUENCE 1191 AA; 138016 MW; 9BD9D776869A57D6 CRC64;

Query Match 38.9%; Score 2316.5; DB 2; Length 1191;
Best Local Similarity 42.4%; Pred. No. 5.1e-134;
Matches 518; Conservative 201; Mismatches 381; Indels 123; Gaps 25;

QY 1 MPAPRCRAVRSLRSHYREVLPATFVRRLG-POGWR--LVQRGDPAAFALVAOCILVC 57
DB 1 MPLRTGGATLILQRLVQGLVIEYDTLQVPGIKVPVLLEGDSEKFRSFAELVVC 60
QY 58 VPMWARPAPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEFTT 117
DB 61 IPRGKTPLPSPVFLQSTQREVVARVQRIKCEKKKNVLAFGYGLVD-EKNSLNIRLTP 119
QY 118 SVRSYLPNTVTDALRGSGAWGLLRRVGGDVVHLLARCALFVLVAPSCAYQVCPPLY- 176
DB 120 NICNYFPNPTTTISTILWETLLTRVGDVVMYWLQCSIFVFVPPRCYQITQPIYT 179
QY 177 -----QLGAATQAR-----PPPHASGPRRLCGERAWNHVRE 209
DB 180 LPSDDVFLFQSFQSTQSNVLLRYIKRVFHLKYLKPKHMTSRM-----LTWRNKP 234
QY 210 AGVPLGLPAGARRGGASRSL-----PLPKPRRGAAP-----PERTVQGG 254
DB 235 SGLLRSKTSMAVTEIHSKRKJCSKDICIPIPKRRNDLKDVTVDHFDLPMCRSVYL 294
QY 255 SWAHPGR-----TRG-PSDRGFCVSPAPAEATSELEGALSGRH----- 294
DB 295 SNMYPKTNVQVTLTSGYKTKTQCPQKPSCEQKTTAFYSVAGDCNLSLKNVNKLI 354
QY 295 SHPSVGRQHAGPPTSPRPWDPCPPVVAETKHELY-SSGDKEQLRPFLSLSLRPS 353
DB 355 TNASV-----PTAQR-----LPSNIFIDFQRTLYLSYKKGFSEFILNLSOST 401
QY 354 LTGARLVETIFLGS-----RPWMPGTPRRLPRLPQRYQWMPRLFLELIGNHAQCPY 405
DB 402 PSGSKLVETIFLSNLAEQNFDPKRDENCRY--KLPKRYWKMPHQELIQNHKKFPY 459
QY 406 GVLLKTHCPRAAVTPAAGVCAREKPOGSVAAPBED-----TDPRLVQLLRQHS 457
DB 460 LVYLNKHCPRSSM-----ACSEKR---SLQKNRIENDGKQLKHTTKANLLSLKQHS 511
QY 458 PMOVYGFVRACLRRLVPPCLAGSRNRRFLNTKFFISL-CXKAKLSLOELTWMSYRD 516
DB 512 IQWVYMFRECLNNVVPDMMGSSNKKRFFRNKVSFLFFSGFKFKISLSELMWSMRVED 571
QY 517 CAWLRSRPGVGVPAAEHRLREILAKFLHMLMSVVVVELLRSFFVYTTTFQKNLFFY 576
DB 572 CSWIBLQSDHVPASEHLLREKILAKFVFWLMDTVYVQLLSFFVYTTTFQKNLFFY 631
QY 577 KXSVNKLQSIGIRQHLRVQLRELSAEVROHREARPALLTSRLRFPKPDGLAPIVM 636
DB 632 KXSVNKLQNLGRKHLKLVKLSLSSLENNQKQNVPLSVRLRFPKTNGLRPISKI 691
QY 637 DYVVGARTFR--REKRAELTSRVVALFSLVNYERARRPGLLGASVGLDDIHRARFTV 694
DB 692 SSTLSQSQSKENQEKIHHFSQIRNLFSLVNYERNRNCSTLGSSVFGMDDIYKKKCFV 751
QY 695 LRV-RAQPPPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKP--QNTYCVRRYAVVQKAA 751

DB 752 LDFEKPQVEKQLQFYFVKTDVKGAYDTIPHSKLDDEVISKVINPANEVYCIIRYATVSDP 811
QY 752 GHVVRKAPKSHVSTLTDLQPYMROFVAHLOETSPLRDAVAVLEQSSSLNEASSGLPDLR 811
DB 812 TGRRIKSPFRHVELADVLPNNKQFVSQQEKLLRLNTILVEONLLNESSVKLLAVFQQ 871
QY 812 FMCHEAVRIRKSYVQCGIPQSGSILSTLLCSLCYGDMMENKLFAGIRRDGLLRVDDFL 871
DB 872 IIRSHILRIKORYMCCGIPQSGSMLSTILCSLCYGDMMENAMLGGIQKNGVLMRLDDFL 931
QY 872 LVTPHLTHAKTFLRTLVRGVEYGCVMNLRTVNVFPVED--EALGGTAFVOMPAGHLP 929
DB 932 LVTPHLDOAKTFLRTLAEIGIPQYGSISPKQTVNVFPVDDIPEC---SEVEQLPSCHLFR 988
QY 930 WCGLLDTRTLEVDQSYSSYARTSTRASLTNRGFKAGRNMRKLFGLVLRKCHSLFLDL 989
DB 989 WCGLLDTRTLDVVDYSSYACTSIRSWTFCSSAAGKYMKKQKIRVLRKCHSLFLDL 1048
QY 990 QVNSLQTVCTNIYKILIQAYRFHACVQLQLPFHQQVKNKPTFFLRVISTDTSALCYSLKA 1049
DB 1049 KVNLSRTVCINTYKIFLLQAYRFHACVQLQFPFGQVNMNPPFELTVISDMAPCFYTFKA 1108
QY 1050 KNAGWSLGAAGAAGPLSEAVOMLCHOAFLKLTRHRYVYVPLGLSLRTAQTQSRKLP 1109
DB 1109 KNKDLTRGYKDVSCQFNPEAVQWLSYQAFLTCLHNNKLVLYKCLIGPLQCKMQLSRRLSQ 1168
QY 1110 TTLTALEAANPALPSPDKTILD 1132
DB 1169 DTIELLSVTDSSLHKDFSCIMD 1191

RESULT 13
Q94807 PRELIMINARY; PRT; 523 AA.
ID O94807
AC O94807
DT 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE Telomerase transcriptase (Fragment).
GN Name=hTERT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99137484; PubMed=9973199;
RA Takakura M., Kyo S., Kanaya T., Hirano H., Takeda J., Yutsudo M.,
RA Inoue M.;
RT "Cloning of human telomerase catalytic subunit (hTERT) gene promoter
RT and identification of proximal core promoter sequences essential for
RT transcriptional activation in immortalized and cancer cells.";
RL Cancer Res. 59:551-557(1999).
DR EMBL; AB016767; BAA74724.1; --
FT NON TER 523
FT SEQUENCE 523 AA; 56555 MW; 8FDE562DDECC93DA CRC64;

Query Match 37.0%; Score 2207.5; DB 2; Length 523;
Best Local Similarity 78.7%; Pred. No. 9.4e-128;
Matches 435; Conservative 3; Mismatches 56; Indels 59; Gaps 6;

QY 1 MPAPRCRAVRSLRSHYREVLPATFVRRLGPOGWRVLRQGDPAAFALVAOCILVCVPW 60
DB 1 MPAPRCRAVRSLRSHYREVLPATFVRRLGPOGWRVLRQGDPAAFALVAOCILVCVPW 60
QY 61 DARPPAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEFTTSVR 120
DB 61 DARPPAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEFTTSVR 120
QY 121 SYLPTNTVTDALRGSGAWGLLRRVGGDVVHLLARCALFVLVAPSCAYQVCPPLYQLGA 180
DB 121 SYLPTNTVTDALRGSGAWGLLRRVGGDVVHLLARCALFVLVAPSCAYQVCPPLYQLGA 180

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QY 181 ATQARPPPHASGPRRLGCERAWNHVSREAGVPLGLPAGARRRGGGSASRLPLPKRPRR 240
Db 181 ATQARPPPHASGPRRLGCERAWNHVSREAGVPLGLPAGARRRGGGSASRLPLPKRPRR 240
QY 241 GAAPPERTPVCGQSWAHPGTRGSDRGFCVSPARPAEATSLLEGALSCTRSHSPSVG 300
Db 241 GAAPPERTPVCGQSWAHPGTRGSDRGFCVSPARPAEATSLLEGALSCTRSHSPSVG 300
QY 301 RQHAGPPSTRPPRPMDTPCPVYAKTHFLYSSGDKQEQLRPSFLSSLRPSLTGARRL 360
Db 301 RQHAGPPSTRPPRPMDTPCPVYAKTHFLYSSGDKQEQLRPSFLSSLRPSLTGARRL 360
QY 361 VETIFLGRPMWGPTRRLPLRPLQRYWQMRPLFLELLGNHACQPGVLLKTHCPRAAVT 420
Db 361 VETIFLGRSPGCGQLPAGCAPSPATGCGPCFWSCLGTTRSAPTG-----CSSRR TAR 414
QY 421 PAAGVCAREKQGSVAAPPEEDTPRRVLQLLRQHSSPQVYGFVRACLRRLVPPGLW-- 478
Db 415 -----CEURSPQPVSVP---GRSPRAL-----W-----RPPRRRTQTPVAVCS 450
QY 479 -----GSRHNERRFLRNTKFFISLGHAKLSLQELTWK 511
Db 451 CSASTAPLAGVRLRAGLPAPAGAPRPLGLQARRRFLRNTKFFISLGHAKLSLQELTWK 510
QY 512 MSVRDCAWLRSP 524
Db 511 MSVRDCAWLRSP 523
RESULT 14
ID Q9JK99 PRELIMINARY; PRT; 575 AA.
AC Q9JK99;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Telomerase catalytic subunit (fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22860253; PubMed=13679242; DOI=10.1016/S0024-3205(03)00670-2;
RA Wong S.C., Ong L.L., Er C.P., Gao S., Yu H., So J.B.;
RT "Cloning of rat telomerase catalytic subunit functional domains,
RT reconstitution of telomerase activity and enzymatic profile of pig and
RT chicken tissues.";
RL Life Sci. 73:2749-2760(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Wong S., Gao S., Xu X., Yu H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF247818; AAF62177.1; -.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO: GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR GO: GO:0016740; F:transferrase activity; IEA.
DR GO: GO:0006278; F:RNA-dependent DNA replication; IEA.
DR InterPro: IPR000477; RVFase.
DR Pfam: PF00078; RVT_1;
DR PRINTS: PR01365; TELOMERASRT.
KW RNA-directed DNA polymerase; transferase.
FT NON_TER 1
SQ SEQUENCE 575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;
```

Query Match 33.8%; Score 2016; DB 2; Length 575;
Best Local Similarity 67.6%; Pred. No. 6, 7e-116;
Matches 391; Conservative 71; Mismatches 110; Indels 6; Gaps 3;

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QY 558 RSFPYVTTTQKNRLFFYRKSVMSKLSQSIGIRHOLKRVQLRELSEAVRQHRARPALL 617
Db 1 RSFPYITESTFQKNRLFFYRKSVMSKLSQSIGVRQHLERVLRELSEBVRHQDTWLAMP 60
QY 618 TSLRFLPKDGLRPIVNMBYVVCARTFRREKRAERLTSRKALFSLVLYEARARPGLLG 677
Db 61 ICRURFLPKNGRLRPIVNMYSYMGTRALGRKKQAHFTQRLKTLFSLMLNRYRTKHPHLMG 120
QY 678 ASVLGLDDIIRAWTFVRLVRAQDPPPELFPVKVDVTGAYDTIPQDRLTEVIASIK-PQ 736
Db 121 SSVLGMDIYRTWRFAVLVRALDQTRMFYFKADVTGAYDAI PQGLVEVVAWNRHSE 180
QY 737 NTYCVRYAVVQKAAHGHVKAFAKSHVSTLTDLQPYMRQFVAHQET--SPLRDAVIEQ 794
Db 181 STYCIQYAVVRDSQGVHKSFRQVTTLSDLQPYMGQFLKHLQDSASALRNSVIEQ 240
QY 795 SSSLINEASSGLFDVFLPFMCHAVIRGKSVVQCGIPQGSILSTLLCSLCYGDMEKLF 854
Db 241 SISNMSSSLDFDLFLRHSVVKIGDRCYTQCGIPQGSLSSTLLCSLCYGDMEKLF 300
QY 855 AGIRRDGLLRLLVDDFLVTPHILTHAKTFLRTLVRGVPYGCVVNLKRTVNVFVDEAL 914
Db 301 AEVQRDGLLRLLVDDFLVTPHILTHAKTFLRTLVRGVPYGCVVNLKRTVNVFVDEAL 360
QY 915 GGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRASLTFRNGFKAGNRMRKL 974
Db 361 GGAAPYQLPAHCLFPWCGLLLDTRTLEVSQSDYSYARTSIRASLTFRNGFKAGNRMRKL 420
QY 975 FGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLOLPHQOVWKNPTPELR 1034
Db 421 LSVLRKCHGLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLOLPHQOVWKNPTPELR 480
QY 1035 VISDTASLCYSILKAKNAGSLGAKGAGPLPSSEAVQWLCHQAFLLKTLHRVTVVPLLG 1094
Db 481 IISQASCCYALLKVKPGMTLKASGS--FPPAAHMLCYQAFLLKLAHSLVYKCLLG 537
QY 1095 SLRTAQTLRSKPLPGTTLTALEAAANPALPSDFKTIID 1132
Db 538 PLRTAQKLLCKLPEATMTILKAAADPALSTDFOTILD 575
RESULT 15
Q673L3
ID Q673L3 PRELIMINARY; PRT; 615 AA.
AC Q673L3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Telomerase reverse transcriptase catalytic subunit splice variant c
DE (Telomerase reverse transcriptase catalytic subunit splice variant
DE b).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BN;
RA Kaneko R., Hirabayashi T., Yagi T.;
RT "Predominant expression of rTERtb, an inactive splicing variant of
RT telomerase reverse transcriptase, in the adult rat brain and heart.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY539720; AAT09127.1; -.
DR EMBL: AY539719; AAT09126.1; -.
DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR RNA-directed DNA polymerase.
SQ SEQUENCE 615 AA; 68614 MW; 2892840D86620B63 CRC64;
```

Query Match 23.6%; Score 1408; DB 2; Length 615;
Best Local Similarity 55.8%; Pred. No. 2, 1e-78;
Matches 305; Conservative 51; Mismatches 135; Indels 56; Gaps 10;

DR	Pfam: PF00078; RVT_1; 1.
DR	PRINTS; PRO1365; TELOMERASERT.
DR	PROSITE; PS00284; SERPIN; UNKNOWN 1.
KW	RNA-directed DNA polymerase; Transferrase.
SQ	SEQUENCE 1123 AA, 130551 MW, 44248295817B7F6 CRC64;
	Query Match 12.2%; Score 724.5; DB 2; Length 1123;
	Best Local Similarity 23.9%; Pred. No. 6e-36;
	Matches 294; Conservative 192; Mismatches 506; Indels 237; Gaps 39;
QY	1 MPRAPRCRAVRSLLRSHRYEVLPLATFV-----RRLGPGQGR-----L 38
DB	1 MPRKPRHVRPEILLWRFGNARNLDALVDLI PNRTIQPEQCRCRGCGCLGSSDKPAFL 60
QY	39 VQRGDPAAFALVAQCLVCVPWDARPPAPSPFQVSLCKELVARVLQRL----CERGANQ 95
DB	61 LRSDDPITHYRKLLHRCFV-VLHEQTPLLDFPTSMWSQSREIVERIETIMQSGD--CQN 117
QY	96 VLAFGFALLDGARGCPPEAFTTSVRSYLPTNTDALRSGAGWGLLRVGDDVLVHLLAR 155
DB	118 VICARYDKYQS-----SPILELT-SGSWEFLLRKHGHVDMVYLQQ 159
QY	156 CALFVLVAPSCAVQVCCPPLYQLGAAT-----QARPPPASHGPRRLGCERAWNHVSRE 209
DB	160 TSIFPLLLGKKHQOVSGPPLCIKHRTLSSHENKRKRDNDVQPPTKRWLSSAVDDCPKD 219
QY	210 AGYPILGIIPAG---ARRRGSSASRSLPKRPRGA-----APEPTPVQGQSWA 257
DB	220 DSATI-TPIVGEDVDQHREKTTTKRSRIYLKRRRKQRKNPKVKDCNAFCITP----- 271
QY	258 HPQTRGPSDRGFCVGPSPAPAEATSLEGALSGTSHSPSVGRQHAGPSTSRPPRPW 317
DB	272 ---STNGKVSTG-----NDEMNLHIGINGSLTDFVKQAQ----- 303
QY	318 DTPCPPVYAEKHPLYS-SGDKEQLRPSFLLSRLPSLTGARRLVFETIFLGSRRWMPCGP 376
DB	304 -----VKRNKNFKFGLSETSYVIPNNHLKTLPNCDSKLMMNHFGEVNVWMTPTS 356
QY	377 RLPLRLPQ---RYWOMRPLFLELGNHAQCPYGVLLKTHCP-----LRAAVTPAAG 424
DB	357 HGKNCPSGISCLYHSLLSKNLGIKTKSHLKMLLDKHCVPULLQEDALKSGTTQSS 416
QY	425 VCAREK-----PQGSVAA-----PEBEDTDPRRLVOLLRQHSPPWQYGFVRACLRLVPPG 476
DB	417 --RQKADKLPHGSSSQTGKPKCPSVEERKL-----YCTNDQVSWFIWAICRYIVPES 468
QY	477 LWSRHNERFRRLNTKTFISLGHAKLSLQELTWKMSVRDCAWLRSPGVCVPAAEHRL 536
DB	469 LLGTTHQMRVLRKMIAFWFSRRNRNEKTVQFLHKVPDSPFPFARKE--LCVMVNGHEL 526
QY	537 REE-----ILAKFLHWLMSVVYVBLLRSFFYVTTTFPOKNRLFFYRKSWSWKLOSIG 588
DB	527 QSESIRSTQMCLCTKWISLWLFLEIVKLVHPNFVATESQGGRLNIYYVRKRSWERLISKE 586
QY	589 IRCHLKEVOLRELSAEVROHREARPALLTSRLRFIPKPDGLRIVNMDDYVVGARTFRE 648
DB	587 ISKALDGYLVLDAAESSRKK-----LSKFRLFKAAGRVRWLID-----FSSS 630
QY	649 KRAERLTSRKVALFSLVNYERARRPGLIGAIVGLDDITHRAWRTFVLRVRAQDPP-PELY 707
DB	631 SRQSGL---RDTHAVLKDQLKEPDLVGSVFDHDDFYRNLCPYLHLRASQSELPLY 686
QY	708 FVKVDVTGAVDTIPQDRLTEVIASIIPKQNTYCVRRYAVVOKAAHG-----VRKAFKS 761
DB	687 FVVADVFEKFDSDVQGGKLLHVIOFLKDE--YILNRCLVCCGKRSNWNVNKILVSSQKNS 744
QY	762 HVSTLTDLQPMRQFVAHOETSPLRDAVITEQSSSLNEASSGLDFVFLRFMRMCHAVRIR 821
DB	745 NFRSFTSTVPYA----LQ-----SIUVDKGENHVRKKOLMWIGNMKNNMLQLD 792
QY	822 GKSYVQCQGIPOGSIILTSLCLSCYGMENKLFAGI-----RRDGL----- 862
DB	793 KSIFYVQIAGIQOGRHLSLLCCFYFHGLERTLIIYPFLEEASKOVSSKECSREEELIPTS 852

QY	863	--LLRLVDPELLVTPHLTHAKFTLRTLVGVPEYGCVMRLKTVNFPVEDE-----	912
Db	853	YKLLREIDYLFVSTSRDQASSFYHLKRGFKDYNCFMNETKFCINFEDKEBHRCSNRM	912
QY	913	--ALGCTAFVQMPAHGLFPWCGLLLDTRLEVQSDYSSYARTSIRASLTFNRRGFKAGRNM	970
Db	913	FVGDNGVPFVR-----WTGLLINSRTFEVQVDVTRYLSGHISSTFSVAMQNKPVRL	964
QY	971	RRKLGVLRLKCHSLFELDLQVNSLQTVCTNIYKILLQAYRFHACVLQLPFHQQVMK-NP	1029
Db	965	RQKLCYFLVPKCHPIFLPDSNINSGEIVRLNIQIIFLLAAMKPHYVEV---SRFWKLHP	1021
QY	1030	TFPLRVISTASLCYSILKAKNAGMSLGAK-GNAGPLPSEAVOWLCHQAFLLKLTTHRV	1088
Db	1022	QTLFKFITTISVRYMFLINRRVRRINTGSSFRVLKLYKEEVITWGLDAYIQVLKKNSR	1081
QY	1089	YVPLIGSLRTA-----QTQGRKLPQT 1111	
Db	1082	YMLLIYLSKSLSKLSQQLSELKYAT 1110	

RESULT 18			
ID	Q9SPU7	PRELIMINARY;	PRT; 1123 AA.
AC	Q9SPU7;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DE	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Telomerase reverse transcriptase.		
GN	Name=AtTERT; Synonyms=F5E19.190;		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.		
OX	NCBI_TaxID=3702;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=99402974; PubMed=10471830; DOI=10.1016/S0014-5793(99)01083-2;		
RA	Oguchi K., Liu H., Tamura K., Takahashi H.;		
RA	"Molecular cloning and characterization of AtTERT, a telomerase		
RT	reverse transcriptase homolog in Arabidopsis thaliana.;"		
RL	FEBS Lett. 457:465-469 (1999).		
RN	[2]		
RN	SEQUENCE FROM N.A.		
RP	Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,		
RA	Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;		
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	EU Arabidopsis sequencing project;		
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF135454; AAD54777.1; -.		
DR	EMBL; AL391147; CAC01849.1; -.		
DR	PIR; T51517; T51517.		
DR	GO; GO:0005634; C:nucleus; IEA.		
DR	GO; GO:0003677; F:DNA binding; IEA.		
DR	GO; GO:0003723; F:RNA binding; IEA.		
DR	GO; GO:0003962; F:RNA-directed DNA polymerase activity; IEA.		
DR	GO; GO:0016740; F:telomeric template RNA reverse transcriptase. .; IEA.		
DR	GO; GO:0006278; P:RNA-dependent DNA replication; IEA.		
DR	InterPro; IPR000215; Prot_inh_serpin.		
DR	InterPro; IPR000477; RVTse.		
DR	InterPro; IPR003545; Telomerase_RT.		
DR	Pfam; PF00078; RVT 1; 1.		
DR	PRINTS; PR01365; TELOMERASERTN.		
DR	PROSITE; PS00284; SERPIN; UNKNOWN 1.		
XW	RNA-directed DNA polymerase; Transferrase.		
SQL	SEQUENCE 1123 AA; 130579 MW; 5645B8295817B7F6 CRC64;		

Query Match	12.2%;	Score	724.5;	DB 2;	Length	1123;
Best Local Similarity	23.8%;	Pred.	No.	6e-36;		

Matches 294; Conservative 199; Mismatches 511; Indels 233; Gaps 39;

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QY 1 MPRAPRCRAVRSLLRSHYREVLPATFV-----RRLGPOGWR-----L 38
Db 1 MPRKPRHRVPEILWELFGNRRANLDAIVDLIPNRIQPEQCRCGQCLGSSDKPAFL 60
QY 39 VORGDPAAFRALVAOCLVCPWDARPPAAPSFRQVSCLELVARVLQRL---CERGAKN 95
Db 61 LRSDDPIHYRKLHLRCFV-VLHEQTFPLDLFSPTSWSQREIVERIIEEMOSGCD--CON 117
QY 96 VLAQFALLDARGGPPPEAFTTSVRSLPNTVTDALRGSGAWGLLRVGGDVLVHLLAR 155
Db 118 VICARYKVDQS-----SPILELT-SSWEFLKRVGHVGVVYLQO 159
QY 156 CALFVLVAPSCAYQVCGPPLYLQGAAT-----QARPPPHASGPRRLGRCERAMNHSVRE 209
Db 160 TSIFPLPLGKXQVSGPPLCKIKHRTLSVHENKRDNDVQPTTKRWLSSAVDDCPKD 219
QY 210 AGVPLGLPAG-----ARRGGSASRLPLPKRPRGA-----APEPTPVGQGSWA 257
Db 220 DSATI-TPIVGEDVDQHKETTKTSRYLKRKRQKRVNFKVDCNAPCITP-----271
QY 258 HPGRTGSDGFCVVSFARPAEATSLEGALSCTRHSHSPSGRQHHAGPSTSRPPRPW 317
Db 272 ---STNGKVSTG-----NDEMNLHIGINGSLTDFVQAKO-----303
QY 318 DTPCPPVYAETKHFlys-SGDKEQLRPSFLSSRLPSLTGARRLVETIFLGRSPPMGP 376
Db 304 -----VKNKNPKFGLSEIYSVIPPNNHILKTLRPNCSDSKLLANNHIFGEVNVSTPS 356
QY 377 RRLPRLPO-----RYQMPRLFLELGNHACPYGVLLKTHCP-----LRAAVTPAAG 424
Db 357 HGKGNCPGSGSLYHSLLSKLSKLNIGTKTSHLKMLLDKPCFVLLLOEDALSKGTTSSQS 416
QY 425 VCAREK-----POGSVAA-----PEEDTDPRLVOLLROHSSPQVYGFVRACLRLVPPG 476
Db 417 --RQKADKLPHGSSSSGTGPKCPSVEERK-----YCTNDQVVSFIWAICRYIPES 468
QY 477 LWSGRHNRRLNRTKFTISLKGAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRL 536
Db 469 LLGTHQWRLKNIAMFVSRREKCTVQNLHKVPSDPPFPARKE--LCCWVNGHEL 526
QY 537 REE-----ILAKFLHMSVYVYVLLRFFVYVTTTFQKNRFFYRKSVWSKLQSIG 588
Db 527 QSESIRSTQMLCTKWISLWLEIVKLVHFNFYATESQGRNLNYYRKRSWERLISKE 586
QY 589 IROHLKRVQLSELSEAVRQREARPAALLTSLRPIPKPDGLRPIVNMVYVVGARTFRE 648
Db 587 ISKALDGVYLVDDAEASSRKK-----LSKFRFLPKANGVRMYLD-----FSSS 630
QY 649 KRAERLTSRVKALFSLVLYERARRPGLLAGASVLGLDDTHRAWRTFVLVRADQDP-PSLY 707
Db 631 SRSQSL-----RDTHAVLDKIQLKEDVLGSSVDFHDDFYRLNLCPLYHLRSQSSELPLY 686
QY 708 FVKVDVTGAYDTIPODRLTEVIASIIKPNQTYCVRRYAVVQKAAHGH-----VRKAFKS 761
Db 687 FVADVFAFSDQVQKLLHVIQSPKDE--YILNRCLVLCGKRKNVWVNLVSSDKNS 744
QY 762 HVSTLTDLPYRQFVAHLOETSPLRDAVLEQSSSLNEASSGLPDLFRFWCHHAVIR 821
Db 745 NPSRFTSVPYNA-----LQ-----SIVVDKGENHRVRKDLMMVITGNMLKNMLQD 792
QY 822 GKSYYVQCGIIPGSLTSLTCLSCYGDMEKLFAGI-----BRDGI-----862
Db 793 KSFYVQIAGIPQGHRLSLCLCFYVGHUERTLIYPFLEASKDVSSKCSREELIIPTS 852
QY 863 ---LRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGVVNLKRTVNVFVEDE-----912
Db 853 YKLLRFIDDLVFSVSRDQASSFYHLRKHGPKYCNCFWNETKFCINFEDKEHRCSNRM 912
QY 913 ---ALGGTAFVQMPAHGLFPWCGLLDRTLLEVQSDYSYARTSTRASITFNRGFKAGNM 970
Db 913 FVGDNGVFPVR-----WTGLLINSRTFEVQVDYTRYLSCHISSTSFSAWQNKPVRL 964
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QY 971 RRKLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAVRPHACVLCQLPFOHQVWK-NP 1029
Db 965 ROKLCYFLVPKCHPILFDSNINSGEIVRLNIYQIFLLAAKMFHCYVYEV---SRFWKLHP 1021
QY 1030 TFFLRVISTDASLCYSILKAKNAGMSLGAK-GAAGPLPSEAVQWLCHOAFLKLKLRHVT 1088
Db 1022 QTLFKFTTISVRYMFRINRRVRINTGSSFRPVLKLYKEEVIWGLDAYIQVLKKNR 1081
QY 1089 YVPLLGSLRTAQTO--LSRKLPGTTLTAAEAANPAL 1123
Db 1082 YRMILLYKLSALSXKLSLQQLSSSLRYATDRSNSSSL 1118
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RESULT 19

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Q9AU13
ID Q9AU13 PRELIMINARY; PRT: 1259 AA.
AC Q9AU13;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Telomerase reverse transcriptase.
GN Name=TER1;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Oguchi K., Tamura K., Takahashi H.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288216; AAK35007.1; -
DR Gramene; Q9AU13; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR001209; Ribosomal_S14.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT_1; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR PROSITE; PS00527; RIBOSOMAL_S14; UNKNOWN_1.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1259 AA; 143710 MW; 15B041789F2D5CAD CRC64;
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Query Match 11.5%; Score 688; DB 2; Length 1259;
Best Local Similarity 23.9%; Pred. No. 1.2e-33;
Matches 305; Conservative 175; Mismatches 486; Indels 312; Gaps 45;

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QY 36 W-RIVQRGDPAARFALVAOCLVCPWD---ARPPPAAPSPFRQVSCLELVARVLQRLC-- 89
Db 66 WEHLRQDPIAYRRLITRAVCAIADDLASPPPRVTPGNSGHSQARLVREMKSIAD 125
QY 90 -ERGAKNVLAQFALLDARGGPPPEAFTTSVRSLPNTVTDALRGSGAWGLLRVGGD 148
Db 126 QSHGTKNLCNG--LHEGGQ-----SICISDLVSSSSWSILLHRIGDLL 167
QY 149 LVHLLARCALFVLVAPSCAYQVCGPPL-----YOLGAATOARPPPHASGPRRLG 203
Db 168 MCVLLRCTSLFPLVKKNNDYFQVSGVPLNVNLRNPIFASTVARKHQPOTTKAKHTC-YLM 226
QY 204 N-----HSVRAGVPLGLPAP-----GARRRGGS--ASRSLFLPKRP 238
Db 227 KSNANWENLSICHSSNSGNSVSSSTCKIVTQSCETCGSIRRAESKDPSEGCNCKPFP 286
QY 239 RRGAAPE-----PERTPVQGGSWAHGPR-----TRGPS- 266
Db 287 SDGRSGCCNCTYHNRKRKRLYQWRRSKKQVCVDSSEASWKLNGSNFNMNSGPF 346
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Qy 267 -----DRGFCV-----VSPARAEATS-----LEGALSGTRHSHPSV-----GRQ--- 302
Db 347 NLAGKMDAQSVLTVNDTSLARNDSSEIKVINATILSSEKSPCFVDIRGSQGLS 406
Qy 303 -HHAGPSTSPRPVDTCPVVAETKHELYS-----SGDKEQLRPSFLLSLRP 352
Db 407 CHY-----SUSEVOYSTCQVQSPSSVYLHNSCSICFNCIIISNASKHLSLDSLSIS--RN 458
Qy 353 SLTGARRLVETIF-----LGSRP----- 370
Db 459 GIFYNNRTTYSVFHCKHLSKRKPDALSIVKHIFGINSCCASLLKYNCHESITRKSNCL 518
Qy 371 --WMPGTPRRPLRPLQRYQWQMRPLFLELLGNHGAQPGVLLKTHCPRAAVTP--AAGVC 426
Db 519 CCWLPKSIKNIIR-----NSKRQYKCLFLKHCSVKCKVAPDVTXNDG 561
Qy 427 AREKPOGSVAPEBEDTDPRLVQLLRQHSPPWVYGFVRACTRLRYLPPGLWGRHNR 486
Db 562 KAHYPPGKAAYD-----RSFRLEAYSTHQVQVAFVMAVLKRIYVFKPLLGNFFGKRS 615
Qy 487 FLRNTKFIISLGGHAKLSLQBLTWKMSVRDCAWLR-----SPGVGCVPAAEH 534
Db 616 LRTNIWFKILRRPETPOLSDICGLKVSHYSWLSNIEFSCFCSAIIGKQTGSSTSAEB 675
Qy 535 RLREILAKFLHMLVSVVBLRSFFVYTTTQKNRLPFYKSVWSKQSIGIROHLK 594
Db 676 QEQRNLHCWISLWFLSDIVIPVWRTYFVYTERESKRYDVYFYPKSVVRDLTISNAIAS--LN 734
Qy 595 RVQRLSEAEVRQHRARPALLTSRLRFIPKDPGLRPIVNDYVVGARTFRREKRAERL 654
Db 735 KKNFRIL--RGEPR--KAVRHNLCSRRVFLPKADMRLVDL-----RAKSK 778
Qy 655 TSRYKALFVNLNERRARRPGLLGASVLGLDIDHRAWRFLVLRVRAQ--DPPPELYFVVDV 713
Db 779 DANLNKCHLIMKLKDEKPEMFGSVFDYNNVHQNLSQFISSEKRSQLMKKLVIVVADV 838
Qy 714 TGAVDTIPQDRLTEVIASIIKQNTYCVRRYAVVOKAAHGRVKAFFKSHVS-----TLTD 768
Db 839 SKAFDCVSHDMVLWMDIDAFK--CDEYTVRKCKVICNRKNSLYRFDNSASIGNGSIYD 897
Qy 769 LQPYMRQFVAHLOETSPLDADVIEQSSLSNEASSGLFDPVLRPMCHH-----AVR 819
Db 898 LS-----IQSS--GGGIFVDQ-----GTICRILKQFHHLYEQIKCNILK 937
Qy 820 IRGSYVQCGIPOGSIILSTLCSLCYGDMMENKLPAGIRRDG-----LLRL 866
Db 938 IGQXYLQOVGIAQGSKLSPLNCSLYGHLENSVLKFLHDSKLNAGEAFSEPEYLLMRP 997
Qy 867 VDDFLVTPHTHAKTFLRTLVRGVPYGVGVNLRKTVNF-----PVEDEALGGTAFV 920
Db 998 IDDFIFISFLEHAQKFLNRRMRGFFVFNMYMDSKYGFNFCAGNSEPSSNRLYRGDDGV 1057
Qy 921 QMPAHLFPWGLLDTLTLVQSDYSYARTSIRASLTFRNGFKAGNMRKLFGLRL 980
Db 1058 -----SFPWGLLINCETLEIOADYTRYLIDITITIV--KMSSTKYHSHKCHYMRP 1111
Qy 981 KCHSLFDLQVNSLQTVCTNLYKIILLQAYRFAHCVLQLPHPHOQWKNPTFFLRVIDSTA 1040
Db 1112 KCHPIFYDSNINSFCTIRVNIYQAFLLCAMKFH--CYIRSVSDANVSK--LELLQVIKRTF 1168
Qy 1041 SLCVSILKAKNAGMSLGAAGAPLPSEAVOWLCHQAF--LLKLTRHVTVVPLGLSLRT 1098
Db 1169 RYMSLSIYRRMQDEL-----HYNRPVFLKRRKETIMGLTAVIRV 1210
Qy 1099 AQTQLSRKLPCTLTALF 1116
Db 1211 LQOKOSRYKMDLTLTAE 1228

RESULT 20
Q8LKW0
ID Q8LKW0 PRELIMINARY; PRT; 1261 AA.
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AC Q8LKW0;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Telomerase reverse transcriptase.
GN Name:TERT;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=22096152; PubMed=12100484;
RA Heller-Uzaynska K., Schnippenkoetter W., Kilian A.;
RT "Cloning and characterization of rice (Oryza sativa L) telomerase
reverse transcriptase, which reveals complex splicing patterns.";
RL Plant J. 31:75-86(2002).
DR EMBL; AF494453; AAM21841.1; -.
DR Gramene; Q8LKW0; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptas. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR001209; Ribosomal_S14.
DR InterPro; IPR00477; RVTae.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT_1; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR PROSITE; PS00527; RIBOSOMAL_S14; UNKNOWN_1.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1261 AA; 143715 MW; 353153D1C8B7D5CB CRC64;

Query Match 11.0%; Score 654.5; DB 2; Length 1261;
Best Local Similarity 23.6%; Pred. No. 1.4e-31;
Matches 312; Conservative 173; Mismatches 500; Indels 337; Gaps 48;

Qy 8 RAVSLLLRSHVREVLPLATFVR-----LGPGQW-RLVQRGDDPAARALVAQCLVCVPWD 61
Db 33 RAVFLLLPSPRHCPSPACGRVASCGLARWEHLRLDRGDPVAYRRLITRAVCAIAD 92
Qy 62 ---ARPPPAAPSQVPSCLKELVARVLQRLC---ERGAKNVLAFGAFLLDGAQGPPEAF 115
Db 93 DLSAPPPPRYTPGNSGHSGHQAQLVREMMSIVAQSHGTKNVLNG--LHEGGQ----- 143
Qy 116 TTSVRSYLPNTVTDALRGSGAWGLLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPL 175
Db 144 -----SICISDLVSSSSSILHLRIGLLMCLYLLRCTSIPLPKKNDYFQVGVPL 194
Qy 176 ---YQLGAATQARPPPHASGPRRLRCERAWN-----HSVRAGVPLGLPAP 219
Db 195 NVLRNPFIFASTVARKHQPOTTKAKCHTC-YLWKSANMAENLSICHSSNGVNSPSSST 253
Qy 220 -----GARRRGGS--ASRSLPLKPRPRGAPE-----PERTPVQGGSWAH 258
Db 254 CKIVTQSCCTCGSIRRAESKDPSEGCNCPKFFSDGRSGCCNCTYHTRKRKELYSWQR 313
Qy 259 PGR-----TROPS-----DRGFCV-----VSPARPAE 280
Db 314 RSKKQVCSVDSESAEWSKLSNGFNNSGPFSENLAGKMDAQSVLTVNDTSLARNDS 373
Qy 281 EATS-----LEGALSGTRHSHPSV-----HHAGPSTSPRPVDTCPVVAET 328
Db 374 DSSEIKVINATILSSEKSPCFVDIRGSQGLSCHY-----SUSEVOYSTCQVQSPSS 427
Qy 329 KHFLYS-----SGDKEQLRPSFLLSLRPSTLGTARLVETIF-----IGSRP-- 370
Db 428 YLHNLSCSICFNCIIISNASKHLSLDSLSIS--RNGIFYNNRTTYSVFHCKHLSKRKPD 485
Qy 371 -----WMPGTPRRPLRPLQRYQWQMRPLFLE 395
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Db 486 LSLVKHIFGINSCLLKYNCHESTIRKSNCLCCWLPKSIKNLIR- 531
QY 396 LLGNEAQCYPYGLLTKXTHCPRAAVTP--AAGVCAKEKQGSVAAPAEEDTDPRRLVQLLR 453
Db 532 ---NKRQYKGLFLKHGCVCKVADPVTDGDKAHYPPGKAAYD-----RSFSRL 582
QY 454 QHSSPWQYVGFVACILRLRVLPPGLMGSRHNERFLRNTKFTSLGKHAKLSLQELTWKMS 513
Db 583 AVSTHQQVASFVAVLKRIVPKPLGNSFGKSLATNIWKFLKRRFTFQLSDICGDLK 642
QY 514 VRDCAWLR-----SPGVGCVPAABHRLREELAKFLHLMVSVYVVELLRSPF 561
Db 643 VSHYSLNIEFSNCFSCSALIGKQTSSTASBEQKQKILHCHWLSFSDIVIPVTVTF 702
QY 562 YVTEFTQKRLFFYKRWKSLQSIGIRGHLKRVQLRSLSAEYVQHQREARPAALLTSRL 621
Db 703 YVTERESKYDYFPYKPSVWRDLTNAIAS-LNKKNFRL-RGEPR--KAVRHLCSSRV 758
QY 622 RPIKPDGLRPIVNDYVVGARTFRREKRAERLTGRKALFGLVNLVNRARRPGLIGASVL 681
Db 759 RFLPKAKMRPLVDL-----RAKSKDANLKHCHLMKKLDEKEMEGSSVF 805
QY 682 GLDDIHRAWRTFVLVRAQ-DPPPELYFYKVDVTGAYDTIPQDRLTEVIASIKPQNTYC 740
Db 806 DYNVHONLSQFISSKRSQMKKLKVIYVADVSKAFDCVSHDWLKMIDDAFK-CDEYT 864
QY 741 VRYAVVQKAAGHVRAKAFKSHVS-----TLTDQPYMQFVAHQETSPDLDAVVISQS 795
Db 865 VRKSKVYCNRSKSLYRFDNSNAGNSIYDLS-----IQLSS--GGGIFVDQ- 912
QY 796 SSLNEASSGLPDVFLRFMCHH-----AVRIRGKSVQCGIPQGSILSTLCSLCY 846
Db 913 -----GTICRIKQEPHLLHYEQIKNLKIGQKYVLOQVGAQSKLSPNLCSLYY 964
QY 847 GDMENKIFAGIRRDG-----LLRLVDLDFLLVTPHPLTHAKTFLRTLVRGVE 893
Db 965 GHLENSVLKFLHDSKLNAGEAFSEPYLLMRFDIDFIFISPSLEHAQKFLNMRERGVP 1024
QY 894 YGVVNLKRTVNVF-----PVEDALGTAFTVQMPAHGLFPWCGLLDDTTLTLEVSQSY 947
Db 1025 YNCYMNSKYGFNFCAGNSEPSNRLYRGDDGV-----SFMWSEGLLNCETLEIQADYT 1079
QY 948 SV-----ARTSIRASLTNRGFKAGNMRKLGVLRLKCHSLFLDLQVNSLOT 996
Db 1080 RYLDTHYLHPSLVRLCHLHQSTSK-----LCPLAV--QNAHFIFDYSNINSPT 1129
QY 997 VCTNIIKILLQAYRPHACVLPQHPHQVKNPTFFLRVISDTASLCYSILKAKNAGMSL 1056
Db 1130 IRVNIYQAFLLCAMKFH-CYIRSVSDANVSK--LELLQVIRKTPRYMHSLIVRRMQDVEL 1186
QY 1057 GAKGAAGPLPSEAVOWLCHQAF--LLKTRHRVTVPVLGSLRATQQLSRKLPOTTLTA 1114
Db 1187 -----HYNVRPVLKLRKETIWLGLTAVIRVLQKQSRVKMDLTLT 1228
QY 1115 LE 1116
Db 1229 AE 1230

RESULT 21

TERT_SCHPO
ID TERT_SCHPO STANDARD; PRT; 988 AA.
AC O13339; O13338;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit).
DE subunit).
GN Name=ttr1; ORFNames=SPBC29A3.14c;
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.
RN NCBI_TaxID=4896;
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=97400623; PubMed=9252327; DOI=10.1126/science.277.5328.955;
RA Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H.,
RA Lingner J., Harley C.B., Cech T.R.;
RT "Telomerase catalytic subunit homologs from fission yeast and human.";
RL Science 277:955-959(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21849401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weijens J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Bozrym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomycetes pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
the replication of chromosome termini in most eukaryotes. It
elongates telomeres. It is a reverse transcriptase that adds
simple sequence repeats to chromosome ends by copying a template
sequence within the RNA component of the enzyme.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
IsoId=O13339-1; Sequence=Displayed;
Name=2;
IsoId=O13339-2; Sequence=VSP_006395;
CC -!- MISCELLANEOUS: Deletion causes telomere shortening and senescence.
CC -!- SIMILARITY: Belongs to the reverse transcriptase family.
Telomerase subfamily.
CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; AF015783; AAC49802.1; -
CC EMBL; AF015783; AAC49803.1; -
CC EMBL; AL022299; CAA18391.1; -
CC F01; T03838; T03838.
CC GeneDB SPombe; SPBC29A3.14c; -
CC InterPro; IPR000477; RVTse.
CC InterPro; IPR003545; Telomerase_RT.
CC Pfam; PF00078; RVT; 2.

543 MTNTKLSYSHLMKLTILNRMFKDPFGFAVNTDDVMRKYEFEVLKWR--QVGRPKLYFVVT 601
 711 VDVGTAYDTIPDRL-----TEVIASIIKPONTYCVRR----YAVVQKAAGHVRKAFK 760
 602 MDIEKCYDSVDREKLSQLLGTTRLLSSEFRIMTVQAMKRNAEVVDLDKCAKNQKCEFR 661
 761 ---SHVSTLTDLQPYMRQFVAHLQETSPISDAVVIEOSSSINEASSGLFDVFLRFMCHHA 817
 662 QRWKIALEGDQYPSLLNVLEDDQNDLNAKETLLVENVKQRPYKKKALLDPVIKICRHNY 721
 818 VRIRGSYVOCQIGPOGSILSTLLSCYCGDMENKLFAGIRRDG-----LLRLRLVD 868
 722 IEFNRKYKTKGIPQGLCVSSLSLSPFYASLEENALGYLRKSMANDANDNITLLRLTLD 781
 869 DFLVTPHPLTHAKTFLRTLVRGVPEYGCVVNLRKTVVFPVEBALG--GTAFV--QMPA 924
 782 DYLLITTKENNAILFTIEKLINVSQRNKFENMKQLQTNFLDPSKLNKYGWASVEDQVIA 841
 925 HGLFPWCGLLLDRTLETVQSDYSYARTSTRASITFN-RGFKAGRNWRKLFGLVRLKCH 988
 842 HDVIDWTIGISDMSTLALMPNI-NLRKKGILCTLNMMQTKASMMILKRKL-----K 892
 984 SLFLDLQVNSLOVTCTN-----IYKILLQAVRHACVQLQLPFHQOVWKNPTFFLRVI 1036
 893 SFLMNNITHFRKTIITNRBSNKTILNKLYTAGAYKMQCCIEYKDHFT--NTEIHPQLD 950
 1037 SDTASLCYSILKA 1049
 951 KIICAIIVSVTRA 963

 RESULT 24
 Q7SD71 PRELIMINARY; PRT; 939 AA.
 ID Q7SD71 AC Q7SD71: 01-MAR-2004 (T-EMBLrel. 26, Created)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=NCU02791.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxId=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OR74A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
 RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
 RA Kamal M., Kamysuselis M., Mauceli E., Bielek C., Rudd S., Frishman D.,
 RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
 RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
 RA Yarden O., Flannan M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
 RL Nature 0:0-0(2003).
 CC -i- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AAE0100062; EAA34711.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003664; F:RNA-directed DNA polymerase activity; IEA.
 DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
 DR InterPro; IPR000477; RVTse.
 DR InterPro; IPR003545; Telomerase_Rt.
 DR Pfam; PF00078; RVT_1; 1.
 DR PRINTS; PR01365; TELOMERASERT.
 KW Hypothetical protein; RNA-directed DNA polymerase; Transferase.
 SQ SEQUENCE 939 AA; 104679 MW; 86F6B140E94056DC CRC64;

Query Match 7.9%; Score 469.5; DB 2; Length 939;
 Best Local Similarity 27.3%; Pred. No. 2.5e-20;
 Matches 148; Conservative 86; Mismatches 205; Indels 103; Gaps 15;

QY 430 KPGSVAPEEDTDRRLVQLLRHQHSPQVGVFVRACLRRLVPPGLWGS----- 480
 DB 400 RPPSTAAVISNSQSQSLDLATPISS---ISAFQAVLSKIIPNDFWGSSEEGHPQ 456
 QY 481 RHNREFLNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSSPGVGVCPAAEHL--RE 538
 DB 457 EHNKSVFLKQIDNFIKRLRFRFSMTLHNLVQGGKSSISWL--ASAAALSHKCSQPELNKRK 515
 QY 539 EILAKELHLMSSVYVELLRSPFYTTTFQKNRFFYRKSVWSKQSIGIRQHLKRVQL 598
 DB 516 EYLFLYTFDSLLIPLIRSNFYTESAHRYLFFFRHDVWLSVTKPAL--ACLKVKMF 574
 QY 599 RELSEAEVQHREARPALTSRLRFPKPDG--LRPIVNDYVVGARTF-----RRE 648
 DB 575 EEVKGAEAVKMLEGR-KLGFQSVRLLPKGVGNSLRPIMNLRRLVRGLSGKGIWQKQ 633
 QY 649 KRAERLTSRKALFSLVINYERARRGLLGASVLGLDDHRAWRTPFLVRVRAQ-----DPPP 704
 DB 634 MLGPSINSVLGPVNSMLKPEKERECRLGGGFVAGDIYQRYKFRFVAVSEVSKKGGK 693
 QY 705 ELVYFVKVDVTGAVDTIPQDLRTEVIASIIKQNTQVRRYAVVOKAAAHGVH----- 755
 DB 694 KTFYKVDVQAAPDTIIPQAAMVELLQKI-----PCHGVYKESKHEVSLPLDYHN 744
 QY 756 -----RKAFKSHVSTLT-----DLQPMRFQVAHLQ 781
 DB 745 PANNDTNDIDNPKYKLPKTRMHSITTSPPSITTTTTSASISILPQQDSVA--- 801
 QY 782 ETSPLRDVAVIOSSSLNEASSGLFDVFLRFWCHAVIRKSVQCGIPQGSILSTLL 841
 DB 802 -TTKQNTLPIPSHSSTPKLTHSALLSLAKEHITQNLVKIGKRYRQKTGIPQGSVLSTL 860
 QY 842 CSLCYGDMENKL-----FAGIRDG--LLRLVDDFLVTPHLTHAKTFLR 885
 DB 861 CNTFYADLRSSQGLAFPLGTGDEDEGRGSRDGNLTMLRLDIFLLITTSRKARFVE 920
 QY 886 TL 887
 DB 921 VM 922

RESULT 25
 QYUN56 PRELIMINARY; PRT; 85 AA.
 AC OSUN56;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Telomerase reverse transcriptase (Fragment).
 GN Name=RTT;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE=99105927; PubMed=9887342; DOI=10.1093/hmg/8.1.137;
 RT Cong Y.S., Wen J., Bacchetti S.;
 RT "The human telomerase catalytic subunit hTERT: organization of the
 RT gene and characterization of the promoter.";
 RL Hum. Mol. Genet. 8:137-142(1999).

GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR GO; GO:0003964; F:RNA-directed DNA polymerase.
 FT NON_TER 85
 SQ SEQUENCE 85 AA; 9601 MW; 67A096FC9ECB53B3 CRC64;

Query Match 7.5%; Score 450; DB 2; Length 85;
 Best Local Similarity 100.0%; Pred. No. 1.8e-20;
 Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVSLRSHYREVLPLATFVRLRGQWELVORGPAPRALVAOCLVCPW 60
 DB 1 MPRAPRCRAVSLRSHYREVLPLATFVRLRGQWELVORGPAPRALVAOCLVCPW 60
 QY 61 DARPPPAAPSPFQVSCLELVARVL 85
 DB 61 DARPPPAAPSPFQVSCLELVARVL 85

RESULT 26
 QYUN56 PRELIMINARY; PRT; 940 AA.
 AC O6C9D0
 DT 25-OCT-2004 (TEMBLrel. 28, Created)
 DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)
 DE Yarrowia lipolytica chromosome D of strain CLIB99 of Yarrowia
 DE lipolytica.
 GN ORFNames=YAL10D12188g;
 OS Yarrowia lipolytica CLIB99.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 OC NCBI_TaxID=284591;
 RX [1]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=CLIB99;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boirame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicell J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennene D., Tekala F., Wesolowski-Louvel M., Weathof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts";
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIB99;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382130; CAG80920.1; -
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
 DR InterPro; IPR000477; RVTse.
 DR InterPro; IPR003545; Telomerase_RT.
 DR Pfam; PF00078; RVT_1; 1.
 DR PRINTS; PR01365; TELOMERASERT.
 KW RNA-directed DNA polymerase; Transferase.
 SQ SEQUENCE 940 AA; 108087 MW; 4EA86CEFF0811FFC CRC64;

Query Match 7.5%; Score 450; DB 2; Length 940;
 Best Local Similarity 25.6%; Pred. No. 3.9e-19;
 Matches 159; Conservative 115; Mismatches 238; Indels 110; Gaps 24;

GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
 DR InterPro; IPR000477; RVTse.
 DR InterPro; IPR003545; Telomerase_Rt.
 DR Pfam; PF00078; RVT_1; 1.
 DR PRINTS; PR01365; TELOMERASERT.
 KW Hypothetical protein; RNA-directed DNA polymerase; Transferase.
 SQ SEQUENCE 939 AA; 104679 MW; 86F6B140E94056DC CRC64;

Query Match 7.9%; Score 469.5; DB 2; Length 939;
 Best Local Similarity 27.3%; Pred. No. 2.5e-20;
 Matches 148; Conservative 86; Mismatches 205; Indels 103; Gaps 15;

QY 430 KPGSVAPEEDTDRRLVQLLRHQHSPQVGVFVRACLRRLVPPGLWGS-----480
 DB 400 RPPSTAAVISNSQSQSLDLATPISS---ISAFQAVLSKIIPNDFWGSSEEGHPQ 456
 QY 481 RHNREFLNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSSFGVGCVPAAEHL--RE 538
 DB 457 EHNKSVFLKQIDNFIKRLRFRFESMTLHNLVQGGKSSISWL--ASAAALSHKCSQPELNKRK 515
 QY 539 EILAKELHLMSSVYVELLRSFYVTTTFQKNRFFYRKSVWSKQSIGIRQHLKRVQL 598
 DB 516 EYILEFLYTFDSLLPIRSNFYTESAHRYLFFFRHDVWLVSYPAL--ACLKVKMF 574
 QY 599 RELSEAEVQHREARPALTSRLRFPKPDG--LRPIVMDYVVGARTF-----RRE 648
 DB 575 EEVKGAEAVKMLEGR-KLGFSQVRLLPKGVGNSLRPIMNLRRLVVRGLSGKGIWQKQ 633
 QY 649 KRAERLTSRKALFSLVINYERARRGLLGASVLGLDDHRAWRTPFLVRVRAQ-----DPPP 704
 DB 634 MLGPSINSVLGPNVSNMLKEPERGRLGGGFVAGDIYQRYKFRFARVSEVSKKGGK 693
 QY 705 ELVYFVKVDVTGAVDTIPQDLRTEVIASIIKQNTQVRRYAVVOKAAAHGV-----755
 DB 694 KTFYKVDVQAAPDTIIPQAAMVELLQKI-----PCHGVYKESKHEVSLPLDYHN 744
 QY 756 -----RKAFKSHVSTLT-----DLQPMRFQVAHLQ 781
 DB 745 PANNDTNDIDNPKYKLPKTRMHSITTSPPSITTTTTSASISILPQQDSVA---801
 QY 782 ETSPLRDVAVIOSSSLNEASSGLFDVFLRFWCHAVIRKSVQCGIPQGSILSTLL 841
 DB 802 -TTKQNTLPIPSHSSTPLKLTSSALLSLAKEHITQNLVKIGKRYQKRTGIPQGSVLSTL 860
 QY 842 CSLCYGDMENKL-----FAGIRDG--LLRLVDDFLVTPHLTHAKTFLR 885
 DB 861 CNTFYADLRSSQGLAFPLGTGDEDEGRGIRSDGNLTMLRLDIFLLITTSRKARFVE 920
 QY 886 TL 887
 DB 921 VM 922

RESULT 25
 QYUN56 PRELIMINARY; PRT; 85 AA.
 AC OSUN56;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Telomerase reverse transcriptase (Fragment).
 GN Name=RTT;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE=99105927; PubMed=9887342; DOI=10.1093/hmg/8.1.137;
 RT Cong Y.S., Wen J., Bacchetti S.;
 RT "The human telomerase catalytic subunit hTERT: organization of the
 RT gene and characterization of the promoter.";
 RL Hum. Mol. Genet. 8:137-142(1999).

GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR InterPro; IPR0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR InterPro; IPR0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR Non_TER 85
 SQ SEQUENCE 85 AA; 9601 MW; 67A096FC9ECB53B3 CRC64;

Query Match 7.5%; Score 450; DB 2; Length 85;
 Best Local Similarity 100.0%; Pred. No. 1.8e-20;
 Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVSLRSHRYEVLPLATFVRLRPGQWELVORGPAPRALVAOCLVCPW 60
 DB 1 MPRAPRCRAVSLRSHRYEVLPLATFVRLRPGQWELVORGPAPRALVAOCLVCPW 60
 QY 61 DARPPPAAPSPFQVSCLELVARVL 85
 DB 61 DARPPPAAPSPFQVSCLELVARVL 85

RESULT 26
 QYUN56 PRELIMINARY; PRT; 940 AA.
 AC O6C9D0
 DT 25-OCT-2004 (TEMBLrel. 28, Created)
 DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)
 DE Yarrowia lipolytica chromosome D of strain CLIB99 of Yarrowia
 DE lipolytica.
 GN ORFNames=YAL10D12188g;
 OS Yarrowia lipolytica CLIB99.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 OC NCBI_TaxID=284591;
 RX [1]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=CLIB99;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boirame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicell J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennene D., Tekala F., Wesolowski-Louvel M., Weathof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIB99;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382130; CAG80920.1; -
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
 DR InterPro; IPR000477; RVTse.
 DR InterPro; IPR003545; Telomerase_RT.
 DR Pfam; PF00078; RVT_1; 1.
 DR PRINTS; PR01365; TELOMERASERT.
 KW RNA-directed DNA polymerase; Transferase.
 SQ SEQUENCE 940 AA; 108087 MW; 4EA86CEFF0811FFC CRC64;

Query Match 7.5%; Score 450; DB 2; Length 940;
 Best Local Similarity 25.6%; Pred. No. 3.9e-19;
 Matches 159; Conservative 115; Mismatches 238; Indels 110; Gaps 24;

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QY 445 PRLVQLLRQHSS---PNOVTGFR-----ACLRRLVPP 475
Db 314 PKRLVFFQIASTIVKKGQQNLFRLDAPFLNDRYDGHVNDVWVFCFAASHLLPPH 373
QY 476 GLWGRSHNERFLRNTKFIISGKHAKLSLQELTWKMSVRDCAWLRRSPGVCVPAAEHR 535
Db 374 VLFSGADNVAVLRSKYVYLLNLPSTSPHLDTMTGGFRLTEINWLFTS--DNMLKKSDDM 432
QY 536 LR-BEILAKFLHLSVYVVELLSFFVTTTFOKRLFFYRKSVMKLSIGIRQHLK 594
Db 433 LKARELPQMLWTVNRPQLPOLRSFFFTDSLTSDQ--IIRHPVQR-KTRSTLQELK 489
QY 595 RVOL--RELSEAVRQREARPAALLTSRLRIPKPDGLRPIVNDYVVGARTPREKRAE 652
Db 490 RTQFSKVLTPSD-----LGISFRMLPKKSGFRPVSLSGRPVQS---PRGKKPI 536
QY 653 RLTSRVKALFSLNVERARRPGLLGASVLGDDIH--RAWRTFVLVRADQDPPELVFV 709
Db 537 SVNKKLSKYLKIL-YQEFR---LGNKKCGLDSDVHLLKKVLGKEKAIKGO--TQGLKFV 590
QY 710 KVDVTGAYDTIPQDRLETVIA-----SIIRKPONTYCVRRYAVVQKAHGHVR 756
Db 591 KIDVTAEDTTPASKVKDISKRLDCESYLSHSHRILPMSKTVLRWFTTSRACNGRSE 650
QY 757 KAFKSHVSTLDLQPMYQFVAHLQETSPLRDVAVVIEOSSLINEASSGLFDFVFLRFMCHH 816
Db 651 CA-----LQAFRELGL-----NKGIIIDENKSDSVGKQLLYKLLNDHLFRN 690
QY 817 AVRIRGKSYVOCGIPGOSILSTLLCYGDMENKLFAGI--REDGLLRLVDDFLVLT 874
Db 691 DVFIDGQVHRQVRGIPQGSILSSULFCSMVYEMVREKFSIDLVRPDTCLMRFPVDFMLIT 750
QY 875 PHLTHAKFTLRLVRGVPYGCWNLRKTVVNFVPEDEALGCTAFVQMPAHGLFPWCGLL 934
Db 751 TDATATETFNALKGLPDYGVSNRSKLVNFPF---SVGVRIALQEEGEMPPFLGK 807
QY 935 LDTTLEVSQSYSSYARTSIRASLTFRNGFK--AGRNRRKRLFGVLRKCHSLFLDLQVN 992
Db 808 IDPCNLQIHRDY-PYS-----SALLVWDVKGVLAAVRHRAKEVYFSA--RFPRLLLNKSVP 859
QY 993 SLQTVCTNI-----YKILLQAVR 1011
Db 860 E-AVVLKNVSAPFRYVFLRAIR 860

RESULT 27
Q80SUS PRELIMINARY; PRT; 116 AA.
AC Q80SUS;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Telomerase reverse transcriptase (Fragment).
GN Name=tert;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer;
RX MEDLINE=22615084; PubMed=12729609; DOI=10.1016/S0003-2697(03)00091-5;
RA Holzmann K., Berger W., Meiri D., Cerni C., Sagary S.;
RT "Detection and quantification of transcripts for the catalytic subunit
RT TERT and the RNA component of telomerase in rat tissue.";
RL Anal. Biochem. 317:120-123(2003).
DR EMBL; AJ440965; CAD29524.1; -
DR EMBL; AJ440966; CAD29525.2; -
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON TER 1
FT NON TER 116
SQ SEQUENCE 116 AA; 12634 MW; BAA7F12F6B23DB35 CRC64;
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Query Match 7.5%; Score 449; DB 2; Length 116;
Best Local Similarity 74.8%; Pred. No. 3.2e-20;
Matches 86; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 47 FRALVAQCLVCPWDARPPAPSPROVSCUKELVARVLQRLCERGAKNVLAFGALLDG 106
Db 2 FRTLVAQCLVCPWGSQPPADLSFHQVSSLUKELSVRVVQKLCERGERNVLAFGALLG 61

QY 107 ARGCPPEAFTTSVRSYLPNTVTDALRGSGAWGLLRRVGDVVLHLLARCALFVL 161
Db 62 ARGCPPEAFTTSVRSYLPNSVTESLCVSGAMWLLLSRVGDDLLVYLLSHCALYLL 116

RESULT 28
TERT_EUPAE STANDARD; PRT; 1031 AA.
AC Q00939;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
DE subunit) (Telomerase subunit P123).
OS Euplotes aediculatus.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC Euplotida; Euplotidae; Euplotes.
OX NCBI_TaxID=5940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97274210; PubMed=9110970; DOI=10.1126/science.276.5312.561;
RA Lingner J., Hughes T.R., Shevchenko A., Mann M., Lundblad V.,
RA Cech T.R.;
RT "Reverse transcriptase motifs in the catalytic subunit of
RT telomerase.";
RL Science 276:561-567(1997).
CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
CC the replication of chromosome termini in most eukaryotes. It
CC elongates telomeres. It is a reverse transcriptase that adds
CC single sequence repeats to chromosome ends by copying a template
CC sequence within the RNA component of the enzyme.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the reverse transcriptase family.
CC Telomerase subfamily.
CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U95964; AAC47515.1; -
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR PROSITE; PS50878; RT_POL; 1.
DR DNA-binding; Nuclear protein; RNA-directed DNA polymerase; Telomere;
DR TRANSFERASE.
FT DOMAIN 498 852 Reverse transcriptase.
SQ SEQUENCE 1031 AA; 122562 MW; 57B87A63A1FED60F CRC64;

Query Match 7.5%; Score 448.5; DB 1; Length 1031;
Best Local Similarity 22.2%; Pred. No. 5.4e-19;
Matches 138; Conservative 125; Mismatches 303; Indels 57; Gaps 16;

QY 464 FVRACLRLVPPGLWGRSHNERFLRNTKFIISGKHAKLSLQELTWKMSVRDCAWLRRS 523
Db 361 FINEFFYNILPKDFLTGR-NRKNFKQVKYKVELNKHLELHNKLLKINTREISMQVVE 419
QY 524 PGVGCVPAAEHRLREEILAKFLHLSVYVVELLSFFVTTTFOKRLFFYRKSVMK 583
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RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AL590451; CAD27002.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase; .; IEA.
DR InterPro; IPR003545; Telomerase RT.
DR PRINTS; PRO1365; TELOMERASERT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 823 AA; 95280 MW; 8FD1BED4CCE68354 CRC64;

Query Match 6.8%; Score 408; DB 2; Length 823;
Best Local Similarity 19.8%; Pred. No. 1.3e-16;
Matches 203; Conservative 159; Mismatches 363; Indels 298; Gaps 33;

QY 66 PAAPSFQVSCLELVARVQLRCERGAKNVLAAGFAL----LDGARGGPPPEAFTTSVRS 121
DQ 48 PVSSFKSTQKQDVLSKAVRTLLIKNRDNHLCAGYKWSGPGPGA-----STKILC 99

QY 122 YLPNTVTDALRGSGAWGLLRVGGDDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGAA 181
DQ 100 YFPNSSRLIR-SHESWMLRSIGDELAFILTECLVQLMNSGYVFL-----146

QY 182 TQARPPPHASGRRRLGGERAMNHSVRBAGVPLGAPCARRRGSGASRSLPLKPRRGG 241
DQ 147 -----AGDPKSLSGMATERSVNAIGRNVLFYKETRR- 177

QY 242 AAPPERTVPGSGWAHPGRTGSDRGFCVVSPPAPAEATSLEG---ALSGTRHSPS 298
DQ 178 -----ISFCSLSAFEYVFEAHNSKYKVIQKARDVLES 211

QY 299 VGRQHHAGPPSTSRPRPDWTPCPVYAETKHFYSSGDKEOL----RPSFLLSLRPSL 354
DQ 212 IERR-----WK-----KISTHAIKFSFKBELAIEDKSSALECGVKQS- 249

QY 355 TGARRLVTIFLGSRPWPGTPRRLPLPQRYQWQMRPLFLELLGNHACQPYGVLLKTHCP 414
DQ 250 ----KLNVNLFLLS-----KKLFKDAFDLHG-----FRILKSLRS 280

QY 415 LRAAVTPAAGVCAREKPGQSVAAPEEDTPRRLVQLLRQHSHPQVYGFVRACLRLVP 474
DQ 281 L-----LIHRNRYETVSKNELVKYFRI-----302

QY 475 POLGMSRHNERRFLNRTKFKFISLGHAKSLQELTWKMSVRDCAMLRSPGVGCVPAAEH 534
DQ 303 ----SRKFFTELECTR-----SEF 318

QY 535 RLREILAKFLHLMVSVVVELLSFFYVTTTQKNLFFYRKSVWSKLSQIGIRQHLK 594
DQ 319 VFRFRVSRFLVYITEKLIPIISKYFYCTETSFSGKFKVHYPPRSIRWHFSSIHIDRFLE 378

QY 595 RVQLBELSEAEVRQREARPAALLTSRLRIFPKPDGLRPIVNDYVVGARTFRREKRAEL 654
DQ 379 KFEPAKSGTTH-----SYSELRCIPKMGARTISNMKSARNGR-----PSI 419

QY 655 TSRVKALFSLNRYERARRPGLIGASVLGDDIHRAWRTFVLRL-VRADPPPELYPVKVDV 713
DQ 420 NKSIVPEFCVLHE---THGLMNSILNHSGMIEKLSLSYLSRSVR-----PLYLKVDL 470

QY 714 TGAYDTIPQDRLTEVIASIIKPNQTYCVRRYAVVQAAHGHVRKAFKSHVS-----TLNLD 769
DQ 471 SGCFDNIQDEVSVLVRLLH-KSRYHTKFSFSLIEVG-GLRSYVCKVTENAEITNEL 528

QY 770 QPYMQFVAHLQETSPLRDADVIEGSS-----SLNEASSGLPDVFLRFMCHAVIRIGSKY 825
DQ 529 -----MMPEGAFNVKVKENASQRIILSREEVEGAWTNMIKR-----NYVKHNGKLF 574

QY 826 VOCQIGPOGSIILSTLCSLCGDMENKLFAGIRRDGLLRLVDDPELLVTPHLTHAKTFLR 885
DQ 575 VQKTGIAQGSVASTLCSLYKSIDDLFYDRVFKEGILTRYVDDFLVISPCIDEIMKFLF 634

QY 886 TLVRGVPPEYGCVVNLRKTVNVPFVDEALGGTAFVQMPAH-----GLFPWCGLLLDIT 937
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Db 635 -VSOSISHLGINFSEKEMESNFGLEHLKAASSISELSKHKSMKITNAPVGCCTKIYS 693
QY 938 RTLEVQSDYSS-YARTSIRASITFNRGFKAGRNMRKLPGLVLRKCHSLFLDLQVNSLQT 996
DQ 694 DGFISKSQTADPYLPFSIAHST-----KPGRALESRRKLLQNRMSRIYID---PNNKK 745
QY 997 VCTNIYKILLQAVRFHACVQLQLPFHQQVQWKNPTFFLRVISDTASLCYSILKAKNAGMSL 1056
DQ 746 AVENIYDTFL-----FYGKGLLLGRMDFINRSFARRTLEHSKRFAPRI--CRKHGISI 798
QY 1057 GAK 1059
DQ 799 TRK 801

RESULT 31
Q9JULM1 PRELIMINARY; PRT; 104 AA.
AC Q9JULM1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Telomerase reverse transcriptase (fragment).
GN Name=tert;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hatakeyama S., Ishikawa F.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF157502; AAF42984.1; -.
DR MGD; MGI:1202709; Tert.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0003720; F:telomerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON TER 104 104
SQ SEQUENCE 104 AA; 11998 MW; 4B649E63476D3D44 CRC64;

Query Match 6.7%; Score 397; DB 2; Length 104;
Best Local Similarity 76.0%; Pred. No. 4.4e-17;
Matches 79; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 MPAPRCBAVPSLSARSHYREVLPATFVRRLGPOGWRVLRVQGDPAARFALVAQCLVCPW 60
DQ 1 MTRAPRCBAVPSLSARSHYREVLPATFVRRLGPEGRLVQPGDPKRYRTLVQAQCLVCMHW 60

QY 61 DARPPPAAPSFRQVSCLELVARVQLRCERGAKNVLAAGFALL 104
DQ 61 GSQPPPADLSFHQVSSLELVARVQVRLCERNVLAAGFALL 104

RESULT 32
Q818Z7 PRELIMINARY; PRT; 1135 AA.
AC Q818Z7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Telomerase.
OS Sterkiella sp. Aspen.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
OC Stichotrichida; Oxytrichidae; Sterkiella.
OX NCBI_TaxID=200599;
RN [1]
RP SEQUENCE FROM N.A.
RA Marandi S., Prescott D.M.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY116501; AAN87866.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
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QY 952 TSIRASLTFRNGFKAGRNMRRLFGVRLKCHSLFDLOVNSLQVCTNVIYKILLQAVR 1011
 Db 972 EGILCTLVNVMQTNESILWLKKLKSFLMNNISFYFKSTINTKQFANITLSKLYIAAEK 1031
 QY 1012 FHACVLQLP-FHQ 1023
 Db 1032 YVACCOEKFRRPHE 1044
 RESULT 34
 Q9UNR4
 ID Q9UNR4 PRELIMINARY; PRT; 73 AA.
 AC Q9UNR4; 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2004 (TReMBLrel. 26, Last annotation update)
 DE Telomerase reverse transcriptase (Fragment).
 GN Name=TERT;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99151529; PubMed=10029071;
 RA Horikawa I., Cable P.L., Afshari C., Barrett J.C.;
 RT "Cloning and characterization of the promoter region of human
 telomerase reverse transcriptase gene.";
 RL Cancer Res. 59:826-830(1999).
 DR EMBL; AF098956; AAD12786.1; -;
 DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 FT RNA-directed DNA polymerase.
 KW NON TER 73
 SQ SEQUENCE 73 AA; 8290 MW; 20097F24B3035134 CRC64;

Query Match 6.6%; Score 394; DB 2; Length 73;
 Best Local Similarity 100.0%; Pred. No. 4.3e-17;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPRAPRCRAVRSLLSHRYEVLPLATFVRRLLGQGWRLVQRGDPAAFRALVAQCLVCPW 60
 Db 1 MPRAPRCRAVRSLLSHRYEVLPLATFVRRLLGQGWRLVQRGDPAAFRALVAQCLVCPW 60
 QY 61 DARPPPAAPSPFQ 73
 Db 61 DARPPPAAPSPFQ 73

RESULT 35
 Q91826
 ID Q91826 PRELIMINARY; PRT; 1108 AA.
 AC Q91826;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Telomerase (Fragment).
 OS Sterkiella sp. Aspen.
 OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
 OC Stichotrichida; Oxytrichidae; Sterkiella.
 OX NCBI_TaxID=200599;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Marandi S.S., Prescott D.M.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY116502; AAN87867.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. . .; IEA.
 DR InterPro; IPR003545; Telomerase_RT.
 DR PRINTS; PR01365; TELOMERASEKT.
 FT NON TER 1
 KW NON TER 1
 SQ SEQUENCE 1108 AA; 131535 MW; EC8262E01B8E0FAD CRC64;

Query Match 6.6%; Score 392; DB 2; Length 1108;
 Best Local Similarity 22.2%; Pred. No. 1.8e-15;
 Matches 136; Conservative 112; Mismatches 307; Indels 58; Gaps 15;
 QY 450 QLLROHSSPWQYGVFRACLRRLVPPGLWGSNRRERFLRNTKFKISLGHAKLSLQELT 509
 Db 427 QLFHEYQDQROISNLFTEFVANVPFKNFLEGG-KKKIFNKKMLQFVKFNRFSTKISLL 485
 QY 510 WKMSVRDCAWLRRSPGVCVPAAEH---RLREIILAKFLHLMWSVVVVELLSFFVVTET 566
 Db 486 NKFRVNEVSWL-----SFCKDENKKFFMNEHVFVKLKWVFDLAILTMCYFSTBK 541
 QY 567 TFQKNRFFYKRSVMSKLSQIGIRQHLKRVQLRELSEAFVRQHRREARPALLTSRLRPIPK 626
 Db 542 AKEYQRIFFYKRNINMIMRLSIDLLAQ-NLKQVEKKEMRIFCESQ-NFAPGKLRLEPK 599
 QY 627 PDGLRPIVMYVVGARTFRRE-----KRAERLTSRVK---ALFSVLNVEARARPLGLG 677
 Db 600 GDTFRPIM-----TFNRKIPNQVGKFSQSRMTTNKKLQTAHMMKLNKSKMLKHSFG 650
 QY 678 ASVLGLDDIHRARWTFVLVRQAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIAS----- 731
 Db 651 FAVENYDDIMKRYENFVQKW-KQINSPKLYFVAMDIKCYDNDVCERVVNFLOKSDLMWK 709
 QY 732 -----IIRPONTYCVRRYAVVQAAHGVKAFKSHVSTLTLDLPYMRQFVAHLQET 783
 Db 710 EVFILANTFVLRKNNIIVERSNFRKLPKIQYFRYKQK-IGIDGSSYPTLPEILEDFND 768
 QY 784 SPLRDANVIRESSSLNEASSGLFDVFLRPMCHAVIRGKSVQCGIGIPQGSILSTLLCS 843
 Db 769 LNMKRTIIEAQEQRKPKPNDLLQVPLKICQNNYVTFNKQYKQKMGIPQGLCVPIYLLS 828
 QY 844 LCYGDMENKLFAGTRD-----GLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPEY 894
 Db 829 FYANLEENALQFLKESMDPEKPEINLMRLMTDYLMTTEKNAMLFIEKLYQSLGN 888
 QY 895 GCVVNLRTVNVFPVEDEALGTAFTVQ---MPAHGLFPWCGLLLTDLTRTLEVSQSYSSVAR 951
 Db 889 FFKFNMKKLTNFALNLQKIGCTNTTQDIDSINDDLFWHIGISIDIKTLNIQNI-NICK 947
 QY 952 TSIRASLTFRNGFKAGRNMRRLFGVRLKCHSLFDLOVNSLQVCTNVIYKILLQAVR 1011
 Db 948 EGILCTLVNVMQTNESILWLKKLKSFLMNNISFYFKSTINTKQFANITLSKLYIAAEK 1007
 QY 1012 FHACVLQLP-FHQ 1023
 Db 1008 YVACCOEKFRRPHE 1020

RESULT 36
 Q6CSS0
 ID Q6CSS0 PRELIMINARY; PRT; 861 AA.
 AC Q6CSS0;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Kluyveromyces lactis strain NRRL Y-1140 chromosome C of strain NRRL Y-1140 of Kluyveromyces lactis.
 GN ORFNames=KLLA0C1831g;
 OS Kluyveromyces lactis NRRL Y-1140.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=284590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Tallia E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boisarane A., Boyer J., Cattolico L., Confaniolero F., de Daruvar A.,

Db 563 QYHNILSSSSHLNCKSLVDKTKTIALQKGNILEVCRSQYDVV-----GSVKDARG 616
 QY 823 K--SVYOCQGIPOGSIITLLCSLCVGMENKLFAGI---RDGILLRLVDDFLAVTPEHL 877
 Db 617 NLHYKRGVQGFSLGSIFCDIILYSAMVHDCQFLWKSQDFLVRVLDLFLVTPD- 675
 QY 878 THAKTFLRLVRG--VPEYGCYVNLKTKTVNPFVDEALGGTAFAVQMPAHGLFPWCGLLL 935
 Db 676 SNIYQVHNILSGKILESYGAFVNDKTV---VNVQTTTKTS-----I 715
 QY 936 DRTLEVSQDYSYARTSIRASLTNRFKAGNMRKLFVGLRLKCHSLFLDLQVNSLQ 995
 Db 716 DFIGLEVNATDLSIKRNSGSISLV-TTNFRTFKTLVKYKTKPYQLNLEGFLDSCFGVLE 774
 QY 996 TVCTNIYKILLQAVRFHACVQLPFPHQVKNPTFFELRVISDTSASLCYSILK 1048
 Db 775 NVLENMGSLLRLVLRREF-----KTKFTSIVKYDTFHCYKFIK 811

RESULT 38

Q9GRCS PRELIMINARY; PRT; 895 AA.
 ID Q9GRCS
 AC Q9GRCS
 DT 01-MAR-2001 (TremBLrel. 16, Created)
 DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
 DE Telomerase reverse transcriptase.
 GN Name=PtERT;
 OS Paramesium caudatum.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
 CC Paramesium.
 OX NCBI_TaxID=5885;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KNZ-5 and KNZ-2;
 RX MEDLINE=21147925; PubMed=11250070; DOI=10.1016/S0378-1119(01)00337-7;
 RA Takenaka Y., Matsuura T., Haga N., Mitsui Y.;
 RT "Expression of telomerase reverse transcriptase and telomere
 elongation during sexual maturation in Paramesium caudatum";
 RL Gene 264:153-161(2001).
 DR EMBL; AB035309; BAB18587.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. . .; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
 DR InterPro; IPR000477; RVTse.
 DR Pfam; PF00078; RVT_1; 2.
 DR PRINTS; PR01365; TELOMERASERT.
 KW RNA-directed DNA polymerase; Transferase.
 SQ SEQUENCE 895 AA; 107086 MW; 130C0DB32FD11C76 CRC64;

Query Match 6.1%; Score 364; DB 2; Length 895;
 Best Local Similarity 22.2%; Pred. No. 7.3e-14;
 Matches 142; Conservative 113; Mismatches 274; Indels 110; Gaps 21;
 QY 448 LVQLRQSSPWQVYGFYRACLRLLVPPGLWGSRRNRRFLNTKFTISLGHAKLSLOE 507
 Db 277 LDHLYLNIHPQQTSLVNFLEIIPIDLFG-QQNLFITLDSDFITLRFEDQSVD 335
 QY 508 LTWKMVRDCAWLRSPGVCVPAAEHLR---REELAKFLHMLVYVVELLSFFIV 563
 Db 336 YIKMNVFEPVWLNK----YFNKKQRLLIIKRQNMPLMKFWQBIIPFLHNFYI 390
 QY 564 TETTFQKNRLFPYKSVNSKLSQIGIQHLKRVQLRELSEAEVQRHREARPALTSRLRF 623
 Db 391 TIRMKDDKFLFYRKEIWHILQLSLTS-LTKNPFEEISVNSIK-----TPYVGKLR 442
 QY 624 IPKPDGLRPVNMDDVVGARTFRREKRAERLTSRVKALFSLVLYNERARRPGLLGASVLG- 682

Db 443 VPKEGTFRPV-----TYNRKAKTSKSLNRK-LVDIKYILNRLIOPLGYSVFN 492
 QY 693 -----LDDIHRAMFTFLVRADOPPELVFKVDVTVGAVDTIPQDRLTEVIASIIKPO 736
 Db 493 PEVFSRLEEFKKW-----IKLQQ--PKTYITMDIOKCYDTIILQLKLLQFIESKOPS 544
 QY 737 NTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDL-----QPYMRQ--FVAHLQ 781
 Db 545 SIYAINKYHYSR-NNRMLKPSF-----SMKDLFILOLTCAPENKQLLKQGYIEHIQ 598
 QY 782 ETSPLRDVAVTQSSSLNEASGLFDVPL-----RFMC-HHAVIRKSVYQCOGIPGSL 837
 Db 599 KN--KOTIIINQGFQ-----NSVTFSEFLNSIKNICQNNIVQFENRYFRQTLGIPQGLNI 651
 QY 838 STLCSLCYGMENKLPAGIRRDGILLRLVDDFLAVTPEHLTHAKTFLRLVRGVPYGCV 897
 Db 652 SGILCSFYLANLEOKLTNKLIGDITLIMRLTDDYCCFLAFSQSSIKILANNFQIEQOIR 711
 QY 898 VNLKRTVNVFVEDEALGGTAFAVQMPAHGLFPWCGLLDDTRTLEVSQDYSYARTSIRAS 957
 Db 712 LNHDKTQHNIERSDR-----YFKWIGKIIDIETLTLPKPAFYLESDTKFQVQ 757
 QY 958 LTFNRGFKAGNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACV 1017
 Db 758 INVNLPTKVTYIKSKLSLILNQFKFFNSKLNLDKPTMK-----VL 801
 QY 1018 QLPHQVQVKNPTFFELRVISDTSASLCYSILKAKNAGMSL 1056
 Db 802 KIFVHSLGLVKLISFLKRL-----KYNYGASKLRNQKSI 835

RESULT 39
 TERT_TERTH STANDARD; PRT; 1117 AA.
 ID AC 077448;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
 subunit) (Telomerase subunit P133).
 GN Name=TERT;
 OS Tetrahymena thermophila.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
 CC Tetrahymenina; Tetrahymenidae; Tetrahymena.
 OX NCBI_TaxID=5911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B7;
 RX MEDLINE=98337940; PubMed=9671703; DOI=10.1073/pnas.95.15.8479;
 RA Bryan T.M., Sperger J.M., Chapman K.B., Cech T.R.;
 RT "Telomerase reverse transcriptase genes identified in Tetrahymena
 thermophila and Oxytricha trifallax";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8479-8484 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98337941; PubMed=9671704; DOI=10.1073/pnas.95.15.8485;
 RA Collins K., Gandhi L.;
 RT "The reverse transcriptase component of the Tetrahymena telomerase
 ribonucleoprotein complex";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8485-8490 (1998).
 CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
 the replication of chromosome termini in most eukaryotes. It
 elongates telomeres. It is a reverse transcriptase that adds
 simple sequence repeats to chromosome ends by copying a template
 sequence within the RNA component of the enzyme.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the reverse transcriptase family.
 CC Telomerase subfamily.
 CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -

Db 405 KLIPKRSFRV/CVPIKRSKLLNKKLELDLTKLEKCR-----EFERYRKE 449
 QY 674 GL-----LGASVLGLDDIHRARWTFV-----LRVRAQD-----PPPELVFKVD 712
 Db 450 VLSPVGQILRLKLSKLRDYESYRASVHSSSDVAEKISDYRDSLLTRGCEIPKILKFD 509
 QY 713 VTGADYTPDRLTEVIASIKPON---TYCVRRYAVQKAAHVRKAFKSHVSTLDTL 769
 Db 510 MKECYDRLSQPVLMKKLEELFENQDNKTSYYVRYA--QLDASHKLKK-----VKTITDT 562
 QY 770 QYMEQFVA---HLQETSPLRD---AVVIEQSSSINEASSGLFDVFLRPMCHHVR-IRG 822
 Db 563 QYHNILNLSHSHLNSCKSLVDKTKTIALQKNILEVRSQYDVV-----GSVDARG 616
 QY 823 K--SYVQCQIGPQGSILSTLLCSLCYGDMEKLFAGI---RDGGLLLRLVDVFLVTPHL 877
 Db 617 NLHLKRGKGVFGFSLISFCDILYSAMVHDFQFLMKSKQDFLFLVRLVDDFLVTPD- 675
 QY 878 THAKTFLRLVRG--VPEYGCVVNLRKTVNPFVDEALGGTAFVQMAHGLFPWCGLL 935
 Db 676 SNIYQVHNILSGKILESYGAFVNDKTVW-----VNOQTTPKSIDFVGLV 722
 QY 936 DRTLEQSDSYSYARTSIRASLTFRNGFKAGRNMRKLFGLVRLKCHSLFLDLQVNSIQ 995
 Db 723 NTDLISK-----RNGSISLV-TTNFRFTKLVKYLKTPYQNLNLEGFLDCSFGVLE 774
 QY 996 TVCTNIYKILLQAYRFHACVILQLPFHQQVWKNPTFFLRVISTDASLCYSILK 1048
 Db 775 NVLENMGSLLRLVLEF-----KTKFTSIVKYDTHCYKFK 811

RESULT 41

TERT YEAST
 ID TERT YEAST STANDARD; PRT; 884 AA.
 AC Q06153.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit).
 DE subunit).
 CN Name=EST2; OrderedLocusNames=YLR318W; ORFNames=L8543.12;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RX MEDLINE=97313267; PubMed=9169871;
 RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansoorge W.,
 RA Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,
 RA Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,
 RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,
 RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,
 RA Mueller-Auer S., Neutwich U., Obermaier B., Piravandi E., Pohl T.M.,
 RA Portetle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
 RA Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,
 RA Vierendeels F., Voet M., Volckaert G., Voss H., Wamburt R., Wedler E.,
 RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hohnsels J.D.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
 RL Nature 387:87-90(1997).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=97274210; PubMed=9110970; DOI=10.1126/science.276.5312.561;
 RA Lingner J., Hughes T.R., Shevchenko A., Mann M., Lundblad V.,
 RA Cech T.R.;
 RT "Reverse transcriptase motifs in the catalytic subunit of
 telomerase.";
 RL Science 276:561-567(1997).
 CC !- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
 the replication of chromosome termini in most eukaryotes. It
 elongates telomeres. It is a reverse transcriptase that adds

CC simple sequence repeats to chromosome ends by copying a template
 CC sequence within the RNA component of the enzyme.
 CC !- SUBCELLULAR LOCATION: Nuclear.
 CC !- MISCELLANEOUS: Deletion causes telomere shortening and senescence.
 CC !- SIMILARITY: Belongs to the reverse transcriptase family.
 CC Telomerase subfamily.
 CC !- SIMILARITY: Contains 1 reverse transcriptase domain.
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U20618; AAB64520.1; -;
 CC PIR; S53396; S53396.
 CC Germonline; 142382; -;
 CC SGD; S000004310; EST2.
 CC GO; GO:0005730; C:nucleolus; IDA.
 CC GO; GO:0005697; C:telomerase holoenzyme complex; IDA.
 CC InterPro; IPR000477; RVTse.
 CC Pfam; PF00078; RVT; 1.
 CC PRINTS; PR01365; TELOMERASERT.
 CC PROSITE; PS50878; RT POL; 1.
 CC DNA-binding; Nuclear protein; RNA-directed DNA polymerase; Telomere;
 KW Transference. 422 725 Reverse transcriptase.
 FT DOMAIN 422 725 Reverse transcriptase.
 SQ SEQUENCE 884 AA; 102663 MW; 788334BB49592340 CRC64;
 Query Match 6.0%; Score 356.5; DB 1; Length 884;
 Best Local Similarity 22.1%; Pred. No. 2.1e-13;
 Matches 167; Conservative 127; Mismatches 309; Indels 151; Gaps 28;
 QY 329 KHFYSSGDKBQLRPS--FLLSLRPSLTGARRLV---ETIFLGSRPWMPGTFRRLPLRP 383
 Db 185 KQFLH----KLNINSSSPFPYSKILPSSSIKLTDLREALF-----PTNLVKIP 230
 QY 384 QRYQWMPRLFLE-LLGNHAQCPYGVLLKTHCPRAVTPAAGVCAREKYPQGSVAAPERED 442
 Db 231 QRLKVRINLTQLKLRHKLRLNYVILNSICP-----PLEGTVL----- 269
 QY 443 TDPRLVQLLRQHSPPWQVGVFVRACLRLVPPGLWGRHNERFLRNTKRFISLGKHA 502
 Db 270 ----DLSHLSQ-SPKERVLFIIIVILQKLPQEMFGSKKNGKIKNLNLLSPLNGY 324
 QY 503 LSLQELTWKMSVRDCAMLRSPGVGCVPAAEHRLR--EEILAKFLHLMVSVVVELLRSP 560
 Db 325 LPFDSLLKLRKDFRWL---FISDIWFTKHNPENLNQALCFISLWFRQLIPKIIQTF 380
 QY 561 FYVTETFPQKRLFFYKRSVWSKLSQIGIROHLKRVQLRELSEAV-RQREARPAALT- 618
 Db 381 FYCTEIS-STVTIVYFRHDTNKLITPFIFYFTY----LVENNVCNHNSTYLSNFH 435
 QY 619 SRLRFPKPGDLRPLVNDYVYV-----GARTFRREKRAERLTSRVKALFVNLVERARR 672
 Db 436 SKMRLPKS-----NNEFRILAIIPCADEEBEFTIYKHNKNAIQTKILEVLRNKR 489
 QY 673 PGLLGASVLGLDDIHRARWTFVLVRV--RAQPPPELVFKVDVDTGAYDTIPQDRLETVIA 730
 Db 490 PTFP-TKIYSPQTADRIKEFKQRLKKFNKNVLPFLYPMKDFKVSICYDSIPRMECMRLK 548
 QY 731 SIIPQNTYCVRRYAVVQKAAHVRKAFKSHVSTLTDLPYMQQFVAHLQETSPLRDV 790
 Db 549 DALKNENGFFVRYSQYFFN--TNTGVKLIF-NVNVASRVKPEY-----EL 589
 QY 791 VIEQSSSINEASSGLFDVFLRPMCHHVRIRGKSVQCGIPQGSILSTLLCSLCYGD- 849
 Db 590 YIDNVRTVHLNQNQVINNVEMEIPKALWVEDKCIREDGLPQGSLSAPIDVLDVDDL 649
 QY 850 --ENKLFAGIRRDGILLRLVDVDFLLVTPHLLTHAKTFLRLTVRGVPEYGCVVNLRKTV-VN 906

DF	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Telomerase reverse transcriptase (TERT) (Fragment).
GN	Name=TERT;
OS	Felis silvestris catus (Cat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX	NCBI_TaxID=9685;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22692837; PubMed=12808208;
RA	Yazawa M., Okuda M., Uyama R., Nakagawa T., Kanaya N., Nishimura R.,
RA	Sasaki N., Masuda K., Ohno K.; Tsujimoto H.;
RT	"Molecular cloning of the feline telomerase reverse transcriptase
RT	(TERT) gene and its expression in cell lines and normal tissues.";
RL	J. Vet. Med. Sci. 65:573-577(2003).
DR	ENBL; AB094677; BAC78444.1; -
DR	GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW	RNA-directed DNA polymerase.
FT	NON_TER 1
FT	NON_TER 79
FT	NON_TER 79
SEQ	SEQUENCE 79 AA; 9086 MW; BSADCD207226308B CRC64;
Query Match 5.7%; Score 339; DB 2; Length 79;	
Best Local Similarity 81.0%; Pred. No. 1.2e-13;	
Matches 64; Conservative 6; Mismatches 9; Indels 0; Gaps 0;	
QY	627 PDGLRPIVNDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLIGASVLGDDI 686
Dd	1 PSGLRPIVNDYVVGARTFRRDKKKRHLTSSQKNLFGLVLYERARRPSLLIGASVLGMDDI 60
: : : : : : : : : :	
QY	687 HRAWRTFVLVRQAODPPPE 705
Dd	1 HRVRSFVLVRQAODPPAPQ 79
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RESULT 45	
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ID	Q76K45
AC	AQ76K45;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Telomerase reverse transcriptase (TERT) (Fragment).
GN	Name=TERT;
OS	Canis familiaris (Dog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX	NCBI_TaxID=9615;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22976522; PubMed=14620776;
RA	Yazawa M., Okuda M., Kanaya N., Hong S.H., Takahashi T., Ohashi E.,
RA	Nakagawa T., Nishimura R., Sasaki N., Masuda K., Ohno K.,
RA	Tsujimoto H.;
RT	"Molecular cloning of the canine telomerase reverse transcriptase gene
RT	and its expression in neoplastic and non-neoplastic cells.";
RL	Am. J. Vet. Res. 64:1395-1400(2003).
DR	ENBL; AB094677; BAD06179.1; -
DR	GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW	RNA-directed DNA polymerase.
FT	NON_TER 1
FT	NON_TER 79
FT	NON_TER 79
SEQ	SEQUENCE 79 AA; 9119 MW; 3C180172A78D4DBF CRC64;
Query Match 5.7%; Score 338; DB 2; Length 79;	
Best Local Similarity 77.2%; Pred. No. 1.3e-13;	
Matches 61; Conservative 12; Mismatches 6; Indels 0; Gaps 0;	
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Dd	1 PSGLRPIVNDYVVGARTFRRDKKKRHLTSSQKNLFGLVLYERARRPSLLIGASVLGMDDI 60
: : : : : : : : :	
QY	687 HRAWRTFVLVRQAODPPPE 705


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DR EMBL; CR380947; CAG57699.1; --
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcripts...; IEA.
DR InterPro; IPR000477; RVase.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RV1_1; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 851 AA; 98673 MW; CCB0F339CEE446BD CRC64;

Query Match
Best Local Similarity 5.2%; Score 309; DB 2; Length 851;
Matches 136; Conservative 117; Mismatches 235; Indels 156; Gaps 25;

QY 464 FVRACLRRLVPPGLMGRSRRNRFLRNTKFKTSLGKHAKLSQELTWKMSVDRCAWLRS 523
D 464 FVRACLRRLVPPGLMGRSRRNRFLRNTKFKTSLGKHAKLSQELTWKMSVDRCAWLRS 523
D 266 FIVILEKLIQLGSRKNSFVLSKISQLKPLNGKINVEFTKLNVNA---VRY 322
QY 524 PGVGVCPAAHRLREILAKFLHMLSVVYVLLRSFFVYVTTTFQKRLFFYRKSVMSK 583
D 524 PGVGVCPAAHRLREILAKFLHMLSVVYVLLRSFFVYVTTTFQKRLFFYRKSVMSK 583
D 323 LSIDPIGQKQSMR-LYLTCCVNYLLSKLPSLLKSFYCTEVS-SYSKILYFRNDEWNS 380
QY 584 LOSIGIRQHLKRVQLREISEAEVQHRARPALLTSR-----LRPIKPDGLRPVNDY 638
D 584 LOSIGIRQHLKRVQLREISEAEVQHRARPALLTSR-----LRPIKPDGLRPVNDY 638
D 381 ISTPFLKEYLDKYLQ-----NTHCNSHFYSMESQFNHCNFRLLPKK----- 422
QY 639 VVGARTF-----REKRAERL-----TSRVKALFSLNYERARRPGL--LGASVLGL 683
D 639 VVGARTF-----REKRAERL-----TSRVKALFSLNYERARRPGL--LGASVLGL 683
D 423 --GNNEFRVIGIPYKGNNAEELQYKQNTKIVTVTKLILDYLRKSRQTTQKLLSAMQI 480
QY 684 DD-----IHRWRTFVLVRAQDPPPELVFVVDVTGAYDTIPQDLTEVIAI1K- 734
D 684 DD-----IHRWRTFVLVRAQDPPPELVFVVDVTGAYDTIPQDLTEVIAI1K- 734
D 481 SDHICQYKCHLSKGYI-----PKLPYKFDHNCYDSIPAKAKSVLNSLINN 530
QY 735 -PQNYCYVRYAV-----QKAAGHVTKAFKSHVSTLTDLPQYRQFVAHLQETS 784
D 735 -PQNYCYVRYAV-----QKAAGHVTKAFKSHVSTLTDLPQYRQFVAHLQETS 784
D 531 COYEEFYVRSVTILNTQNEVRYDTIVNGHIN----- 562
QY 785 PLRD--AVVEIQSSLINEASSGLFDVFLPMCHHVRIRKSVVOCQIPQSGILSLTLC 843
D 785 PLRD--AVVEIQSSLINEASSGLFDVFLPMCHHVRIRKSVVOCQIPQSGILSLTLC 843
D 563 -IRDFEIVNDSTTTFLTKEDIMDLIEFEMEMTSIRLPDKYLRKXGLFQGLSATIVD 621
QY 844 LCYGDV--ENKLFAGI-RDGLLLRLVDLFLVTPH---LTHAKTFLRLVGRVPEYGV 897
D 844 LCYGDV--ENKLFAGI-RDGLLLRLVDLFLVTPH---LTHAKTFLRLVGRVPEYGV 897
D 622 ILYDMLKRNKRVFKDILNNDGLVLRHADDFLISPSKEIISVRLKIN---EGFTEYNAQ 678
QY 898 VNLRTVNVFVEDEALGCTAFVQMPAHGLPWCGLLDLTRLFVOSDYSSVARTSI--- 954
D 898 VNLRTVNVFVEDEALGCTAFVQMPAHGLPWCGLLDLTRLFVOSDYSSVARTSI--- 954
D 679 VNRKIVFS---ESDNIAITA-----IPFCGVEIIPRTLEVIFKFSAMNETDISD 726
QY 955 -----RASLTFRNGFKAG-----RNRRKLFGLVRLKCHSLFLDLQVNSLQ 995
D 955 -----RASLTFRNGFKAG-----RNRRKLFGLVRLKCHSLFLDLQVNSLQ 995
D 727 EGNIVSKAVLPKMLNVTGMNANLNSITMLKQVENATINVIILNSHIATSVSFS 786
QY 996 TVCTNIYKILLIQAQYRFHACVQLQLPFPQVQVKNPTFFLRVSDT 1039
D 996 TVCTNIYKILLIQAQYRFHACVQLQLPFPQVQVKNPTFFLRVSDT 1039
D 787 SPVNELYNICLLSSRN-----LNLNHRDLQR-----FLTSIKKT 821

RESULT 48
Q57EQ2
ID Q67EQ2 PRELIMINARY; PRT; 261 AA.
AC Q67EQ2;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Telomerase reverse transcriptase catalytic subunit (Fragment).
GN Name=TERT;
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
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OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root tips;
RA Sykorova E.;
RT "Comparison of protein subunits of plant telomerases.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY363163; AAR11376.1; -
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 261
SQ SEQUENCE 261 AA; 30247 MW; 70DC6AC97D2D0BFD CRC64;

Query Match
Best Local Similarity 4.2%; Score 250.5; DB 2; Length 261;
Matches 69; Conservative 52; Mismatches 126; Indels 29; Gaps 4;

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D 455 HSSPQVYGVFVACLRRLVPPGLMGRSRRNRFLRNTKFKTSLGKHAKLSQELTWKMSV 514
D 3 YSTHDQVSVFVAVLTRIIPQPLGNPSSKRALRMNIWKFIIRRPETFOVTDICELKA 62
QY 515 RDCAWLRSPGVGCVPA-----EHLREEILAKFLHMLSVVYVLLRSFFY 562
D 515 RDCAWLRSPGVGCVPA-----EHLREEILAKFLHMLSVVYVLLRSFFY 562
D 63 PEYLSKIGFTGFCFCVLLREETGLSNGMEEQKQNLHCHWISWLFSDIVPLINTLY 122
QY 563 VTETTFQKRLFFYRKSVMSKLSQISGIRQHLKRVQLREISEAEVQHRARPALLTSRL 622
D 563 VTETTFQKRLFFYRKSVMSKLSQISGIRQHLKRVQLREISEAEVQHRARPALLTSRL 622
D 123 VTERETKYDYFYPKSVNRNLTSNTVAS-LNAQSFKLCGT---SRAIKHLYESSVR 178
QY 623 FIPKPDGLRPVNDYVVGARTFVRKRAERLTSRVKALFSLNYERARRPGLLGASVLG 682
D 623 FIPKPDGLRPVNDYVVGARTFVRKRAERLTSRVKALFSLNYERARRPGLLGASVLG 682
D 179 FLPAKDIRPLVNF-----KAQSKDGLTNKCHLVIKKLRODNPMSFGSSAFD 225
QY 683 LDDIHRWRTFVLVRAQDPPPELVFVVDVTGAYD 718
D 683 LDDIHRWRTFVLVRAQDPPPELVFVVDVTGAYD 718
D 226 YDGVTKNLSSFMSSVYRGQLKESKIYVVADVSKAFD 261

RESULT 49
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AC Q9ROB3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE Telomerase catalytic subunit (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Drissi R., Cleveland J.L.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090439; AAD54013.1; -
FT NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 6479 MW; 41473425E44BDA9C CRC64;

Query Match
Best Local Similarity 3.4%; Score 200; DB 2; Length 52;
Matches 37; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 567 TFQKRLFFYRKSVMSKLSQISGIRQHLKRVQLREISEAEVQHR 611
D 567 TFQKRLFFYRKSVMSKLSQISGIRQHLKRVQLREISEAEVQHR 611
D 1 TFQKRLFFYRKSVMSKLSQISGIRQHLKRVQLREISEAEVQHR 45

RESULT 50
Q6W8T6
ID Q6W8T6 PRELIMINARY; PRT; 260 AA.
AC Q6W8T6;
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Search completed: August 5, 2005, 14:11:06
Job time : 205 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 5, 2005, 14:11:13 ; Search time 173 Seconds
(without alignments)
2554.511 Million cell updates/sec

Title: US-10-053-758-225
Perfect score: 5961
Sequence: 1 MPAPRCRAVRSLLRSHYRE.....TALSAANPALPDSFKTILD 1132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters: 1752860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5961	100.0	1132	9 US-09-990-080-2	Sequence 2, Appli
2	5961	100.0	1132	9 US-09-749-728B-31	Sequence 31, Appl
3	5961	100.0	1132	9 US-09-843-676-225	Sequence 225, App
4	5961	100.0	1132	9 US-09-953-052-2	Sequence 2, Appli
5	5961	100.0	1132	11 US-09-788-110A-23	Sequence 23, Appl
6	5961	100.0	1132	14 US-10-053-758-225	Sequence 225, App
7	5961	100.0	1132	14 US-10-208-243-2	Sequence 2, Appli
8	5961	100.0	1132	14 US-10-054-295-225	Sequence 225, App
9	5961	100.0	1132	14 US-10-054-611-225	Sequence 225, App
10	5961	100.0	1132	14 US-10-105-963-2	Sequence 2, Appli
11	5961	100.0	1132	14 US-10-044-692-2	Sequence 2, Appli

12	5961	100.0	1132	14	US-10-044-539-2	Sequence 2, Appli
13	5961	100.0	1132	14	US-10-295-681-57	Sequence 57, Appli
14	5961	100.0	1132	15	US-10-325-810-2	Sequence 2, Appli
15	5961	100.0	1132	15	US-10-388-578-2	Sequence 2, Appli
16	5961	100.0	1132	16	US-10-602-441-2	Sequence 2, Appli
17	5961	100.0	1132	16	US-10-389-431-2	Sequence 2, Appli
18	5961	100.0	1132	16	US-10-877-124-2	Sequence 2, Appli
19	5961	100.0	1132	16	US-10-877-022-2	Sequence 2, Appli
20	5961	100.0	1132	16	US-10-862-698-3	Sequence 3, Appli
21	5961	100.0	1132	17	US-10-831-266-4	Sequence 4, Appli
22	5961	100.0	1132	17	US-10-492-034-2	Sequence 2, Appli
23	5961	100.0	1132	17	US-10-831-267-4	Sequence 2, Appli
24	5961	100.0	1132	17	US-10-877-146-2	Sequence 4, Appli
25	5961	100.0	1132	17	US-10-917-853-2	Sequence 2, Appli
26	5961	100.0	1132	17	US-10-918-739-2	Sequence 2, Appli
27	5961	100.0	1132	17	US-10-637-443-2	Sequence 2, Appli
28	5961	100.0	1132	17	US-10-490-143A-19	Sequence 19, Appli
29	5961	100.0	1132	17	US-10-794-514A-3	Sequence 3, Appli
30	5961	100.0	1132	18	US-10-143-536-2	Sequence 2, Appli
31	5961	100.0	1154	14	US-10-044-692-323	Sequence 323, App
32	5961	100.0	1154	14	US-10-044-539-323	Sequence 323, App
33	5961	100.0	1154	15	US-10-325-810-611	Sequence 611, App
34	5961	100.0	1154	16	US-10-877-124-611	Sequence 611, App
35	5961	100.0	1154	16	US-10-877-022-611	Sequence 611, App
36	5961	100.0	1154	17	US-10-877-146-611	Sequence 611, App
37	5961	100.0	1189	14	US-10-044-539-325	Sequence 325, App
38	5961	100.0	1189	14	US-10-044-539-325	Sequence 325, App
39	5961	100.0	1189	15	US-10-325-810-613	Sequence 613, App
40	5961	100.0	1189	16	US-10-877-124-613	Sequence 613, App
41	5961	100.0	1189	16	US-10-877-022-613	Sequence 613, App
42	5961	100.0	1189	17	US-10-877-146-613	Sequence 613, App
43	5961	100.0	1200	14	US-10-044-692-324	Sequence 324, App
44	5961	100.0	1200	14	US-10-044-539-324	Sequence 324, App
45	5961	100.0	1200	15	US-10-325-810-612	Sequence 612, App

ALIGNMENTS

RESULT 1

US-09-990-080-2
; Sequence 2, Application US/09990080
; Patent No. US20020102686A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Genon Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 018/258C
; CURRENT APPLICATION NUMBER: US/09/990,080
; CURRENT FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 09/052,864
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-990-080-2

Query Match 100.0%; Score 5961; DB 9; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPAPRCRAVRSLLRSHYREVLPATFVRRILGPGQWRILVQRGDPAAFPALVAQCILVCVFW 60
Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRRILGPGQWRILVQRGDPAAFPALVAQCILVCVFW 60
Qy 61 DARPPAPSPROVSCLEKELVARVLORLCERGAKNVLAFFGALLDGGRGPEAFTTSVR 120
Db 61 DARPPAPSPROVSCLEKELVARVLORLCERGAKNVLAFFGALLDGGRGPEAFTTSVR 120
Qy 121 SYLENTVTDALRGSGAWGLLRLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

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121 SYLNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYVQCGPLYQLGA 180
181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKPRR 240
181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKPRR 240
241 GAAPEPERTVQGGSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 300
241 GAAPEPERTVQGGSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 300
301 ROHAGPSTSRPRPMDTPCPVYAEKTHLYSSGDKQELRPSFLSSLPSTGARRL 360
301 ROHAGPSTSRPRPMDTPCPVYAEKTHLYSSGDKQELRPSFLSSLPSTGARRL 360
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361 VETIFLGSRRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
421 PAAGVCAREKPGQGSVAAPBEEDTDPRLVQLLRQHSPPWQYGVFVRACLRRLVPPGLWGS 480
421 PAAGVCAREKPGQGSVAAPBEEDTDPRLVQLLRQHSPPWQYGVFVRACLRRLVPPGLWGS 480
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661 LPSVLNTERARRPGLGASVLGLDDIHRAWTFVLRVRAQDPPPELVKVDVTVGAYDTI 720
661 LPSVLNTERARRPGLGASVLGLDDIHRAWTFVLRVRAQDPPPELVKVDVTVGAYDTI 720
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781 QETSPRLDAVIEQSSSLNEASGLFDVFLRFPMCHHAVIRKGSYVQCQGIPOQSILSTL 840
781 QETSPRLDAVIEQSSSLNEASGLFDVFLRFPMCHHAVIRKGSYVQCQGIPOQSILSTL 840
841 LCSLCYGMENKLPAGIRDDGLLRLVDDFLLVTPHLTHAKTFLRTLVRGVEYGCVVNL 900
841 LCSLCYGMENKLPAGIRDDGLLRLVDDFLLVTPHLTHAKTFLRTLVRGVEYGCVVNL 900
901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLDTTLEVSQSDYSSYARTSIRASITF 960
901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLDTTLEVSQSDYSSYARTSIRASITF 960
961 NRGFKAGNMRKLPGLVRLKCHSLFDLQVNSLQTVCTNLYKILLQAYRHFACVLQLP 1020
961 NRGFKAGNMRKLPGLVRLKCHSLFDLQVNSLQTVCTNLYKILLQAYRHFACVLQLP 1020
1021 FHQQWKNMPTFFLRVISDTSIACYSLKAKNAGMSLGAGAPLPSEAVOMLCHQAPLL 1080
1021 FHQQWKNMPTFFLRVISDTSIACYSLKAKNAGMSLGAGAPLPSEAVOMLCHQAPLL 1080
1081 KLTRHRVTYVPLGLSLRTAQQLSRKLPGLTTLTALAAANPALPSDFKTIILD 1132
1081 KLTRHRVTYVPLGLSLRTAQQLSRKLPGLTTLTALAAANPALPSDFKTIILD 1132

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RESULT 2

US-09-749-728B-31
; Sequence 31, Application US/09749728B
; Patent No. US20020142457A1
; GENERAL INFORMATION:

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; APPLICANT: Umezawa, Akihiro
; APPLICANT: Hata, Jun-Ichi
; APPLICANT: Fukuda, Keiichi
; APPLICANT: Ogawa, Satoshi
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Gojo, Satoshi
; APPLICANT: Yamada, Yoji
; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMY
; FILE REFERENCE: 00766.000043
; CURRENT APPLICATION NUMBER: US/09/749,728B
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: H11-372826
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: PCT-JP00-01148
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT-JP00-07741
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver.2.0
; SEQ ID NO 31
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-749-728B-31

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Query Match 100.0%; Score 5961; DB 9; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MPRAPRCRAVRSLLRSHYREVLPPLATEFVRLPGQWMLVQRGDPAAPALVAOCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPPLATEFVRLPGQWMLVQRGDPAAPALVAOCLVCVPW 60
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Db 61 DARPPPPAAPSFROVSCIKELVARVLQRLCERGANVLAFGFPALLDARGGPEAFTTSVR 120
Qy 121 SYLPNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYVQCGPLYQLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYVQCGPLYQLGA 180
Qy 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKPRR 240
Db 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKPRR 240
Qy 241 GAAPEPERTVQGGSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 300
Db 241 GAAPEPERTVQGGSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 300
Qy 301 ROHAGPSTSRPRPMDTPCPVYAEKTHLYSSGDKQELRPSFLSSLPSTGARRL 360
Db 301 ROHAGPSTSRPRPMDTPCPVYAEKTHLYSSGDKQELRPSFLSSLPSTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQGSVAAPBEEDTDPRLVQLLRQHSPPWQYGVFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQGSVAAPBEEDTDPRLVQLLRQHSPPWQYGVFVRACLRRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKKFISLGKHAKLISLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREI 540
Db 481 RHNERRFLRNTKKFISLGKHAKLISLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREI 540
Qy 541 LAKFLHLMWSVYVVELLRSFFYVTTTFOKNRLLFFYKSVMSKLSQSIGIRHLKRVQURE 600
Db 541 LAKFLHLMWSVYVVELLRSFFYVTTTFOKNRLLFFYKSVMSKLSQSIGIRHLKRVQURE 600
Qy 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMMDYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMMDYVVGARTFRREKRAERLTSRVKA 660

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661 LFSVLNYERARRPGLGASVGLDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
661 LFSVLNYERARRPGLGASVGLDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
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781 QETSPLRDVAVIEQSSSLEASSGLFDVFLRFMCHHAVIRGKSYVQCQIGIQQSILSTL 840
781 QETSPLRDVAVIEQSSSLEASSGLFDVFLRFMCHHAVIRGKSYVQCQIGIQQSILSTL 840
841 LCSLCYGDMMENKLFAGIRDDGLLLRLVDDFLVTPHLLTHAKTFLRLVGRVPEYGCVMNL 900
841 LCSLCYGDMMENKLFAGIRDDGLLLRLVDDFLVTPHLLTHAKTFLRLVGRVPEYGCVMNL 900
901 RKTUVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQDYSSYARTSIRASLTF 960
901 RKTUVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQDYSSYARTSIRASLTF 960
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961 NRGFKAGRNMRKLFVLRKCHSLFDLQVNSLQVCTNIVKILLQAYRHACVQLQP 1020
1021 FHOQVKNPTFFLRVISTDTSYLSYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
1021 FHOQVKNPTFFLRVISTDTSYLSYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
1081 KLTRHRVTVPVLLGSLRTAQTOLSRKLPCTTITALEAANPALPSDFKTILD 1132
1081 KLTRHRVTVPVLLGSLRTAQTOLSRKLPCTTITALEAANPALPSDFKTILD 1132

RESULT 3

US-09-843-676-225
; Sequence 225, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US/08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US/08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US/08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-09-843-676-225
Query Match 100.0%; Score 5961; DB 9; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVORGDPAAFRALVAQCLVCPW 60
QY 61 DARPPAAPSPFQVSCLEKELVARVQLRCERCAGKNVLAFFGALLDGCARGGPEAFTTSVR 120
DB 61 DARPPAAPSPFQVSCLEKELVARVQLRCERCAGKNVLAFFGALLDGCARGGPEAFTTSVR 120
QY 121 SYLNTVNTDALRGSGANGLLLRVGGDVLVHLLARCALFVLVAPSCAYVCCPPLYQLGA 180
DB 121 SYLNTVNTDALRGSGANGLLLRVGGDVLVHLLARCALFVLVAPSCAYVCCPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLGRCERAWNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRPR 240
DB 181 ATQARPPPHASGPRRLGRCERAWNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRPR 240
QY 241 GAAPERTPVQGSWAHPGTRGPDSDRGFCVVSAPAEAEATSELEGALSGTRHSHPSVG 300
DB 241 GAAPERTPVQGSWAHPGTRGPDSDRGFCVVSAPAEAEATSELEGALSGTRHSHPSVG 300
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DB 301 RQHHAGPSTSRPPRPWDTPCPVYAEYKHFYSSGDKQLRPSFLLSLRSLTGARL 360
QY 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHACQPIGVLLKTHCPRAAVT 420
DB 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHACQPIGVLLKTHCPRAAVT 420
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DB 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSSPMQVYGFVRACLRLVPPGLWGS 480
QY 481 RHNERFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHLRREI 540
DB 481 RHNERFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHLRREI 540
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DB 541 LAKFLHLMWSVYVVELLSFFVTETTFQKRLFFYRKSVMKLSQISIGIRHKLKRVQRE 600
QY 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNYERARRPGLLGASVGLDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNYERARRPGLLGASVGLDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PDRLTEVIASIIKPONTYCVRRYAVVQAAHGHVKAFAKSHVSTLTDLPYMRQFVAHL 780
DB 721 PDRLTEVIASIIKPONTYCVRRYAVVQAAHGHVKAFAKSHVSTLTDLPYMRQFVAHL 780
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Db 781 QETSLRDAVVEQSSSLNEASSGLFVFLRFMCHAVIRGKSYVQCQGIPOQSILSTL 840
Qy 841 LCSICYGDMENKLFAGIRRDGELLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
Db 841 LCSICYGDMENKLFAGIRRDGELLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
Qy 901 RKTWNFFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSSYARTSTRASLTFF 960
Db 901 RKTWNFFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSSYARTSTRASLTFF 960
Qy 961 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIIKYILLQAYRPHACVLQLP 1020
Db 961 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIIKYILLQAYRPHACVLQLP 1020
Qy 1021 FHQQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPCTTLTALAAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPCTTLTALAAAANPALPSDFKTILD 1132

RESULT 4

US-09-953-052-2
; Sequence 2, Application US/09953052
; Patent No. US20020173476A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Antisense Compositions for Detecting and
; Inhibiting Telomerase Reverse Transcriptase
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,052
; FILING DATE: 14-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/052,919
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/974,549
; FILING DATE: 19-NOV-1997

; APPLICATION NUMBER: US 08/974,584
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 015389-00360005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-953-052-2

Query Match 100.0%; Score 5961; DB 9; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRLGPGQWRLVQRGDPAAPRALVAOCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRLGPGQWRLVQRGDPAAPRALVAOCLVCVPW 60

Qy 61 DARPPPAAPSFQVSCIKELVARVLQRLCERGAKNVLAFGFALLDARGGPEAFTTSVR 120
Db 61 DARPPPAAPSFQVSCIKELVARVLQRLCERGAKNVLAFGFALLDARGGPEAFTTSVR 120

Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPLYQLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPLYQLGA 180

Qy 181 ATQARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAPGARRRGGSASRSLPKRPRR 240
Db 181 ATQARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAPGARRRGGSASRSLPKRPRR 240

Qy 241 GAAPEPERTVPGQSWAHPGRTGRGSDRGFCVSPARPAEATSEALSTRHSHPSVG 300
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Db 301 ROHHAGPSTSRPPRWDTPCPPVYAEKHFYSSGDKCOLRPSFLLSSLRPSLTGARRL 360

Qy 361 VETIFLGSRPWMPGTTPRRLPRLPORYWQMRPLFLELLGNHAQCYPYVLLKTHCPLRAVT 420
Db 361 VETIFLGSRPWMPGTTPRRLPRLPORYWQMRPLFLELLGNHAQCYPYVLLKTHCPLRAVT 420

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Db 421 PAAGVCAREKPGQSVAAPEEEDTPRLVOLLROHSSFPWQYGVFVACLRRLVPPGLWGS 480

Qy 481 RHNERRFLRNTKFPISLGKHAKLSQLBTWQMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERRFLRNTKFPISLGKHAKLSQLBTWQMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy 541 LAKFLHLMSSVYVVELLSRFFYVTTTTFQKNRLFFYRKSVMKLSQSIGIRQHLKRVQURE 600
Db 541 LAKFLHLMSSVYVVELLSRFFYVTTTTFQKNRLFFYRKSVMKLSQSIGIRQHLKRVQURE 600

Qy 601 LSEAEVQHREARPAALLTSRLRFPKDDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVQHREARPAALLTSRLRFPKDDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 660

Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720

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DB 781 QETSPLRDVAVTEQSSSINEASSGLFDVFLRPMCHHVRIRGKSVVQCGIPQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLTLVRGPEYGCNVNL 900
DB 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLTLVRGPEYGCNVNL 900
QY 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLTF 960
DB 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLTF 960
QY 961 NRGFKAGNMRKLFVGLRLKCHSLFDLDVNSLQTVCTNIIKILLQAYRPHACVLOLP 1020
DB 961 NRGFKAGNMRKLFVGLRLKCHSLFDLDVNSLQTVCTNIIKILLQAYRPHACVLOLP 1020
QY 1021 FHOQVWKNTFFLRVISTASIIKPNQTYCVRVYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 1080
DB 1021 FHOQVWKNTFFLRVISTASIIKPNQTYCVRVYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 1080
QY 1081 KLTHRVTVVPLGLSLRTAQTSLSKLPGLTTLTALAAAAANPALPSDFKTILD 1132
DB 1081 KLTHRVTVVPLGLSLRTAQTSLSKLPGLTTLTALAAAAANPALPSDFKTILD 1132

RESULT 5
US-09-788-110A-23
; Sequence 23, Application US/09788110A
; Publication No. US20040086518A1
; GENERAL INFORMATION:
; APPLICANT: Zanetti, Maurizio
; TITLE OF INVENTION: A Universal Vaccine and Method for Treating Cancer Employing
; FILE REFERENCE: UCSD-07017
; CURRENT APPLICATION NUMBER: US/09/788,110A
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 23
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-110A-23

Query Match 100.0%; Score 5961; DB 11; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLSHRYEVLPLATFVRRLGPOGWRVLVQRGDPAAFRALVAQCILVCPW 60
DB 1 MPRAPRCRAVRSLLSHRYEVLPLATFVRRLGPOGWRVLVQRGDPAAFRALVAQCILVCPW 60

QY 61 DARPPPAAPSFRQVSKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPEAFTTSVR 120
DB 61 DARPPPAAPSFRQVSKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPEAFTTSVR 120

QY 121 SYLPTNTVDALRGSGAWGLLRVGDVLLVLLARCALFVLVAPSCVQCGPPPLYQLGA 180
DB 121 SYLPTNTVDALRGSGAWGLLRVGDVLLVLLARCALFVLVAPSCVQCGPPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLGRCERAWNSVREAGVPLGLPAPGARRRGSGASRSLPLPKRPR 240
DB 181 ATQARPPPHASGPRRLGRCERAWNSVREAGVPLGLPAPGARRRGSGASRSLPLPKRPR 240

QY 241 GAAPSPERTPVQCGSWAHPGRTGSDRGFCVVSAPRABEATSLEGALSGTRHSHPSVG 300
DB 241 GAAPSPERTPVQCGSWAHPGRTGSDRGFCVVSAPRABEATSLEGALSGTRHSHPSVG 300
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QY 301 RQHIAGPSTSRPRPMDTPCPVYVAETKHFYSSGDKQELRPSFLLSSLRPSLTGARRL 360
DB 301 RQHIAGPSTSRPRPMDTPCPVYVAETKHFYSSGDKQELRPSFLLSSLRPSLTGARRL 360
QY 361 VETIFLGSRRPMPGTPRRLPRLPORYWQMRPLFLELLGNHQAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRRPMPGTPRRLPRLPORYWQMRPLFLELLGNHQAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKQGSVAAPPEEDTDPRLVLQRLRHSSPWQVYGVFRACLRRLVPPGLMGS 480
DB 421 PAAGVCAREKQGSVAAPPEEDTDPRLVLQRLRHSSPWQVYGVFRACLRRLVPPGLMGS 480
QY 481 RHNERRFLRNTKFTISLGKHAHKLQELTWMKSVRDCAWLRRSPGVGCPVAAEHLRBEI 540
DB 481 RHNERRFLRNTKFTISLGKHAHKLQELTWMKSVRDCAWLRRSPGVGCPVAAEHLRBEI 540
QY 541 LAKFLHLMWSVYVVELLRSFFVTETTFQKRLFFYKRSVMSKQSGIGIROHLKRVQJRE 600
DB 541 LAKFLHLMWSVYVVELLRSFFVTETTFQKRLFFYKRSVMSKQSGIGIROHLKRVQJRE 600
QY 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPNQTYCVRVYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
DB 721 PODRLTEVIASIIKPNQTYCVRVYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSPLRDVAVTEQSSSINEASSGLFDVFLRPMCHHVRIRGKSVVQCGIPQGSILSTL 840
DB 781 QETSPLRDVAVTEQSSSINEASSGLFDVFLRPMCHHVRIRGKSVVQCGIPQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLTLVRGPEYGCNVNL 900
DB 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLTLVRGPEYGCNVNL 900
QY 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLTF 960
DB 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLTF 960
QY 961 NRGFKAGNMRKLFVGLRLKCHSLFDLDVNSLQTVCTNIIKILLQAYRPHACVLOLP 1020
DB 961 NRGFKAGNMRKLFVGLRLKCHSLFDLDVNSLQTVCTNIIKILLQAYRPHACVLOLP 1020
QY 1021 FHOQVWKNTFFLRVISTASIIKPNQTYCVRVYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 1080
DB 1021 FHOQVWKNTFFLRVISTASIIKPNQTYCVRVYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 1080
QY 1081 KLTHRVTVVPLGLSLRTAQTSLSKLPGLTTLTALAAAAANPALPSDFKTILD 1132
DB 1081 KLTHRVTVVPLGLSLRTAQTSLSKLPGLTTLTALAAAAANPALPSDFKTILD 1132
```

RESULT 6

```
US-10-053-758-225
; Sequence 225, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.
; ; Morin, Gregg B.
; ; Harley, Calvin
; ; Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Crew LLP
```

STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-10-053-758-225

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRVLVQRGDPAAFRALVAQCLVCPW	60
Db	1	MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRVLVQRGDPAAFRALVAQCLVCPW	60
Qy	61	DARPPAAPSPROVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR	120
Db	61	DARPPAAPSPROVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR	120
Qy	121	SYLPTNTVDALRGSGAWGLLRVGGDVLVHLARCALFVLVAPSCAYQVCGPPLYQIGA	180
Db	121	SYLPTNTVDALRGSGAWGLLRVGGDVLVHLARCALFVLVAPSCAYQVCGPPLYQIGA	180
Qy	181	ATQARPPPHAGPRRRLCERAWNHSVREAGVPLGPAPGARRRGGSASRLPLPKRPRR	240
Db	181	ATQARPPPHAGPRRRLCERAWNHSVREAGVPLGPAPGARRRGGSASRLPLPKRPRR	240
Qy	241	GAAPERTPVQGSWAHPGTRGSDRGFCVSPAPAEATSLGALSCTRHSHPVG	300
Db	241	GAAPERTPVQGSWAHPGTRGSDRGFCVSPAPAEATSLGALSCTRHSHPVG	300
Qy	301	RQHAGPSTSRPPRPWTTPCPVVAETKHFYSSGDKQLRPSFLSSRLPSLTGARRL	360
Db	301	RQHAGPSTSRPPRPWTTPCPVVAETKHFYSSGDKQLRPSFLSSRLPSLTGARRL	360
Qy	361	VETIFLGRPNWPGTPRRLPRLPQRYWQMRPLFLELLGNHACQPGVLLKTHCPLRAAVT	420
Db	361	VETIFLGRPNWPGTPRRLPRLPQRYWQMRPLFLELLGNHACQPGVLLKTHCPLRAAVT	420

Qy	421	PAAGVCAREKPOGSSVAAPBEEDTPRLVLQRLROHSSPWQYGVFRACLRRLVPPGLWGS	480
Db	421	PAAGVCAREKPOGSSVAAPBEEDTPRLVLQRLROHSSPWQYGVFRACLRRLVPPGLWGS	480
Qy	481	RHNERRFLRNTKFIISLGKIAKLSQBLTWKMSVRDCAWLRSPGVGCVPAAEHLRREI	540
Db	481	RHNERRFLRNTKFIISLGKIAKLSQBLTWKMSVRDCAWLRSPGVGCVPAAEHLRREI	540
Qy	541	LAKFLHLMSSVYVVELLRSFFYVTTTTFQKNRLFYKRSVMSKLSQSIGIRQHLKRVQRE	600
Db	541	LAKFLHLMSSVYVVELLRSFFYVTTTTFQKNRLFYKRSVMSKLSQSIGIRQHLKRVQRE	600
Qy	601	LSEAEVQHREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFREKRAERLTSRYKA	660
Db	601	LSEAEVQHREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFREKRAERLTSRYKA	660
Qy	661	LFSVLYNERARRPGLLGASVLGLDDIHRAWRTFVLVRQAODPPPELVFKVDVTGAYDTI	720
Db	661	LFSVLYNERARRPGLLGASVLGLDDIHRAWRTFVLVRQAODPPPELVFKVDVTGAYDTI	720
Qy	721	PODLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTLDQPYMRQFVAHL	780
Db	721	PODLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTLDQPYMRQFVAHL	780
Qy	781	QETSPLRDAVVIEQSSSINEASSGLFDVFLRPMCHHAVIRGKSYVOCQGIPOGSIILSTL	840
Db	781	QETSPLRDAVVIEQSSSINEASSGLFDVFLRPMCHHAVIRGKSYVOCQGIPOGSIILSTL	840
Qy	841	LCSLCYGD MENKLPAGIRRDGLLRVDDLLVTPHLLTHAKTFLRTRTVRGVPEYGCVVNL	900
Db	841	LCSLCYGD MENKLPAGIRRDGLLRVDDLLVTPHLLTHAKTFLRTRTVRGVPEYGCVVNL	900
Qy	901	RKTVPNPFVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVSQSDYSYARTSIRASLT	960
Db	901	RKTVPNPFVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVSQSDYSYARTSIRASLT	960
Qy	961	NRGFKAGNNRRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRPHACVLQLP	1020
Db	961	NRGFKAGNNRRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRPHACVLQLP	1020
Qy	1021	FHQVWKNPFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAFLL	1080
Db	1021	FHQVWKNPFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAFLL	1080
Qy	1081	KLTRHRVTVYVPLLGSLTAQTQLSRKLPGTTLTALAAAAANPALPSDFKTILD	1132
Db	1081	KLTRHRVTVYVPLLGSLTAQTQLSRKLPGTTLTALAAAAANPALPSDFKTILD	1132

RESULT 7

US-10-208-243-2
; Sequence 2, Application US/10208243
; Publication No. US20030044394A1
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; TITLE OF INVENTION: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/10/208,243
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/675,321
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-208-243-2

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCPWM 60
DB 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCPWM 60

QY 61 DARPPAPSPFQVSCLEKELVARVQLRCERAKNVLAAGFALLDARGCPPEATTTSVR 120
DB 61 DARPPAPSPFQVSCLEKELVARVQLRCERAKNVLAAGFALLDARGCPPEATTTSVR 120

QY 121 SYLPTNTVDALRGSAWGLLLRRVGDVLLHLLARCALFVLVAPSCAVQCGPPPLYQLGA 180
DB 121 SYLPTNTVDALRGSAWGLLLRRVGDVLLHLLARCALFVLVAPSCAVQCGPPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLGRCERAWNHSVREAGVPLGLPAPGARRRGGASRSLLPKRPRR 240
DB 181 ATQARPPPHASGPRRLGRCERAWNHSVREAGVPLGLPAPGARRRGGASRSLLPKRPRR 240

QY 241 GAAPERTPVQCGSWAHPGRTGRGSDRGFCVVSAPAPABEATSLEGALSGTRHSPSVG 300
DB 241 GAAPERTPVQCGSWAHPGRTGRGSDRGFCVVSAPAPABEATSLEGALSGTRHSPSVG 300

QY 301 RQHAGAPSTSRPPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLLSRLPSLTGARRL 360
DB 301 RQHAGAPSTSRPPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLLSRLPSLTGARRL 360

QY 361 VETIFLGRPMWPGTFRRLPRLPQRYQWMPRLFLELLGNHACPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGRPMWPGTFRRLPRLPQRYQWMPRLFLELLGNHACPYGVLLKTHCPLRAAVT 420

QY 421 PAAGCAEKEKPGSVAAPEBEDTPRRLVOLLRQHSHPQVYGFVRACLRRLVPPGLWGS 480
DB 421 PAAGCAEKEKPGSVAAPEBEDTPRRLVOLLRQHSHPQVYGFVRACLRRLVPPGLWGS 480

QY 481 RHNERFRNTKFTSLGHAKLSLQELTWKMSVRDCAWLRSVGCVPAAEHLRREI 540
DB 481 RHNERFRNTKFTSLGHAKLSLQELTWKMSVRDCAWLRSVGCVPAAEHLRREI 540

QY 541 LAKFLHLMSSVYVVELLSFFVYTTTFOKNLFFYRKSVMKLSQIGIRQHLKRVQLE 600
DB 541 LAKFLHLMSSVYVVELLSFFVYTTTFOKNLFFYRKSVMKLSQIGIRQHLKRVQLE 600

QY 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660

QY 661 LFSVLNYSRARPGLLGASVLGLDDIHRARWTFVLVRADQDPPPELYFKVDVTCAYDTI 720
DB 661 LFSVLNYSRARPGLLGASVLGLDDIHRARWTFVLVRADQDPPPELYFKVDVTCAYDTI 720

QY 721 PODRLTEVIASIIKQNTYCVRYAVVQKAAGHVRKAFKSHVSTLTLDQPYMROFVAHL 780
DB 721 PODRLTEVIASIIKQNTYCVRYAVVQKAAGHVRKAFKSHVSTLTLDQPYMROFVAHL 780

QY 781 QETSLRDAVVIQESSLSNEASSGLFVFLRFMCHAVRIRKSVYVQCGIPQGSILSTL 840
DB 781 QETSLRDAVVIQESSLSNEASSGLFVFLRFMCHAVRIRKSVYVQCGIPQGSILSTL 840

QY 841 LCSLCYGMENKLFAGIRDDGLLRLVDDFLAVTTHLTHAKTFLRLVRGVEYCVNVL 900
DB 841 LCSLCYGMENKLFAGIRDDGLLRLVDDFLAVTTHLTHAKTFLRLVRGVEYCVNVL 900

QY 901 RKTVMNFPVEDALGATFVQMPAHGLFPWCGLLDTRTLEVQSDYSSVARTSIRASLTF 960
DB 901 RKTVMNFPVEDALGATFVQMPAHGLFPWCGLLDTRTLEVQSDYSSVARTSIRASLTF 960

QY 961 NRGFKAGRNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
DB 961 NRGFKAGRNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020

RESULT 8

US-10-054-295-225
; Sequence 225, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/POCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225:

SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 225:

US-10-054-295-225

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCPWM 60
DB 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCPWM 60

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QY 61 DARPPAAPSPROVSCLELVARVLORLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
Db 61 DARPPAAPSPROVSCLELVARVLORLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYLQGA 180
Db 121 SYLPTNTVDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYLQGA 180
QY 181 ATQARPPPHAGSPRRRLCERAWNHSVREAGVPLGLPAPGARRRGSSASRLPLPKRPRR 240
Db 181 ATQARPPPHAGSPRRRLCERAWNHSVREAGVPLGLPAPGARRRGSSASRLPLPKRPRR 240
QY 241 GAAPPEPTPGQSGWAHPGTRGSDRGFCVSPARPAEATSLEGALSSTRSHPSVG 300
Db 241 GAAPPEPTPGQSGWAHPGTRGSDRGFCVSPARPAEATSLEGALSSTRSHPSVG 300
QY 301 RQHAGPSTSRPPRPMDTPCPVVAETKHFLYSSGDEQLRPSFLSSLRPSLTGARRL 360
Db 301 RQHAGPSTSRPPRPMDTPCPVVAETKHFLYSSGDEQLRPSFLSSLRPSLTGARRL 360
QY 361 VETIFLGRPMWGPTRRLPLRQRYQWRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGRPMWGPTRRLPLRQRYQWRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKQGSVAAPBEEDTPRRLVOLLRHSSPWQYVGFVRACLRRLVPPGLWS 480
Db 421 PAAGVCAREKQGSVAAPBEEDTPRRLVOLLRHSSPWQYVGFVRACLRRLVPPGLWS 480
QY 481 RHNERFLRNTKFTSLGKHAKLSQELTWKMSVRDCAWLRRSPGVCPVPAEHLRREI 540
Db 481 RHNERFLRNTKFTSLGKHAKLSQELTWKMSVRDCAWLRRSPGVCPVPAEHLRREI 540
QY 541 LAKFLHLMWSVVVVELLSFFVTTFTQKNRLFYRKSVMSKLSQSIGIRQHLKRVQRE 600
Db 541 LAKFLHLMWSVVVVELLSFFVTTFTQKNRLFYRKSVMSKLSQSIGIRQHLKRVQRE 600
QY 601 LSEAEVROHREARPAALLTSRLRFIPKPGCLRPINMDYVVGARTFRREKRAERLTSRKA 660
Db 601 LSEAEVROHREARPAALLTSRLRFIPKPGCLRPINMDYVVGARTFRREKRAERLTSRKA 660
QY 661 LFSVLNYSERARRPGLLGASVLGLDDIHRARWTFVLVRADQPPPLPVKVDVDTGAYDTI 720
Db 661 LFSVLNYSERARRPGLLGASVLGLDDIHRARWTFVLVRADQPPPLPVKVDVDTGAYDTI 720
QY 721 PQDRUTEVIASIIKPQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
Db 721 PQDRUTEVIASIIKPQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
QY 781 QETSPLRDVAVTEQSSSLEASSGLFDVFLRFMCHHAVRIKSVVQCGIPQGSILSTL 840
Db 781 QETSPLRDVAVTEQSSSLEASSGLFDVFLRFMCHHAVRIKSVVQCGIPQGSILSTL 840
QY 841 LCSCYGDWENKLFAGIRDDGLLLRLVDDFLIVTPHLTHAKTFLTLVRGVPYGCVVNL 900
Db 841 LCSCYGDWENKLFAGIRDDGLLLRLVDDFLIVTPHLTHAKTFLTLVRGVPYGCVVNL 900
QY 901 RKTVNVFVEDBALGCTAFVQMPAHGLFPWCGLLDDTLTEVQSYSSYARTSIRASLTF 960
Db 901 RKTVNVFVEDBALGCTAFVQMPAHGLFPWCGLLDDTLTEVQSYSSYARTSIRASLTF 960
QY 961 NRGFKAGNMRKLFGLRLKCHSLFLDLQVNSLQTVCTNIIKILLQAYRPHACVLQLP 1020
Db 961 NRGFKAGNMRKLFGLRLKCHSLFLDLQVNSLQTVCTNIIKILLQAYRPHACVLQLP 1020
QY 1021 FHQQWKNPTFFLRVISTASICYILKAKNAGMSLGAKGAGPLPSEAVOWLCHOAFL 1080
Db 1021 FHQQWKNPTFFLRVISTASICYILKAKNAGMSLGAKGAGPLPSEAVOWLCHOAFL 1080
QY 1081 KLTHRVTVVPLLSRLTAQTSRLPGTTLTALAEAAANPALPSDFKTI 1132
Db 1081 KLTHRVTVVPLLSRLTAQTSRLPGTTLTALAEAAANPALPSDFKTI 1132

```

```

RESULT 9
US-10-054-611-225
; Sequence 225, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;             Lingner, Joachim
;             Nakamura, Toru
;             Chapman, Karen B.
;             Morin, Gregg B.
;             Harley, Calvin
;             Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054.611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 225:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-10-054-611-225

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVQRGDPAAFRALVAQCCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVQRGDPAAFRALVAQCCLVCVPW 60
QY 61 DARPPAAPSPROVSCLELVARVLORLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
Db 61 DARPPAAPSPROVSCLELVARVLORLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYLQGA 180
Db 121 SYLPTNTVDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYLQGA 180
QY 181 ATQARPPPHAGSPRRRLCERAWNHSVREAGVPLGLPAPGARRRGSSASRLPLPKRPRR 240

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Db 181 ATQARPPPHASGRRRLGGERAWNHSVREAGVPLGLPAPGARRRGSGASRSPLPKRPRR 240
Qy 241 GAAPERTPVQGGSWAHPCRTGSDRGFCVVSPPARPAEAEATSLGALSGLTSHSPSVG 300
Db 241 GAAPERTPVQGGSWAHPCRTGSDRGFCVVSPPARPAEAEATSLGALSGLTSHSPSVG 300
Qy 301 ROHAGPPTSPRPPWDTPCPVYAEKHFYSSGDKQLRPSFLLSLRSLTGAARL 360
Db 301 ROHAGPPTSPRPPWDTPCPVYAEKHFYSSGDKQLRPSFLLSLRSLTGAARL 360
Qy 361 VETIFLGSPPWPGTTPRRLPRLPQRYWQMRPLFLELLGNHACQPYGVLLKTHCPLRAAYT 420
Db 361 VETIFLGSPPWPGTTPRRLPRLPQRYWQMRPLFLELLGNHACQPYGVLLKTHCPLRAAYT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPWQVYGFVRACLRLRVLPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPWQVYGFVRACLRLRVLPPGLWGS 480
Qy 481 RHNERFLRNTKFFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREI 540
Db 481 RHNERFLRNTKFFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREI 540
Qy 541 LAKFLHMLSVVYVVELLRSPFYVTTTFQKNRLFYRKSVWSKLSIGIRQHLKRVOLRE 600
Db 541 LAKFLHMLSVVYVVELLRSPFYVTTTFQKNRLFYRKSVWSKLSIGIRQHLKRVOLRE 600
Qy 601 LSEAEVRQREARPPALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQREARPPALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNAYERARRPGLLGASVLGLDDIHRARWTFVLRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNAYERARRPGLLGASVLGLDDIHRARWTFVLRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780
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Qy 781 QETSPLRDAVIEQSSSLEASGLFDVFLRPMCHHAVIRGKSVYQCOGIPQGSILSTL 840
Db 781 QETSPLRDAVIEQSSSLEASGLFDVFLRPMCHHAVIRGKSVYQCOGIPQGSILSTL 840
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Db 841 LCSLCYGDMEKLFAGIRDGILLRLVDLFTVPLTHAKTFLRLTVRGVPEYGCVMNL 900
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Db 901 RKTVMNPFVEDEALGCTAFVQMPAHGLFPWCGLLDTLRLVQSDSYSSYARTSIRASLTF 960
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Db 961 NRGFKAGRNMRKLFGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Qy 1021 FHOQVWKNPTFLRVIDSTASLCYSLKAKNAGMSLGAKGAAGPLPSEAVQMLCHQAFLL 1080
Db 1021 FHOQVWKNPTFLRVIDSTASLCYSLKAKNAGMSLGAKGAAGPLPSEAVQMLCHQAFLL 1080
Qy 1081 KLTHRVTVVPLLSLRTAQTQLSRKLPGTTLTALAAANPALPSDFKTILD 1132
Db 1081 KLTHRVTVVPLLSLRTAQTQLSRKLPGTTLTALAAANPALPSDFKTILD 1132

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RESULT 10
 US-10-105-963-2
 ; Sequence 2, Application US/10105963
 ; Publication No. US20030068818A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Geron Corporation
 ; APPLICANT: Denning, Chris
 ; APPLICANT: Clark, A. John
 ; APPLICANT: Schiff, J. Michael
 ; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human

; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
 ; FILE OF INVENTION: 731/002
 ; CURRENT APPLICATION NUMBER: US/10/105,963
 ; CURRENT FILING DATE: 2002-03-21
 ; PRIOR APPLICATION NUMBER: US 60/277,811
 ; PRIOR FILING DATE: 2001-03-21
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 1132
 ; TYPE: PR1
 ; ORGANISM: Homo sapiens
 ; US-10-105-963-2

Query Match 100.0%; Score 5961; DB 14; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MPRAPRCAVRSLLSRSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
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Db 61 DARPPAAPSPFQVSCLEKELVARVQLRCERGAKNVLAFGFALLDGAAGGPEAFITSVR 120
Qy 121 SYLPNTVTDALRGSGAWGLLRVDDVLLHLLARCALFVLVAPSCAYVCGPPPLYOLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLRVDDVLLHLLARCALFVLVAPSCAYVCGPPPLYOLGA 180
Qy 181 ATQARPPPHASGRRRLGGERAWNHSVREAGVPLGLPAPGARRRGSGASRSPLPKRPRR 240
Db 181 ATQARPPPHASGRRRLGGERAWNHSVREAGVPLGLPAPGARRRGSGASRSPLPKRPRR 240
Qy 241 GAAPERTPVQGGSWAHPCRTGSDRGFCVVSPPARPAEAEATSLGALSGLTSHSPSVG 300
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Qy 301 ROHAGPPTSPRPPWDTPCPVYAEKHFYSSGDKQLRPSFLLSLRSLTGAARL 360
Db 301 ROHAGPPTSPRPPWDTPCPVYAEKHFYSSGDKQLRPSFLLSLRSLTGAARL 360
Qy 361 VETIFLGSPPWPGTTPRRLPRLPQRYWQMRPLFLELLGNHACQPYGVLLKTHCPLRAAYT 420
Db 361 VETIFLGSPPWPGTTPRRLPRLPQRYWQMRPLFLELLGNHACQPYGVLLKTHCPLRAAYT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPWQVYGFVRACLRLRVLPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPWQVYGFVRACLRLRVLPPGLWGS 480
Qy 481 RHNERFLRNTKFFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREI 540
Db 481 RHNERFLRNTKFFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREI 540
Qy 541 LAKFLHMLSVVYVVELLRSPFYVTTTFQKNRLFYRKSVWSKLSIGIRQHLKRVOLRE 600
Db 541 LAKFLHMLSVVYVVELLRSPFYVTTTFQKNRLFYRKSVWSKLSIGIRQHLKRVOLRE 600
Qy 601 LSEAEVRQREARPPALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQREARPPALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNAYERARRPGLLGASVLGLDDIHRARWTFVLRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNAYERARRPGLLGASVLGLDDIHRARWTFVLRAQDPPPELYFVKVDVTGAYDTI 720
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Db 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780
Qy 781 QETSPLRDAVIEQSSSLEASGLFDVFLRPMCHHAVIRGKSVYQCOGIPQGSILSTL 840

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Db 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHAVIRKGSVVOQGIPQGSILSTL 840
Qy 841 LCSLCYGDMEKNLFGIRRDGILLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
Db 841 LCSLCYGDMEKNLFGIRRDGILLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
Qy 901 RKTUVNFEVEALGCTAFVOMPAGHLPWCGLLDDTFLVQSDYSSYARTSIRASLTF 960
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Qy 961 NRGFKAGNMRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHACVLQLP 1020
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Qy 1081 KLTRHRVTYVPLLSGLRTAQTLRSKLPGTTLTALAAAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLLSGLRTAQTLRSKLPGTTLTALAAAAANPALPSDFKTILD 1132

RESULT 11

US-10-044-692-2
; Sequence 2, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-044-692-2

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Beet Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLRIGPQGWRLVQRGDPAAFPALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLRIGPQGWRLVQRGDPAAFPALVAQCLVCVPW 60
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Db 241 GAAPERTPVQGSWAHPGRTGSDRGFCVSPARPABEATSILEGALSCTRHSHPVSG 300
Qy 301 RQHAGPSTSRPPMDTPCPVYAETKHFLYSSGDKQLRPSFLSSLSPLSGARRL 360
Db 301 RQHAGPSTSRPPMDTPCPVYAETKHFLYSSGDKQLRPSFLSSLSPLSGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRLLPRLPQRYQWQMRPLFLELGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRLLPRLPQRYQWQMRPLFLELGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPOGSAVAPEEEDTPRLVQLLRHSSPQVYGVFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPOGSAVAPEEEDTPRLVQLLRHSSPQVYGVFVRACLRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKFI SLGKIAKLSLQELTWKMSVRDCAWLRSPGVCPVAAEHLRBEI 540
Db 481 RHNERRFLRNTKFI SLGKIAKLSLQELTWKMSVRDCAWLRSPGVCPVAAEHLRBEI 540
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Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRAWTFFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
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Db 721 PQDLTEVIASIIKPNQTYCVRRYAVQKAAHVRKAFKSHVSTLTDLQPMRQFVAHL 780
Qy 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHAVIRKGSVVOCGIPQGSILSTL 840
Db 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHAVIRKGSVVOCGIPQGSILSTL 840
Qy 841 LCSLCYGDMEKNLFGIRRDGILLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
Db 841 LCSLCYGDMEKNLFGIRRDGILLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900

901 RKTVMNPFVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSSVARTSIRASLTF 960
 901 RKTVMNPFVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSSVARTSIRASLTF 960
 961 NGGFKAGNRMRKLFVLRKCHSLFDLDQVNSLQVCTNIIYKILLQAYRHFACVQLP 1020
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 1021 FHOQWKNTFFELRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHQAFLL 1080
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RESULT 12
 US-10-044-539-2
 Sequence 2, Application US/10044539
 Publication No. US20030100093A1
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin
 Andrews, William H.
 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
 THERAPEUTIC METHODS
 NUMBER OF SEQUENCES: 335
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/044,539
 FILING DATE: 11-Jan-2002
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/912,951
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002600US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid

TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-044-539-2
 Query Match 100.0%; Score 5961; DB 14; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRVLVQRGDPAAFRALVAQCLVCPW 60
 Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRVLVQRGDPAAFRALVAQCLVCPW 60
 QY 61 DARPPAAPSPRQVSKLKVRLQRLCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120
 Db 61 DARPPAAPSPRQVSKLKVRLQRLCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120
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 Db 121 SYLNTVTDALRGSGAWGLLRRVGGDDVLLHLLARCALFVLVAPSCAVQVCPPIYQLGA 180
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 QY 241 GAAPEPERTVQGGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSGTRHSHPSVG 300
 Db 241 GAAPEPERTVQGGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSGTRHSHPSVG 300
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 Db 301 RQHAGPSTSRPRPMDTPCPVYAEATKHFYSSGDEQLRPSFLLSRLPSLTGARRL 360
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 Db 361 VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFLELLGNHACQPYGVLLKTHCPRAAYT 420
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 Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSPPWQVYGFVRACLRLVPPGLMGS 480
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 Db 481 RHNERFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVCPVAAEHLREBI 540
 QY 541 LAKFLHLMVSVVVELLSFFVTTTETTFQKRLFPYKSVMSKLOSIGIRQHLKRVQRE 600
 Db 541 LAKFLHLMVSVVVELLSFFVTTTETTFQKRLFPYKSVMSKLOSIGIRQHLKRVQRE 600
 QY 601 LSEAEVRQHREARPAALTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
 Db 601 LSEAEVRQHREARPAALTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
 QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRARWTFVLRVAQDPPPELYFVKVDVTGAYDTI 720
 Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRARWTFVLRVAQDPPPELYFVKVDVTGAYDTI 720
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 Db 781 QETSPDRDAVVEIOSSSLNEASSGLFDVFLRFMCHHVRIRGKSVYVQCGIPOGSIILSTL 840
 QY 841 LCSLCYGDMEKNLPAFIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVEYCVVNL 900
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 QY 901 RKTVMNPFVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSSVARTSIRASLTF 960
 Db 901 RKTVMNPFVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSSVARTSIRASLTF 960

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QY 961 NRGFKAGRNMRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIYKILLLOAYRPHACVLQLP 1020
DB 961 NRGFKAGRNMRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIYKILLLOAYRPHACVLQLP 1020
QY 1021 FHQQVWKNPFFLRVISTASLCYSLKAKNAGSLGAKGAGPLPSEAVOMLCHOAFLL 1080
DB 1021 FHQQVWKNPFFLRVISTASLCYSLKAKNAGSLGAKGAGPLPSEAVOMLCHOAFLL 1080
QY 1081 KLTRHRVTYVPLGLSLRTAQOLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
DB 1081 KLTRHRVTYVPLGLSLRTAQOLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132

RESULT 13
US-10-295-681-57
; Sequence 57, Application US/10295681
; Publication No. US20030166270A1
; GENERAL INFORMATION:
; APPLICANT: E. Premkumar Reddy
; APPLICANT: Sushil G. Kane
; APPLICANT: Richard V. Mettus
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REVERSIBLY
; TITLE OF INVENTION: INDUCING CONTINUAL GROWTH IN NORMAL CELLS
; FILE REFERENCE: 6056-307
; CURRENT APPLICATION NUMBER: US/10/295,681
; PRIORITY FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1132
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-295-681-57

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRLSLRSHREVLPATFVRRLLGPQGMRLVQRGDPAARFALVAQCILVCVPM 60
DB 1 MPRAPRCRAVRLSLRSHREVLPATFVRRLLGPQGMRLVQRGDPAARFALVAQCILVCVPM 60

QY 61 DARPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
DB 61 DARPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

QY 121 SYLPTNTVDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPTNTVDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLGRCERAWNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKRPRR 240
DB 181 ATQARPPPHASGPRRLGRCERAWNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKRPRR 240

QY 241 GAAPPERTPVQGSWAHPGRTGSDRGFCVVSAPARPAEATSLEGALSGTRHSHPSVG 300
DB 241 GAAPPERTPVQGSWAHPGRTGSDRGFCVVSAPARPAEATSLEGALSGTRHSHPSVG 300

QY 301 RQHAGAPSTSRPPRPWDTPCPVVAETHKFLYSSGDKQELRPSFLLSLRPSLTGARRL 360
DB 301 RQHAGAPSTSRPPRPWDTPCPVVAETHKFLYSSGDKQELRPSFLLSLRPSLTGARRL 360

QY 361 VETIFLGSRPWMPGTPRRLPRLPQRYQWOMRPUFLLELLGNHQAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRPWMPGTPRRLPRLPQRYQWOMRPUFLLELLGNHQAQCPYGVLLKTHCPLRAAVT 420

QY 421 PAAGYCAKEKPGSVAAPPEEDTPDRRLVQLLRQHSPPQVYGFVRACLRLRVLPPGLWGS 480
DB 421 PAAGYCAKEKPGSVAAPPEEDTPDRRLVQLLRQHSPPQVYGFVRACLRLRVLPPGLWGS 480

QY 481 RHNERFLRNTKFTSLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAEHLRREI 540
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DB 481 RHNERFLRNTKFTSLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAEHLRREI 540
QY 541 LAKFLHLMMSVYVVELLRSFYVTTTFQKNRLEFFYRKSVMSKLQSIGIRQHLKRVQLRE 600
DB 541 LAKFLHLMMSVYVVELLRSFYVTTTFQKNRLEFFYRKSVMSKLQSIGIRQHLKRVQLRE 600
QY 601 LSEAEVQHRREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVA 660
DB 601 LSEAEVQHRREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVA 660
QY 661 LFSVLNYERARRRPGILGASVLGLDDIHRAMPTFVLVRAPDPPBELYFKVDVTGAYDTI 720
DB 661 LFSVLNYERARRRPGILGASVLGLDDIHRAMPTFVLVRAPDPPBELYFKVDVTGAYDTI 720
QY 721 PQDLRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
DB 721 PQDLRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSPLRDADVIEOSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYVOCQGIPOQSILSTL 840
DB 781 QETSPLRDADVIEOSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYVOCQGIPOQSILSTL 840
QY 841 LCSLCYGD MENKLFAGIRRDGLLRLVDDFLLVTPHLLTHAKTFLRTLVRGYPGYCVNVL 900
DB 841 LCSLCYGD MENKLFAGIRRDGLLRLVDDFLLVTPHLLTHAKTFLRTLVRGYPGYCVNVL 900
QY 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGILLDTRTLLEVQSDYSSYARTSIRASLTF 960
DB 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGILLDTRTLLEVQSDYSSYARTSIRASLTF 960
QY 961 NRGFKAGRNMRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIYKILLLOAYRPHACVLQLP 1020
DB 961 NRGFKAGRNMRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIYKILLLOAYRPHACVLQLP 1020
QY 1021 FHQQVWKNPFFLRVISTASLCYSLKAKNAGSLGAKGAGPLPSEAVOMLCHOAFLL 1080
DB 1021 FHQQVWKNPFFLRVISTASLCYSLKAKNAGSLGAKGAGPLPSEAVOMLCHOAFLL 1080
QY 1081 KLTRHRVTYVPLGLSLRTAQOLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
DB 1081 KLTRHRVTYVPLGLSLRTAQOLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
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RESULT 14

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US-10-325-810-2
; Sequence 2, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICANT: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-325-810-2
Query Match 100.0%; Score 5961; DB 15; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLFGQWRLVQRGDPAAFRALVAQCLVCPW 60
DB 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLFGQWRLVQRGDPAAFRALVAQCLVCPW 60
QY 61 DARPPAPSPFQVSCLEKELVARVLQRCERGAKNVLAFGPALLDGCARGGPPPEAFTTSVR 120
DB 61 DARPPAPSPFQVSCLEKELVARVLQRCERGAKNVLAFGPALLDGCARGGPPPEAFTTSVR 120
QY 121 SYLPNTVTDALRGSGAWGLLRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPNTVTDALRGSGAWGLLRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAGARRRGSGASRSLPLPKRRR 240
DB 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAGARRRGSGASRSLPLPKRRR 240
QY 241 GAAPPERTPVQGSWAHPGRTGRGDFCVVSPARPAEATSLEGALSGTRHSHPSVG 300
DB 241 GAAPPERTPVQGSWAHPGRTGRGDFCVVSPARPAEATSLEGALSGTRHSHPSVG 300
QY 301 ROHAGPSTSPRRPMDTPCPVVAETHKFLYSSGDKQLRPSFLSLRSLTGARRL 360
DB 301 ROHAGPSTSPRRPMDTPCPVVAETHKFLYSSGDKQLRPSFLSLRSLTGARRL 360
QY 361 VETIFLGSPPMGPTRRLPRLPQRYWQMRPLFELLLGNHACQPGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSPPMGPTRRLPRLPQRYWQMRPLFELLLGNHACQPGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEDTPRRLVQLLRQHSHPMQVYGFVRACLRRLVPPFLMGS 480
DB 421 PAAGVCAREKPGQSVAAPEEDTPRRLVQLLRQHSHPMQVYGFVRACLRRLVPPFLMGS 480

RESULT 15

US-10-388-578-2
; Sequence 2, Application US/10388578
; Publication No. US20030224411A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Stanton, Lawrence
; APPLICANT: Ralph, Brandenberger
; APPLICANT: Joseph, Gold D.
; APPLICANT: John, Irving
; APPLICANT: Mandalam, Ramkumar
; APPLICANT: Mok, Michael
; APPLICANT: Shelton, Dawne
; TITLE OF INVENTION: Genes that are Up- or Down-Regulated During Differentiation of H
; TITLE OF INVENTION: Embryonic Stem Cells
; FILE REFERENCE: 135/001
; CURRENT APPLICATION NUMBER: US/10/388,578
; CURRENT FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: Custom
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-388-578-2

Query Match 100.0%; Score 5961; DB 15; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0; Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRR	LGPOGWR	LVRQGD	PAAFRAL	VAQC	LVCP	VPW 60
Db	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRR	LGPOGWR	LVRQGD	PAAFRAL	VAQC	LVCP	VPW 60
Qy	61	DARPPAAPSPROVSKL	VARVLR	QRCER	GAKNV	LAFG	FALLD	GARG	GPPEAFTTSVR 120
Db	61	DARPPAAPSPROVSKL	VARVLR	QRCER	GAKNV	LAFG	FALLD	GARG	GPPEAFTTSVR 120
Qy	121	SYLNTVTDALRGSAWGL	LLRRVGGD	VLVHLL	ARCAL	FVL	VAPSCA	YVCG	PPLYQLGA 180
Db	121	SYLNTVTDALRGSAWGL	LLRRVGGD	VLVHLL	ARCAL	FVL	VAPSCA	YVCG	PPLYQLGA 180
Qy	181	ATQARPPPHASGPRR	RLGCER	AWNHS	VREAG	VP	LGLPAP	GARR	RGGSASRS
Db	181	ATQARPPPHASGPRR	RLGCER	AWNHS	VREAG	VP	LGLPAP	GARR	RGGSASRS
Qy	241	GAAPEPERTVQGS	WAHPGTR	GRPS	DRGFC	VVSP	PARPAE	ATS	LEGALSGTRHSPSVG 300
Db	241	GAAPEPERTVQGS	WAHPGTR	GRPS	DRGFC	VVSP	PARPAE	ATS	LEGALSGTRHSPSVG 300
Qy	301	RQHAGPSTSRPP	PMDT	PCPP	VYAE	TKH	FYLS	SGD	KEQLRPS
Db	301	RQHAGPSTSRPP	PMDT	PCPP	VYAE	TKH	FYLS	SGD	KEQLRPS
Qy	361	VETIFLGS	RPMWPGT	PRRL	PRL	PQY	WQMR	PL	FLELLGN
Db	361	VETIFLGS	RPMWPGT	PRRL	PRL	PQY	WQMR	PL	FLELLGN
Qy	421	PAAGVCA	REKPOGS	VAAP	EEED	TDPR	RLVOLL	ROH	SSPWQY
Db	421	PAAGVCA	REKPOGS	VAAP	EEED	TDPR	RLVOLL	ROH	SSPWQY
Qy	481	RHNERRFL	NRTK	KT	ISL	GK	AKLS	LOEL	WTWMS
Db	481	RHNERRFL	NRTK	KT	ISL	GK	AKLS	LOEL	WTWMS
Qy	541	LAKFLH	LWLS	VVYV	VELLS	RP	FFVT	TET	TFQK
Db	541	LAKFLH	LWLS	VVYV	VELLS	RP	FFVT	TET	TFQK

Db	1021	FHQQWKNPTFF	LRVISD	TASLCYSIL	KAKNAG	MSLGAK	GAAGPLP	SEAVQW	LCHQ	AFL	1080
Qy	1081	KLTRHRYVY	PLPLGL	SLRTAQ	TLSRKL	PGTTLT	AL	EAAA	NPAL	PSDF	KTILD 1132
Db	1081	KLTRHRYVY	PLPLGL	SLRTAQ	TLSRKL	PGTTLT	AL	EAAA	NPAL	PSDF	KTILD 1132
RESULT 16											
US-10-602-441-2											
; Sequence 2, Application US/10602441											
; Publication No. US20040106128A1											
; GENERAL INFORMATION:											
; APPLICANT: Geron Corporation											
; APPLICANT: Majumdar, Anish Sen											
; APPLICANT: Ferber, Iris											
; APPLICANT: Frolkis, Maria											
; APPLICANT: Wang, Zhuo											
; TITLE OF INVENTION: Cancer Vaccines Containing Xenogeneic Epitopes of Telomerase Reverse Transcriptase											
; FILE REFERENCE: 086/002											
; CURRENT APPLICATION NUMBER: US/10/602,441											
; CURRENT FILING DATE: 2003-06-24											
; PRIOR APPLICATION NUMBER: 60/393,295											
; PRIOR FILING DATE: 2002-06-27											
; NUMBER OF SEQ ID NOS: 12											
; SOFTWARE: Patent in version 3.1											
; SEQ ID NO 2											
; LENGTH: 1132											
; TYPE: PRT											
; ORGANISM: Homo sapiens											
US-10-602-441-2											
Query Match 100.0%; Score 5961; DB 16; Length 1132;											
Best Local Similarity 100.0%; Pred. No. 0;											
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
Qy	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRR	LGPOGWR	LVRQGD	PAAFRAL	VAQC	LVCP	VPW 60		
Db	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRR	LGPOGWR	LVRQGD	PAAFRAL	VAQC	LVCP	VPW 60		
Qy	61	DARPPAAPSPROVSKL	VARVLR	QRCER	GAKNV	LAFG	FALLD	GARG	GPPEAFTTSVR 120		
Db	61	DARPPAAPSPROVSKL	VARVLR	QRCER	GAKNV	LAFG	FALLD	GARG	GPPEAFTTSVR 120		
Qy	121	SYLNTVTDALRGSAWGL	LLRRVGGD	VLVHLL	ARCAL	FVL	VAPSCA	YVCG	PPLYQLGA 180		
Db	121	SYLNTVTDALRGSAWGL	LLRRVGGD	VLVHLL	ARCAL	FVL	VAPSCA	YVCG	PPLYQLGA 180		
Qy	181	ATQARPPPHASGPRRRLGCER	AWNHSVREAG	VP	LGLPAPGARR	RGGSASRS	SLP	LP	KR	PRR 240	
Db	181	ATQARPPPHASGPRRRLGCER	AWNHSVREAG	VP	LGLPAPGARR	RGGSASRS	SLP	LP	KR	PRR 240	
Qy	241	GAAPEPERTVQGS	WAHPGTRGRPS	DRGFCVVSP	PARPAE	ATS	LEGALSGTRHSP	SVG 300			
Db	241	GAAPEPERTVQGS	WAHPGTRGRPS	DRGFCVVSP	PARPAE	ATS	LEGALSGTRHSP	SVG 300			
Qy	301	RQHAGPSTSRPP	PMDT	PCPPVYAE	TKHFLYSSGD	KEQLRPS	LT	GARR	L 360		
Db	301	RQHAGPSTSRPP	PMDT	PCPPVYAE	TKHFLYSSGD	KEQLRPS	LT	GARR	L 360		
Qy	361	VETIFLGS	RPMWPGT	PRRL	PRL	PQY	WQMR	PL	FLELLGN	HAQC	PYGV
Db	361	VETIFLGS	RPMWPGT	PRRL	PRL	PQY	WQMR	PL	FLELLGN	HAQC	PYGV
Qy	421	PAAGVCA	REKPOGS	VAAP	EEED	TDPR	RLVOLL	ROHSS	PWQY	VF	VR
Db	421	PAAGVCA	REKPOGS	VAAP	EEED	TDPR	RLVOLL	ROHSS	PWQY	VF	VR
Qy	481	RHNERRFL	NRTK	KT	ISL	GK	AKLS	LOEL	WTWMS	VR	DC
Db	481	RHNERRFL	NRTK	KT	ISL	GK	AKLS	LOEL	WTWMS	VR	DC
Qy	541	LAKFLH	LWLS	VVYV	VELLS	RP	FFVT	TET	TFQK	NRL	FP
Db	541	LAKFLH	LWLS	VVYV	VELLS	RP	FFVT	TET	TFQK	NRL	FP


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Db 541 LAKFLHLMSSVYVLELRFYFYTETTFQKRLFFYKSVMSKQIGIROHLKRVQLRE 600
Qy 601 LSEAEVRQREARPAALLTSRLRPIPKPDGLRPVNMNDYVVGARTFPRKRAELRTSRVKA 660
Db 601 LSEAEVRQREARPAALLTSRLRPIPKPDGLRPVNMNDYVVGARTFPRKRAELRTSRVKA 660
Qy 661 LFSVLNYSERARRPGLLGASVLGDDIHRARWTFVLRVRAQDPPPELYFVKVDVDTGAYDTI 720
Db 661 LFSVLNYSERARRPGLLGASVLGDDIHRARWTFVLRVRAQDPPPELYFVKVDVDTGAYDTI 720
Qy 721 PODRLTEVIASIIKPONTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPONTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
Qy 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVYQCOGIPQGSILSTL 840
Db 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVYQCOGIPQGSILSTL 840
Qy 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYEGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYEGCVVNL 900
Qy 901 RKTVMNFPVEDEALGCTAFVQMPAHGLFPWCGLLDDTRTLEVOSSDYSSVARTSIRASLTF 960
Db 901 RKTVMNFPVEDEALGCTAFVQMPAHGLFPWCGLLDDTRTLEVOSSDYSSVARTSIRASLTF 960
Qy 961 NRGFKAGNRMRKLFVGLRLKCHSLFDLDQVNSLQVCTNIIKILLQAYRHACVLQPL 1020
Db 961 NRGFKAGNRMRKLFVGLRLKCHSLFDLDQVNSLQVCTNIIKILLQAYRHACVLQPL 1020
Qy 1021 FHQVWKNTFFLRLVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
Db 1021 FHQVWKNTFFLRLVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
Qy 1081 KLTRHRVTYVPLLGSLRTAQOLSRKLPCTTTLTALEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLLGSLRTAQOLSRKLPCTTTLTALEAAANPALPSDFKTILD 1132

RESULT 17
US-10-389-431-2
; Sequence 2, Application US/10389431
; Publication NO. US20040180347A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence
; APPLICANT: Ralph, Brandenberger
; APPLICANT: Joseph, Gold D.
; APPLICANT: John, Irving
; APPLICANT: Mandalam, Ramkumar
; APPLICANT: Mok, Michael
; TITLE OF INVENTION: A Marker System for Preparing and Characterizing High-Quality Hum
; TITLE OF INVENTION: Embryonic Stem Cells
; FILE REFERENCE: 135/002
; CURRENT APPLICATION NUMBER: US/10/389,431
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-389-431-2

Query Match 100.0%; Score 5961; DB 16; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPCRRAVRSLLSHRYEVLPLATFVRRLGQWRLVQRGDPAAFRALVAQCLVCPW 60
Db 1 MPRAPCRRAVRSLLSHRYEVLPLATFVRRLGQWRLVQRGDPAAFRALVAQCLVCPW 60
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RESULT 18

US-10-877-124-2
; Sequence 2, Application US/10877124
; Publication No. US20040242529A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,124
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-Apr-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-Apr-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-May-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-May-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-Oct-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-Oct-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-10-877-124-2

Query Match 100.0%; Score 5961; DB 16; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPOGWRLVQRGDPAAAPRALVAQCLVCVPW	60
DB	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPOGWRLVQRGDPAAAPRALVAQCLVCVPW	60
QY	61	DARPPAAPSPROVSCIKELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEAFTTSVR	120
DB	61	DARPPAAPSPROVSCIKELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEAFTTSVR	120
QY	121	SYLENTVTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA	180
DB	121	SYLENTVTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA	180
QY	181	ATQARPPPHASGPRRRRLGCERAWNHSYREAGVPLGLPAPGARRRGGSSASRSILPLPKRRR	240
DB	181	ATQARPPPHASGPRRRRLGCERAWNHSYREAGVPLGLPAPGARRRGGSSASRSILPLPKRRR	240
QY	241	GAAPERTPVGQGSWAHPGTRGDRGFCVSPARPABEATSLLEGALSSTRSHSPSVG	300
DB	241	GAAPERTPVGQGSWAHPGTRGDRGFCVSPARPABEATSLLEGALSSTRSHSPSVG	300
QY	301	RQHHAGPPSTSRPPRMDTPCPPVYAEKTFHYSSGDKQLRPSFLSSLPSTGARRL	360
DB	301	RQHHAGPPSTSRPPRMDTPCPPVYAEKTFHYSSGDKQLRPSFLSSLPSTGARRL	360
QY	361	VETIFLGSRRPMPCTPRRLPRLPORYQWMLRPLFLELLGNHAOCYPYGVLLKTHCPLRAAVT	420
DB	361	VETIFLGSRRPMPCTPRRLPRLPORYQWMLRPLFLELLGNHAOCYPYGVLLKTHCPLRAAVT	420
QY	421	PAAGVCAREKPGQSVAAPEBEDTDRRLVQLLRHSSSPWQVYGFVRACLRRLVPPGLWGS	480
DB	421	PAAGVCAREKPGQSVAAPEBEDTDRRLVQLLRHSSSPWQVYGFVRACLRRLVPPGLWGS	480
QY	481	RHNERFLRNTKTFISLGKHAKLSQLBELTWQMSVRDCAWLRSPGVGCVPAAEHRLREI	540
DB	481	RHNERFLRNTKTFISLGKHAKLSQLBELTWQMSVRDCAWLRSPGVGCVPAAEHRLREI	540
QY	541	LAKFLHMLMSYVVVLELRSFFYVTTFTFQKNRLFYKSVMSKLOSIGIROHLKRVQURE	600
DB	541	LAKFLHMLMSYVVVLELRSFFYVTTFTFQKNRLFYKSVMSKLOSIGIROHLKRVQURE	600
QY	601	LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA	660
DB	601	LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA	660
QY	661	LFSVLNYERARRPGLLGASVLGDDIIHRAWTFVLRVRAQDPPPELYFVKVDVTGAYDTI	720
DB	661	LFSVLNYERARRPGLLGASVLGDDIIHRAWTFVLRVRAQDPPPELYFVKVDVTGAYDTI	720
QY	721	PODRLTEVIASIIKPNQTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL	780
DB	721	PODRLTEVIASIIKPNQTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL	780
QY	781	QETSPLRDVAVIEOSSSLNEASSGLFDVFLRFMCHAVRIRGKSVYVQCGIPQGSILSTL	840
DB	781	QETSPLRDVAVIEOSSSLNEASSGLFDVFLRFMCHAVRIRGKSVYVQCGIPQGSILSTL	840
QY	841	LCSLCYGDMENKLPAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGPEYGCVVNL	900
DB	841	LCSLCYGDMENKLPAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGPEYGCVVNL	900
QY	901	RKTVNPFEVEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSTRASLTF	960
DB	901	RKTVNPFEVEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSTRASLTF	960
QY	961	NRGFKAGNMRKLFVLRLLKCHSLFDLQVNSLQTVCTNIYKILLQAYRPHACVLQLP	1020
DB	961	NRGFKAGNMRKLFVLRLLKCHSLFDLQVNSLQTVCTNIYKILLQAYRPHACVLQLP	1020
QY	1021	FHQQWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHQAFLL	1080
DB	1021	FHQQWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHQAFLL	1080
QY	1081	KLTRHRTVTVPLGSLRTPAQTQLSRKLPGTTLTALAAANPALPSDFKTLTD 1132	

Db 1081 KLTRHRTVYVPLGLSLRTAQTLQRKLPCTTLTALEAANPALPSDFKTILD 1132

RESULT 19

US-10-877-022-2

; Sequence 2, Application US/10877022

; Publication NO. US20040247613A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin B.

; Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; FILING DATE: 24-Jun-2004

; CLASSIFICATION: US/10/877,022

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/432,503

; FILING DATE: 02-Nov-1999

; APPLICATION NUMBER: 08/974,549

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-Apr-1997

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-Apr-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-May-1997

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-May-1997

; APPLICATION NUMBER: US 08/911,312

; FILING DATE: 14-Aug-1997

; APPLICATION NUMBER: US 08/912,951

; FILING DATE: 14-Aug-1997

; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-Aug-1997

; APPLICATION NUMBER: WO PCT/US97/17618

; FILING DATE: 01-Oct-1997

; APPLICATION NUMBER: WO PCT/US97/17885

; FILING DATE: 01-Oct-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph Ted

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002610US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1132 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-877-022-2

Query Match 100.0%; Score 5961; DB 16; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRRLQPCQWRLLVQRGDDPAAFRALVAQCLVCVPM 60
DB 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRRLQPCQWRLLVQRGDDPAAFRALVAQCLVCVPM 60

QY 61 DARPPPAAPSFRQVSKLKLVARVLQRLCERCAKKNVLAFGFALLDGCARGCPPEAFTTSVR 120
DB 61 DARPPPAAPSFRQVSKLKLVARVLQRLCERCAKKNVLAFGFALLDGCARGCPPEAFTTSVR 120

QY 121 SYLPTNTVDALRGSGAWGLLLRRVGDVVLVHLLARCALFVLVAPSCAYVCGPPPLYQLGA 180
DB 121 SYLPTNTVDALRGSGAWGLLLRRVGDVVLVHLLARCALFVLVAPSCAYVCGPPPLYQLGA 180

QY 181 ATOARPPPHASGPRRLGCRANWHSVREAGVPLGLPAPGARRRGGSASRSIPLPKRPRR 240
DB 181 ATOARPPPHASGPRRLGCRANWHSVREAGVPLGLPAPGARRRGGSASRSIPLPKRPRR 240

QY 241 GAAPEPERTVQGGSWAHPGRTRGSDRGFCVVSAPABEATSLEGALSGTRHSHPSVG 300
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QY 301 RQHAGPPSTSRPRPMDTPCPVYAETKHFYSSGDKQLRPSFLLSSRLPSLTGARRL 360
DB 301 RQHAGPPSTSRPRPMDTPCPVYAETKHFYSSGDKQLRPSFLLSSRLPSLTGARRL 360

QY 361 VETIFLGSRPWMPGTPRRLPRLPQRYQWMRPLFLELLGNHAOCYPYGVLLKTHCPIRAAVT 420
DB 361 VETIFLGSRPWMPGTPRRLPRLPQRYQWMRPLFLELLGNHAOCYPYGVLLKTHCPIRAAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVOLLROHSSPWQVYGFVRACLRLLVPCLWGS 480
DB 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVOLLROHSSPWQVYGFVRACLRLLVPCLWGS 480

QY 481 RHNERRFLRNTKCFISLGHAKLSLQELTWKMSVRDCAWLRSPGVCVPAAEHLRREI 540
DB 481 RHNERRFLRNTKCFISLGHAKLSLQELTWKMSVRDCAWLRSPGVCVPAAEHLRREI 540

QY 541 LAKFLHLMMSVYVVELLSRFFVYVTTTQKNRLFFYRKSVMSKLSQIGIRHQLKRVQRE 600
DB 541 LAKFLHLMMSVYVVELLSRFFVYVTTTQKNRLFFYRKSVMSKLSQIGIRHQLKRVQRE 600

QY 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTPRERKRAERLSRVKA 660
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QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRVRAQDPPPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRVRAQDPPPPPELYFVKVDVTGAYDTI 720

QY 721 PODRLTEVIASIIKPQNTYCVRRYAVQKAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
DB 721 PODRLTEVIASIIKPQNTYCVRRYAVQKAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780

QY 781 QETSPLRDAVTEQSSSINEASSGLFDVFLFPMCHHVRIRKSVYQCGIIPGGSILSTL 840
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QY 841 LCSICYGDMENKLPAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYCVVNL 900
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QY 901 RKTVMNPFVEDEALGGTAFVQMPAHLFPWCGLLDTRTLEVSQSYSSYARTSIRASLTFF 960
DB 901 RKTVMNPFVEDEALGGTAFVQMPAHLFPWCGLLDTRTLEVSQSYSSYARTSIRASLTFF 960

QY 961 NRGFKAGNMRKLPGLVRLKCHSLFLDLQVNSLOTVCTNIYKILLLOAYRFHACVLQLP 1020
DB 961 NRGFKAGNMRKLPGLVRLKCHSLFLDLQVNSLOTVCTNIYKILLLOAYRFHACVLQLP 1020

QY 1021 FHQQVWKNPFTFLRVISDTASILCAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Db 1021 FHQQWKNPTFLRVIDSTALCSYLKAKAGMSLGAAGPLPSAVQWLCHQAPLL 1080
Qy 1081 KLTRHRTVTVPLGLSLRTAQQLSKLPGTTLTALAAANPALPSDFKTILD 1132
Db 1081 KLTRHRTVTVPLGLSLRTAQQLSKLPGTTLTALAAANPALPSDFKTILD 1132

RESULT 20

US-10-862-698-3

Sequence 3, Application US/10862698

Publication No. US20040253701A1

GENERAL INFORMATION:

APPLICANT: Morin, Gregg B.
Allsopp, Richard
DePinho, Ronald
Greenberg, Roger

TITLE OF INVENTION: Mouse Telomerase Reverse Transcriptase

NUMBER OF SEQUENCES: 101

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/862,698

FILING DATE: 07-Jun-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/042,460

FILING DATE: 16-MAR-1998

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: US 08/974,549

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US 08/974,584

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US 08/979,742

FILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:

NAME: Einhorn, Gregory P.

REGISTRATION NUMBER: 38,440

REFERENCE/DOCKET NUMBER: 015389-003110US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1132 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1132
OTHER INFORMATION: /note= "human telomerase reverse
transcriptase (hTERT)"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-862-698-3

Query Match 100.0%; Score 5961; DB 16; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLPGOGWRLVORGDPAAAFALVAQCILVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLPGOGWRLVORGDPAAAFALVAQCILVCVPW 60
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Db 61 DARPPPAAPSFQVSCCLKELVARVQLRCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
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Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
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Db 181 ATQARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRPR 240
Qy 241 GAAPEPERTVGGQSWAHPGRTGRGSDRGFCVSPARPABEATSLEGALSCTRHSHPVG 300
Db 241 GAAPEPERTVGGQSWAHPGRTGRGSDRGFCVSPARPABEATSLEGALSCTRHSHPVG 300
Qy 301 RQHHAGPPSTSRPPRPMWDTPCPPVYAEKHLFYSSGDKQLRPSFLSSLPSLTGAARL 360
Db 301 RQHHAGPPSTSRPPRPMWDTPCPPVYAEKHLFYSSGDKQLRPSFLSSLPSLTGAARL 360
Qy 361 VETIFLGSRPWMPGTPRRLPRLPORYWQMRPLFLELGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPWMPGTPRRLPRLPORYWQMRPLFLELGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSSPWQYVGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSSPWQYVGFVRACLRRLVPPGLWGS 480
Qy 481 RHNERFLRNTKKFISLGKHAKLQBELTWQMSVRDCAWLRSPGVGCVPAAEHRLREI 540
Db 481 RHNERFLRNTKKFISLGKHAKLQBELTWQMSVRDCAWLRSPGVGCVPAAEHRLREI 540
Qy 541 LAKFLHLMMSVYVVELLRSFPYVTTFTQKRLFFYKRSVWSKLQSIGIRHKLKRVQURE 600
Db 541 LAKFLHLMMSVYVVELLRSFPYVTTFTQKRLFFYKRSVWSKLQSIGIRHKLKRVQURE 600
Qy 601 LSEAEVRQHREARPALITSRLRFIPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRYKA 660
Db 601 LSEAEVRQHREARPALITSRLRFIPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRYKA 660
Qy 661 LFSVLYNTERARRPGLLGASVLGLDDIHRAMTTFVLRVAQDPPPELYPVKVDVTGAYDTI 720
Db 661 LFSVLYNTERARRPGLLGASVLGLDDIHRAMTTFVLRVAQDPPPELYPVKVDVTGAYDTI 720
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Db 781 QETSPLRDVAVIEQSSSINEASSGLFDVFLRFMCHHAVIRKGSYVQCQGIPOQSILSTL 840

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QY 841 LCSLCYGDMMENKLFAGIRRDGGLLLRLVDDFLVTPHLLTHAKTFLRLTVRGVPEYGCNVN 900
DB 841 LCSLCYGDMMENKLFAGIRRDGGLLLRLVDDFLVTPHLLTHAKTFLRLTVRGVPEYGCNVN 900
QY 901 RKTUVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDTRILEVQSDYSSVARTSIRASLTF 960
DB 901 RKTUVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDTRILEVQSDYSSVARTSIRASLTF 960
QY 961 NRGFKAGNRMRKLFGLVRLKCHSLFLLDQVNSLQVTCVNIYKILLQAYRHACVQLQP 1020
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QY 1021 FHOQVWKNPTFFLRVISTASLCYSLKAKNAGMSLGAKGAGPLPSEAVQMLCHOAFLL 1080
DB 1021 FHOQVWKNPTFFLRVISTASLCYSLKAKNAGMSLGAKGAGPLPSEAVQMLCHOAFLL 1080
QY 1081 KLTRHRVTYVPLGLSRTAQTLRSKLPCTTLTAAEAAANPALPSDFKTILD 1132
DB 1081 KLTRHRVTYVPLGLSRTAQTLRSKLPCTTLTAAEAAANPALPSDFKTILD 1132

RESULT 21
US-10-831-266-4
; Sequence 4, Application US/10831266
; Publication No. US20050003404A1
; GENERAL INFORMATION:
; APPLICANT: Rowley, Peter T.
; TITLE OF INVENTION: TELOMERASE INTERFERENCE
; FILE REFERENCE: A-71506-1/RFT/THR
; CURRENT APPLICATION NUMBER: US/10/831,266
; CURRENT FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: PCT/US 02/33065
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/345,326
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/359,196
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/383,195
; PRIOR FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-831-266-4

Query Match 100.0%; Score 5961; DB 17; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSILRSHYEVLPATFVRRLPGQWRLVORGDPAAFRALVAQCLVCVPM 60
DB 1 MPRAPRCRAVRSILRSHYEVLPATFVRRLPGQWRLVORGDPAAFRALVAQCLVCVPM 60
QY 61 DARPPAAPSFQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGCARGPPEAFTTSVR 120
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DB 301 ROHAGPPSTPRPPWDTPCPVVAETHKFLYSSGDKQLRPSFLLSLRPSLTGARLL 360
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QY 541 LAKFLHMLMSVVVVELLSRFFVYVTTTFOKNRLLFFYRKSVWKSLOSIGIRQHLKRVLRE 600
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DB 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRKA 660
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DB 841 LCSLCYGDMMENKLFAGIRRDGGLLLRLVDDFLVTPHLLTHAKTFLRLTVRGVPEYGCNVN 900
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QY 961 NRGFKAGNRMRKLFGLVRLKCHSLFLLDQVNSLQVTCVNIYKILLQAYRHACVQLQP 1020
DB 961 NRGFKAGNRMRKLFGLVRLKCHSLFLLDQVNSLQVTCVNIYKILLQAYRHACVQLQP 1020
QY 1021 FHOQVWKNPTFFLRVISTASLCYSLKAKNAGMSLGAKGAGPLPSEAVQMLCHOAFLL 1080
DB 1021 FHOQVWKNPTFFLRVISTASLCYSLKAKNAGMSLGAKGAGPLPSEAVQMLCHOAFLL 1080
QY 1081 KLTRHRVTYVPLGLSRTAQTLRSKLPCTTLTAAEAAANPALPSDFKTILD 1132
DB 1081 KLTRHRVTYVPLGLSRTAQTLRSKLPCTTLTAAEAAANPALPSDFKTILD 1132
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RESULT 22

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US-10-492-034-2
; Sequence 2, Application US/10492034
; Publication No. US20050008621A1
; GENERAL INFORMATION:
; APPLICANT: Kirkland, James
; APPLICANT: Tchkonla, Tamara
; TITLE OF INVENTION: PREADIPOCYTE CELL STRAINS AND USES THEREFORE
; FILE REFERENCE: BUI-011US
; CURRENT APPLICATION NUMBER: US/10/492,034
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: PCT/US02/31635
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327650
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 60/327651
; PRIOR FILING DATE: 2001-10-06
; NUMBER OF SEQ ID NOS: 12
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-492-034-2

Query Match      100.0%; Score 5961; DB 17; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCAVRSLLRSHYREVLPATFVRRILGPOQWRLVQRGDPAAFRALVAQCLVCPW 60
DB 1 MPRAPRCAVRSLLRSHYREVLPATFVRRILGPOQWRLVQRGDPAAFRALVAQCLVCPW 60

QY 61 DARPPPAAPSFQVSCLEKELVARVLQRCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
DB 61 DARPPPAAPSFQVSCLEKELVARVLQRCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

QY 121 SYLNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGGASRSILPLKRRR 240
DB 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGGASRSILPLKRRR 240

QY 241 GAAPEPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSGRHSHPSVG 300
DB 241 GAAPEPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSGRHSHPSVG 300

QY 301 ROHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLLSRPSLTGARRL 360
DB 301 ROHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLLSRPSLTGARRL 360

QY 361 VETIFLGSRRPMPGTPRRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAAT 420
DB 361 VETIFLGSRRPMPGTPRRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAAT 420

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-831-267-4

Query Match      100.0%; Score 5961; DB 17; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCAVRSLLRSHYREVLPATFVRRILGPOQWRLVQRGDPAAFRALVAQCLVCPW 60
DB 1 MPRAPRCAVRSLLRSHYREVLPATFVRRILGPOQWRLVQRGDPAAFRALVAQCLVCPW 60

QY 61 DARPPPAAPSFQVSCLEKELVARVLQRCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
DB 61 DARPPPAAPSFQVSCLEKELVARVLQRCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

QY 121 SYLNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGGASRSILPLKRRR 240
DB 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGGASRSILPLKRRR 240

QY 241 GAAPEPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSGRHSHPSVG 300
DB 241 GAAPEPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSGRHSHPSVG 300

QY 301 ROHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLLSRPSLTGARRL 360
DB 301 ROHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLLSRPSLTGARRL 360

QY 361 VETIFLGSRRPMPGTPRRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAAT 420
DB 361 VETIFLGSRRPMPGTPRRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAAT 420

; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-831-267-4

Query Match      100.0%; Score 5961; DB 17; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCAVRSLLRSHYREVLPATFVRRILGPOQWRLVQRGDPAAFRALVAQCLVCPW 60
DB 1 MPRAPRCAVRSLLRSHYREVLPATFVRRILGPOQWRLVQRGDPAAFRALVAQCLVCPW 60

QY 61 DARPPPAAPSFQVSCLEKELVARVLQRCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
DB 61 DARPPPAAPSFQVSCLEKELVARVLQRCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

QY 121 SYLNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGGASRSILPLKRRR 240
DB 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGGASRSILPLKRRR 240

QY 241 GAAPEPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSGRHSHPSVG 300
DB 241 GAAPEPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSGRHSHPSVG 300

QY 301 ROHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLLSRPSLTGARRL 360
DB 301 ROHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLLSRPSLTGARRL 360

QY 361 VETIFLGSRRPMPGTPRRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAAT 420
DB 361 VETIFLGSRRPMPGTPRRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAAT 420
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421 PAAGVCAREKPKQSGVAAPBEEDTDPRLVOLLQHSHPQVYGFVRACLRLRLLVPPGLWGS 480
421 PAAGVCAREKPKQSGVAAPBEEDTDPRLVOLLQHSHPQVYGFVRACLRLRLLVPPGLWGS 480
481 RHNERFLRNTKFFISLGHAKLSLOELTWKMSVRDCAMLRSPGVGCVPAAEHRLREI 540
481 RHNERFLRNTKFFISLGHAKLSLOELTWKMSVRDCAMLRSPGVGCVPAAEHRLREI 540
541 LAKFLHMLSVVYVELLRSPFFVYTTETTFQKNRFFYRKSVWSKLSQIGIRQHLKRVQLRE 600
541 LAKFLHMLSVVYVELLRSPFFVYTTETTFQKNRFFYRKSVWSKLSQIGIRQHLKRVQLRE 600
601 LSAEVRQREARPPALLTSRLRPIPKPDGLRPIVNMVYVVGARTPRREKRAELTSRVKA 660
601 LSAEVRQREARPPALLTSRLRPIPKPDGLRPIVNMVYVVGARTPRREKRAELTSRVKA 660
661 LFSVLNVERARRPGLGASVLGLDDIHRARWTFVLRAQDPPPELYFVKVDVVTGAYDTI 720
661 LFSVLNVERARRPGLGASVLGLDDIHRARWTFVLRAQDPPPELYFVKVDVVTGAYDTI 720
721 PODRLTEVIASIIKPNQTYCVRYAVVQKAAHGHVKAFAKSHVSTLTDLPYMRQFVAHL 780
721 PODRLTEVIASIIKPNQTYCVRYAVVQKAAHGHVKAFAKSHVSTLTDLPYMRQFVAHL 780
781 QETSPLRDVAVIEQSSSLNEASGLFDVFLRFMCHHAVIRGKSVYVQCQI PQGSILSTL 840
781 QETSPLRDVAVIEQSSSLNEASGLFDVFLRFMCHHAVIRGKSVYVQCQI PQGSILSTL 840
841 LCSLCYGDENKLFAGIRDDGLLLRLVDDFLVTPHLTHAKTFLRLTVRGVPEYGCVNL 900
841 LCSLCYGDENKLFAGIRDDGLLLRLVDDFLVTPHLTHAKTFLRLTVRGVPEYGCVNL 900
901 RKTVMNPFVEDEALGTAFOVQPAHGLFPWCGLLDTRILEVQSDYSSVARTSIRASLTF 960
901 RKTVMNPFVEDEALGTAFOVQPAHGLFPWCGLLDTRILEVQSDYSSVARTSIRASLTF 960
961 NRGFKAGRNRRKLFVGLRLKCHSLFLDIQVNSLQVCTNIYKILLQAYRFHACVQLP 1020
961 NRGFKAGRNRRKLFVGLRLKCHSLFLDIQVNSLQVCTNIYKILLQAYRFHACVQLP 1020
1021 FHOQVWKNPTFLRVISDTFASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
1021 FHOQVWKNPTFLRVISDTFASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
1081 KLTRHRVTYVPLGLSLRTAQTLQSLKPLGTTITALEAANPALPSDFKTILD 1132
1081 KLTRHRVTYVPLGLSLRTAQTLQSLKPLGTTITALEAANPALPSDFKTILD 1132

RESULT 24
US-10-877-146-2
Sequence 2, Application US/10877146
Publication No. US20050013825A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,146
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-877-146-2

Query Match 100.0%; Score 5961; DB 17; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAPRCRAVRSLRSHYREVLPATFVRRLPGQWRLVORGDPAAFRALVAQCLVCVPW 60
Db 1 MPAPRCRAVRSLRSHYREVLPATFVRRLPGQWRLVORGDPAAFRALVAQCLVCVPW 60
QY 61 DARPPPAAPSFQVSCSLKELVARVLQRLCERCAKVNLAFGFALLDGARGPPEAFTTSVR 120
Db 61 DARPPPAAPSFQVSCSLKELVARVLQRLCERCAKVNLAFGFALLDGARGPPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGAWGLLRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVDALRGSGAWGLLRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAGRRRGGSSASRSLPLKRRPR 240
Db 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAGRRRGGSSASRSLPLKRRPR 240
QY 241 GAAPEPPTVQSGSWAHPGTRGSDRGFCVVSFARPAEEATSLGALSGLTRHSHPSVG 300
Db 241 GAAPEPPTVQSGSWAHPGTRGSDRGFCVVSFARPAEEATSLGALSGLTRHSHPSVG 300
QY 301 RQHAGPSTSRPPRPWDTPCPVVAETKHFYSSGDKEQRLAPSPFLLSLRSLTGARLL 360
Db 301 RQHAGPSTSRPPRPWDTPCPVVAETKHFYSSGDKEQRLAPSPFLLSLRSLTGARLL 360

Db 961 NRGPAGNRMRKLFVLRKCHSLFVLDQVNSLQTVCTNYIKILLQAYRFHACVQLQP 1020
QY 1021 FHQQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
Db 1021 FHQQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
QY 1081 KLTHRVTVVPLGLSLRTHAQOLSRKLPOTTTTALAEAAANPALPSDFKTILD 1132
Db 1081 KLTHRVTVVPLGLSLRTHAQOLSRKLPOTTTTALAEAAANPALPSDFKTILD 1132

RESULT 26
US-10-918-739-2
; Sequence 2, Application US/10918739
; Publication No. US20050054093A1
; GENERAL INFORMATION:
; APPLICANT: Haas, Martin
; TITLE OF INVENTION: MULTIPOTENT AMNIOTIC FETAL STEM CELLS
; FILE REFERENCE: HAAS.004A
; CURRENT APPLICATION NUMBER: US/10/918,739
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/495,437
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: 60/495,513
; PRIOR FILING DATE: 2003-08-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-918-739-2

Query Match 100.0%; Score 5961; DB 17; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLRSHRYEVLPATFVRRGLPQGWRLVQRGDPAAFRALVAQCLVCPW 60
Db 1 MPAPRCRAVRSLRSHRYEVLPATFVRRGLPQGWRLVQRGDPAAFRALVAQCLVCPW 60

QY 61 DARPPAPSPFQVSCLELVARVLQRCERGAKNVLPAGFALLDGAAGGPPPEAFTTSVR 120
Db 61 DARPPAPSPFQVSCLELVARVLQRCERGAKNVLPAGFALLDGAAGGPPPEAFTTSVR 120

QY 121 SYLPTNTVDALGSGANGLLIRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVDALGSGANGLLIRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLGRCERAWNHSVREAGVPLGLPAGARRRGSASRSLPLKPRR 240
Db 181 ATQARPPPHASGPRRLGRCERAWNHSVREAGVPLGLPAGARRRGSASRSLPLKPRR 240

QY 241 GAAPPERTPVQGSWAHPGRTGSDRGFCVVSAPARAEATSLEGALSGTRHSHPSVG 300
Db 241 GAAPPERTPVQGSWAHPGRTGSDRGFCVVSAPARAEATSLEGALSGTRHSHPSVG 300

QY 301 ROHAGPSTSPRPPMDTPCPVVAETHKFLYSSGDKQLRPSFLSLRSLTGARRL 360
Db 301 ROHAGPSTSPRPPMDTPCPVVAETHKFLYSSGDKQLRPSFLSLRSLTGARRL 360

QY 361 VETIFLGRPMWPGTPRRLPLRPLQRYQWOMRPLFLELLGNHACQPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGRPMWPGTPRRLPLRPLQRYQWOMRPLFLELLGNHACQPYGVLLKTHCPRAAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSSPMQVYGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSSPMQVYGFVRACLRRLVPPGLWGS 480

QY 481 RHNERFLNTKKFISLGHAKLSLOELTWKMSVRDCAWLRRSPGVCGVPAAEHLRBEI 540
Db 481 RHNERFLNTKKFISLGHAKLSLOELTWKMSVRDCAWLRRSPGVCGVPAAEHLRBEI 540

QY 541 LAKFLHLMSSVVVVELLSFFVVTETTTQKNRLLFFYRKSVMSKLSQSIGIRHOLKRVQRE 600
Db 541 LAKFLHLMSSVVVVELLSFFVVTETTTQKNRLLFFYRKSVMSKLSQSIGIRHOLKRVQRE 600
QY 601 LSEAEVROHREARPAALLTSRLRFPKPGRLPIVMDYVVGARTTFRKRAERLTSRVKA 660
Db 601 LSEAEVROHREARPAALLTSRLRFPKPGRLPIVMDYVVGARTTFRKRAERLTSRVKA 660
QY 661 LFSVLNYSERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYSERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPONTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPQYMRQFAHL 780
Db 721 PODRLTEVIASIIKPONTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPQYMRQFAHL 780
QY 781 QETSLRDVAVVEQSSSLNEASSGLFDVFLRFMCHAVRIRKSVYVOCQIGPQGSILSTL 840
Db 781 QETSLRDVAVVEQSSSLNEASSGLFDVFLRFMCHAVRIRKSVYVOCQIGPQGSILSTL 840
QY 841 LCSLCYGDWENKLPAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVEYGCVNL 900
Db 841 LCSLCYGDWENKLPAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVEYGCVNL 900
QY 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLLEVQSDYSYARTSIRASLTF 960
Db 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLLEVQSDYSYARTSIRASLTF 960
QY 961 NRGPAGNRMRKLPVLRKCHSLFVLDQVNSLQTVCTNYIKILLQAYRFHACVQLQP 1020
Db 961 NRGPAGNRMRKLPVLRKCHSLFVLDQVNSLQTVCTNYIKILLQAYRFHACVQLQP 1020
QY 1021 FHQQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
Db 1021 FHQQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
QY 1081 KLTHRVTVVPLGLSLRTHAQOLSRKLPOTTTTALAEAAANPALPSDFKTILD 1132
Db 1081 KLTHRVTVVPLGLSLRTHAQOLSRKLPOTTTTALAEAAANPALPSDFKTILD 1132

RESULT 27

US-10-637-443-2
; Sequence 2, Application US/10637443
; Publication No. US20050070492A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Antisense Compositions for Detecting and
; Inhibiting Telomerase Reverse Transcriptase
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/637,443
; FILING DATE: 08-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/953,052
FILING DATE: 14-Sep-2001
APPLICATION NUMBER: 09/052,919
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-00360005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-637-443-2

Query Match 100.0%; Score 5961; DB 17; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Gaps 0;

QY 1 MPAPRCRAVSLRLSHYREVLPVPLATFVRRLLGPOGWRVLVQRGDPAAPRALVAQCCLVCPW 60
DB 1 MPAPRCRAVSLRLSHYREVLPVPLATFVRRLLGPOGWRVLVQRGDPAAPRALVAQCCLVCPW 60

QY 61 DARPPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFFGFPALLDGARGGPEAFTTSVR 120
DB 61 DARPPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFFGFPALLDGARGGPEAFTTSVR 120

QY 121 SYLNTVNTDALRGSGAWGILLRRVDDVTLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVNTDALRGSGAWGILLRRVDDVTLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLCERAWNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRPRR 240
DB 181 ATQARPPPHASGPRRLCERAWNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRPRR 240

QY 241 GAAPEPERTVQGSWAHPGRTRGSDRGFCVSPARPAEATSLLEGALSCTRHSHPVSG 300
DB 241 GAAPEPERTVQGSWAHPGRTRGSDRGFCVSPARPAEATSLLEGALSCTRHSHPVSG 300

QY 301 RQHAGPSTSRPPRPWTPCPVVAETKHYLYSSGDKQLRPSFLLSRPSLTGARRL 360
DB 301 RQHAGPSTSRPPRPWTPCPVVAETKHYLYSSGDKQLRPSFLLSRPSLTGARRL 360

QY 361 VETIFLGRPWMPGTFRPLRPLQRYWQMRPLFLELLGNHAQCQPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGRPWMPGTFRPLRPLQRYWQMRPLFLELLGNHAQCQPYGVLLKTHCPLRAAVT 420

QY 421 PAAGVCAREKPOGSAAPBEEDTDPRRLVQLLRQHSFPWQYGVFVRACLRLVPPGLMGS 480
DB 421 PAAGVCAREKPOGSAAPBEEDTDPRRLVQLLRQHSFPWQYGVFVRACLRLVPPGLMGS 480

QY 481 RHNERREFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRSSPGVGCVPAAEHLREEI 540
DB 481 RHNERREFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRSSPGVGCVPAAEHLREEI 540

QY 541 LAKFLHLMSSVYVVELLRSFFYVTTTFQKNRLFYFKSVMSKLSQICIRQHLKRVOLRE 600
DB 541 LAKFLHLMSSVYVVELLRSFFYVTTTFQKNRLFYFKSVMSKLSQICIRQHLKRVOLRE 600

QY 601 LSEAEVRQHREARPAALLTSRLRFPKDPGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVRQHREARPAALLTSRLRFPKDPGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660

QY 661 LFSVLNYERARRPGLLGASVLGLDDDIHRAWRTFVLVRAODPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNYERARRPGLLGASVLGLDDDIHRAWRTFVLVRAODPPPELYFVKVDVTGAYDTI 720

QY 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMQFVAHL 780
DB 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMQFVAHL 780

QY 781 QETSPLRDADVIEQSSSLNEASSGLPDVFLRFMCHHVAIRGKSYVQCQGIPOQSILSTL 840
DB 781 QETSPLRDADVIEQSSSLNEASSGLPDVFLRFMCHHVAIRGKSYVQCQGIPOQSILSTL 840

QY 841 LCSLCYGD MENKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
DB 841 LCSLCYGD MENKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900

QY 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVVQSDYSYARTSIRASLTF 960
DB 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVVQSDYSYARTSIRASLTF 960

QY 961 NRGFKAGRNMRRLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLOLP 1020
DB 961 NRGFKAGRNMRRLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLOLP 1020

QY 1021 FHOQVWKNPTFFLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL 1080
DB 1021 FHOQVWKNPTFFLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL 1080

QY 1081 KLTFHRVTVYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTILD 1132
DB 1081 KLTFHRVTVYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTILD 1132

RESULT 28
US-10-490-143A-19
; Sequence 19, Application US/10490143A
; Publication No. US20050079606A1
; GENERAL INFORMATION:
; APPLICANT: TETSURO TAMAKI
; APPLICANT: KIYOSHI ANDO
; TITLE OF INVENTION: MULTIPOTENT STEM CELL IN THE INTERSTITIAL TISSUES OF SKELETAL MUS
; FILE REFERENCE: 766.108
; CURRENT APPLICATION NUMBER: US/10/490,143A
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: JP2001-286332
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: JP2002-133575
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-490-143A-19

Query Match 100.0%; Score 5961; DB 17; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRLSLSHYREVLPPLATFVRRLLGPOGWRVLRQGDPAAFRALVAQCVCVPM 60
DB 1 MPAPRCRAVRLSLSHYREVLPPLATFVRRLLGPOGWRVLRQGDPAAFRALVAQCVCVPM 60

QY 61 DARPPAAPSPROQSVCLKELVARVLQRLCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120
DB 61 DARPPAAPSPROQSVCLKELVARVLQRLCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120

QY 121 SYLNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAGARRRGGSSASRSLLPKRPRR 240
DB 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAGARRRGGSSASRSLLPKRPRR 240

QY 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSCTRHSHPVSG 300
DB 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSCTRHSHPVSG 300

QY 301 RQHAGPSTSRPPRWDTPCPVVAETKHFYSSGDKQLRPSFLLSLRPSLTGARRL 360
DB 301 RQHAGPSTSRPPRWDTPCPVVAETKHFYSSGDKQLRPSFLLSLRPSLTGARRL 360

QY 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMLRFLLELGNHAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMLRFLLELGNHAQCPYGVLLKTHCPLRAAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQVYGFVRACLRLRVPPLGWS 480
DB 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQVYGFVRACLRLRVPPLGWS 480

QY 481 RHNERRFLRNTKFTISLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAEHLRREI 540
DB 481 RHNERRFLRNTKFTISLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAEHLRREI 540

QY 541 LAKFLHLMMSVYVVELLSRFFVTETTPQKRLFFYRKSVMKLSQSIGIROLKRVQLRE 600
DB 541 LAKFLHLMMSVYVVELLSRFFVTETTPQKRLFFYRKSVMKLSQSIGIROLKRVQLRE 600

QY 601 LSEAEVROHREARPAALLSRFLFKPKDGLRPIVNDVYVVGARTPRRKRABRLTSRYKA 660
DB 601 LSEAEVROHREARPAALLSRFLFKPKDGLRPIVNDVYVVGARTPRRKRABRLTSRYKA 660

QY 661 LFSVLNYSERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNYSERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720

QY 721 PQDRLETVIASIIKQNTYCYRRYAVQKAAGHVRAKFKSHVSTLTDLQPMRQFVAHL 780
DB 721 PQDRLETVIASIIKQNTYCYRRYAVQKAAGHVRAKFKSHVSTLTDLQPMRQFVAHL 780

QY 781 QETSLRDAVTEIOSSSINEASSGLFDVFLPMCHHVRIRKSVVOCQIPQGSILSTL 840
DB 781 QETSLRDAVTEIOSSSINEASSGLFDVFLPMCHHVRIRKSVVOCQIPQGSILSTL 840

QY 841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGPEYGCNNL 900
DB 841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGPEYGCNNL 900

QY 901 RKTVNVFVEDEALGCTAFVQMPAHLFPWCGLLDTRTLEVSQSYASRTSIRASLTF 960
DB 901 RKTVNVFVEDEALGCTAFVQMPAHLFPWCGLLDTRTLEVSQSYASRTSIRASLTF 960

QY 961 NRGFKAGNMRRLKFGVRLKCHSLFDLQVNSLQTVCTNIIKILLQAYRFHACVLOLP 1020
DB 961 NRGFKAGNMRRLKFGVRLKCHSLFDLQVNSLQTVCTNIIKILLQAYRFHACVLOLP 1020

QY 1021 FHQVWKNTFFLRVISDTASILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

DB 1021 FHQVWKNTFFLRVISDTASILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

QY 1081 KLTRHRVTYVPLGSLRTAQTOLSKRLPGTTLTALEAANPALPSDFKTILD 1132
DB 1081 KLTRHRVTYVPLGSLRTAQTOLSKRLPGTTLTALEAANPALPSDFKTILD 1132

RESULT 29
US-10-794-514A-3
; Sequence 3, Application US/10794514A
; Publication No. US20050112134A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas
; APPLICANT: Laus, Reiner
; APPLICANT: Diegel, Michael
; APPLICANT: Vidovic, Damir
; TITLE OF INVENTION: Compositions and Methods Employing Alternative
; TITLE OF INVENTION: Reading Frame Polypeptides for the Treatment of
; FILE REFERENCE: 11311.1003U
; CURRENT APPLICATION NUMBER: US/10/794,514A
; CURRENT FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 733
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Human
US-10-794-514A-3

Query Match 100.0%; Score 5961; DB 17; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRLSLSHYREVLPPLATFVRRLLGPOGWRVLRQGDPAAFRALVAQCVCVPM 60
DB 1 MPAPRCRAVRLSLSHYREVLPPLATFVRRLLGPOGWRVLRQGDPAAFRALVAQCVCVPM 60

QY 61 DARPPAAPSPROQSVCLKELVARVLQRLCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120
DB 61 DARPPAAPSPROQSVCLKELVARVLQRLCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120

QY 121 SYLNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAGARRRGGSSASRSLLPKRPRR 240
DB 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAGARRRGGSSASRSLLPKRPRR 240

QY 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSCTRHSHPVSG 300
DB 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSCTRHSHPVSG 300

QY 301 RQHAGPSTSRPPRWDTPCPVVAETKHFYSSGDKQLRPSFLLSLRPSLTGARRL 360
DB 301 RQHAGPSTSRPPRWDTPCPVVAETKHFYSSGDKQLRPSFLLSLRPSLTGARRL 360

QY 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMLRFLLELGNHAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMLRFLLELGNHAQCPYGVLLKTHCPLRAAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQVYGFVRACLRLRVPPLGWS 480
DB 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQVYGFVRACLRLRVPPLGWS 480

QY 481 RHNERRFLRNTKFTISLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAEHLRREI 540
DB 481 RHNERRFLRNTKFTISLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAEHLRREI 540

QY 541 LAKFLHLMMSVYVVELLSRFFVTETTPQKRLFFYRKSVMKLSQSIGIROLKRVQLRE 600
DB 541 LAKFLHLMMSVYVVELLSRFFVTETTPQKRLFFYRKSVMKLSQSIGIROLKRVQLRE 600

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Db 541 LAKFLHMLMSVYVVELLRSFPVYVTTETTPQKRLRFFYRKSVWSKLQSIGIRQHLLKRVQIRE 600
Qy 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFREKRAERLTSRVKA 660
Db 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFREKRAERLTSRVKA 660
Qy 661 LFSVLNVERARRPGLIGASVGLDDIHRAMWTFVLRVAQDPPPELFFVKVDVVTGAYDTI 720
Db 661 LFSVLNVERARRPGLIGASVGLDDIHRAMWTFVLRVAQDPPPELFFVKVDVVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMQFVAHL 780
Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMQFVAHL 780
Qy 781 QETSPLRDVAVIEQSSSINEASSGLFDVFLRFMCHHAVIRKGSYVQCGIPQGSILSTL 840
Db 781 QETSPLRDVAVIEQSSSINEASSGLFDVFLRFMCHHAVIRKGSYVQCGIPQGSILSTL 840
Qy 841 LCSLCYGD MENKLFAGIRBDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCYVNL 900
Db 841 LCSLCYGD MENKLFAGIRBDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCYVNL 900
Qy 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDYSYARTSIRASLTF 960
Db 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDYSYARTSIRASLTF 960
Qy 961 NRGFKAGNNMRKLFVGLRLKCHSLFLLDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
Db 961 NRGFKAGNNMRKLFVGLRLKCHSLFLLDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
Qy 1021 FHOQWKNPTFRLVISDTSILCYSLKAKNAGSLGAKGAAGPLPSEAVOWLCHQAFLL 1080
Db 1021 FHOQWKNPTFRLVISDTSILCYSLKAKNAGSLGAKGAAGPLPSEAVOWLCHQAFLL 1080
Qy 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPCTTTLTALEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPCTTTLTALEAAANPALPSDFKTILD 1132

RESULT 30
US-10-143-536-2
; Sequence 2, Application US/10143536
; Publication No. US20040147465A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Jiang, Xu-Rong
; APPLICANT: Chiu, Choy-Pik
; APPLICANT: Harley, Calvin B.
; TITLE OF INVENTION: Treatment for Wounds
; FILE REFERENCE: 120/200
; CURRENT APPLICATION NUMBER: US/10/143,536
; CURRENT FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 60/289,903
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-143-536-2

Query Match 100.0%; Score 5961; DB 18; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPCRCAVSLRSHREVLPATFVRRLGPOGWRVQRCDDPAAFALVAQCVCVPM 60
Db 1 MPRAPCRCAVSLRSHREVLPATFVRRLGPOGWRVQRCDDPAAFALVAQCVCVPM 60

Qy 61 DARPPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEFTTSVR 120
Db 61 DARPPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEFTTSVR 120
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Qy 121 SYLPNTVTDALRGSGAWGLLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGRRRLGRCERANNHSVREAGVPLGLPAPGARBRGGSASLSLPLPKPRR 240
Db 181 ATQARPPPHASGRRRLGRCERANNHSVREAGVPLGLPAPGARBRGGSASLSLPLPKPRR 240
Qy 241 GAAPEPERTVPGQGSWAHPGRTGRGFCVVSPPARPABEATSLEGALSGTRSHSPSVG 300
Db 241 GAAPEPERTVPGQGSWAHPGRTGRGFCVVSPPARPABEATSLEGALSGTRSHSPSVG 300
Qy 301 RQHHAGPPSTRPPRMDTFCPPVYAEKTHFLYSSGDKQOLRPSFLLSLRPSLTGARRL 360
Db 301 RQHHAGPPSTRPPRMDTFCPPVYAEKTHFLYSSGDKQOLRPSFLLSLRPSLTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAVT 420
Db 361 VETIFLGSRRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAVT 420
Qy 421 PAAGVCAREKPOGSVAAPAEEDTDPRLVOLLQHSHPWQVYGFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPOGSVAAPAEEDTDPRLVOLLQHSHPWQVYGFVRACLRLVPPGLWGS 480
Qy 481 RHNERPRLNTKKPISLGKHAKLSLOBLTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
Db 481 RHNERPRLNTKKPISLGKHAKLSLOBLTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
Qy 541 LAKFLHMLMSVYVVELLRSFPVYVTTETTPQKRLRFFYRKSVWSKLQSIGIRQHLLKRVQIRE 600
Db 541 LAKFLHMLMSVYVVELLRSFPVYVTTETTPQKRLRFFYRKSVWSKLQSIGIRQHLLKRVQIRE 600
Qy 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFREKRAERLTSRVKA 660
Db 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFREKRAERLTSRVKA 660
Qy 661 LFSVLNVERARRPGLIGASVGLDDIHRAMWTFVLRVAQDPPPELFFVKVDVVTGAYDTI 720
Db 661 LFSVLNVERARRPGLIGASVGLDDIHRAMWTFVLRVAQDPPPELFFVKVDVVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMQFVAHL 780
Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMQFVAHL 780
Qy 781 QETSPLRDVAVIEQSSSINEASSGLFDVFLRFMCHHAVIRKGSYVQCGIPQGSILSTL 840
Db 781 QETSPLRDVAVIEQSSSINEASSGLFDVFLRFMCHHAVIRKGSYVQCGIPQGSILSTL 840
Qy 841 LCSLCYGD MENKLFAGIRBDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCYVNL 900
Db 841 LCSLCYGD MENKLFAGIRBDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCYVNL 900
Qy 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDYSYARTSIRASLTF 960
Db 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDYSYARTSIRASLTF 960
Qy 961 NRGFKAGNNMRKLFVGLRLKCHSLFLLDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
Db 961 NRGFKAGNNMRKLFVGLRLKCHSLFLLDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
Qy 1021 FHOQWKNPTFRLVISDTSILCYSLKAKNAGSLGAKGAAGPLPSEAVOWLCHQAFLL 1080
Db 1021 FHOQWKNPTFRLVISDTSILCYSLKAKNAGSLGAKGAAGPLPSEAVOWLCHQAFLL 1080
Qy 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPCTTTLTALEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPCTTTLTALEAAANPALPSDFKTILD 1132

RESULT 31
US-10-044-692-323
; Sequence 323, Application US/10044692
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Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Inventors: Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 323:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 323:
US-10-044-692-323

Query Match 100.0%; Score 5961; DB 14; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MPRAPRCRAVRSLLSHREVLPATFVRRLLGPOGWRVLRVQGDPAAFALVAQCILVCVPW	60
DB	1	MPRAPRCRAVRSLLSHREVLPATFVRRLLGPOGWRVLRVQGDPAAFALVAQCILVCVPW	60
QY	61	DARPPPAAPSFQVSLCKELVARVLQRCERGAKNVLAFGFALLDCARGGPEAFETTSVR	120
DB	61	DARPPPAAPSFQVSLCKELVARVLQRCERGAKNVLAFGFALLDCARGGPEAFETTSVR	120
QY	121	SYLPNTVTDALRGSGAWGALLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA	180
DB	121	SYLPNTVTDALRGSGAWGALLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA	180

QY	181	ATQARPPPHASGPRRLRGCEAWNHSVREAGVPLGLPAPGARRRGGSASRSILPLPKRR	240
DB	181	ATQARPPPHASGPRRLRGCEAWNHSVREAGVPLGLPAPGARRRGGSASRSILPLPKRR	240
QY	241	GAPEPERTVPGQSGWAHPGTRGSDRGFCVSPARPAEATSLEGALSGRHSHPSVG	300
DB	241	GAPEPERTVPGQSGWAHPGTRGSDRGFCVSPARPAEATSLEGALSGRHSHPSVG	300
QY	301	ROHAGAPSTSRPPRPMDTPCPVVAETKHFLYSSGDEQRLRPSFLLSRLSLTGARRL	360
DB	301	ROHAGAPSTSRPPRPMDTPCPVVAETKHFLYSSGDEQRLRPSFLLSRLSLTGARRL	360
QY	361	VETIFLGSRPWMPGTPRRLPRLPQRYMQRPLFLELLGNHAQCPCYGVLLKTKCPRAAVT	420
DB	361	VETIFLGSRPWMPGTPRRLPRLPQRYMQRPLFLELLGNHAQCPCYGVLLKTKCPRAAVT	420
QY	421	PAAGVCAREKPGQSGVAAPPEEDTPRRLVQLLRHSSPWQVYGFVRACLRRLVPPGLWGS	480
DB	421	PAAGVCAREKPGQSGVAAPPEEDTPRRLVQLLRHSSPWQVYGFVRACLRRLVPPGLWGS	480
QY	481	RHNERRLNNTKFTISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVGCVAEHLRBEI	540
DB	481	RHNERRLNNTKFTISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVGCVAEHLRBEI	540
QY	541	LAKFLHMLMSVYVVELLRSFFYVTTTFQKNRLFYFKSVMSKLSQSIGIROHLKEVQLRE	600
DB	541	LAKFLHMLMSVYVVELLRSFFYVTTTFQKNRLFYFKSVMSKLSQSIGIROHLKEVQLRE	600
QY	601	LSEAEVQRHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVA	660
DB	601	LSEAEVQRHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVA	660
QY	661	LFSVLNTERARRPGLLGASVLGLDDIHRAWETFLVRVRAQDPPPELYFVKVDVTGAYDTI	720
DB	661	LFSVLNTERARRPGLLGASVLGLDDIHRAWETFLVRVRAQDPPPELYFVKVDVTGAYDTI	720
QY	721	PODLRLTEVIASIIKPNQTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL	780
DB	721	PODLRLTEVIASIIKPNQTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL	780
QY	781	QETSPLRDAVVEQSSSLNEASSGLFDVFLRFMCHHVRIRGKSYVQCGIPQGSILSTL	840
DB	781	QETSPLRDAVVEQSSSLNEASSGLFDVFLRFMCHHVRIRGKSYVQCGIPQGSILSTL	840
QY	841	LCSLCYGDMEKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGYPEYCVNVL	900
DB	841	LCSLCYGDMEKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGYPEYCVNVL	900
QY	901	RKTVPNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTLTLVQSDYSYARTSIRASLTF	960
DB	901	RKTVPNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTLTLVQSDYSYARTSIRASLTF	960
QY	961	NRGFKAGRNMRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLQP	1020
DB	961	NRGFKAGRNMRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLQP	1020
QY	1021	FHQQWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAFLL	1080
DB	1021	FHQQWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAFLL	1080
QY	1081	KLTRHRTVYVPLLGSLRTAQTOLSKPLPGTTLTALAAANPALPSDFKTIID	1132
DB	1081	KLTRHRTVYVPLLGSLRTAQTOLSKPLPGTTLTALAAANPALPSDFKTIID	1132

RESULT 32
US-10-044-539-323
; Sequence 323, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim

; Nakamura, Toru
 ; Chapman, Karen B.
 ; Morin, Gregg B.
 ; Harley, Calvin
 ; Andrews, William H.
 ; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
 ; THERAPEUTIC METHODS
 ; NUMBER OF SEQUENCES: 335
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94111
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/044,539
 ; FILING DATE: 11-Jan-2002
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/912,951
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 08/854,050
 ; FILING DATE: 09-MAY-1997
 ; APPLICATION NUMBER: US 08/851,843
 ; FILING DATE: 06-MAY-1997
 ; APPLICATION NUMBER: US 08/846,017
 ; FILING DATE: 25-APR-1997
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-APR-1997
 ; APPLICATION NUMBER: US 08/724,643
 ; FILING DATE: 01-OCT-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Apple, Randolph T.
 ; REGISTRATION NUMBER: 36,429
 ; REFERENCE/DOCKET NUMBER: 015389-002600US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 323:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1154 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 323:
 ; US-10-044-539-323
 ;
 ; Query Match 100.0%; Score 5961; DB 14; Length 1154;
 ; Best Local Similarity 100.0%; Pred. No. 0;
 ; Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ;
 ; 1 MPRAPRCAVRSLLRSHYREVLPVPLATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCPW 60
 ; 1 MPRAPRCAVRSLLRSHYREVLPVPLATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCPW 60
 ; 61 DARPPPAAPSPQVSCLEKELVARVLQRCERGAKNVLAFGPALLDARGGPPPEAFTTSVR 120
 ; 61 DARPPPAAPSPQVSCLEKELVARVLQRCERGAKNVLAFGPALLDARGGPPPEAFTTSVR 120
 ; 121 SYLPTNTVTDALRGSGAGLLRRYVDDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 ; 121 SYLPTNTVTDALRGSGAGLLRRYVDDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 ; 181 ATOARPPPPHSGPRRLRGCEAMNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKPRR 240
 ; 181 ATOARPPPPHSGPRRLRGCEAMNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKPRR 240

Qy 241 GAAPEPERTVVGQGSWAHPQRTGRGSDRGFCVVSPPARPAEATSLEGALSTRHSPSVG 300
 Db |||||
 Db 241 GAAPEPERTVVGQGSWAHPQRTGRGSDRGFCVVSPPARPAEATSLEGALSTRHSPSVG 300
 Qy 301 ROHHAGPPSTRPRPMDTFCPPVYAEKTHFLYSSGDKQOLRPSFLSSRPSLTGARRL 360
 Db |||||
 Db 301 ROHHAGPPSTRPRPMDTFCPPVYAEKTHFLYSSGDKQOLRPSFLSSRPSLTGARRL 360
 Qy 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMPLEFLILGNHAQCPYGVLLKTHCPLRAVT 420
 Db |||||
 Db 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMPLEFLILGNHAQCPYGVLLKTHCPLRAVT 420
 Qy 421 PAAGVCAREKPOGSVAAPPEEDTPRRLVOLLRQHSPPWQYGVFVACLRRLVPPGLWGS 480
 Db |||||
 Db 421 PAAGVCAREKPOGSVAAPPEEDTPRRLVOLLRQHSPPWQYGVFVACLRRLVPPGLWGS 480
 Qy 481 RHNERFLRNTKKFISLGHAKLSLOBLTWKMSVRDCAWLRSSPGVCVPAAEHRLREEI 540
 Db |||||
 Db 481 RHNERFLRNTKKFISLGHAKLSLOBLTWKMSVRDCAWLRSSPGVCVPAAEHRLREEI 540
 Qy 541 LAKFLHLMMSVYVVELLSRFYVTTETTFQKNRFFYFKSVMSKLSQSIGIRQLKRVQLRE 600
 Db |||||
 Db 541 LAKFLHLMMSVYVVELLSRFYVTTETTFQKNRFFYFKSVMSKLSQSIGIRQLKRVQLRE 600
 Qy 601 LSAEVRQHRARPALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKAERLTSRKA 660
 Db |||||
 Db 601 LSAEVRQHRARPALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKAERLTSRKA 660
 Qy 661 LFSVLNVERARRRGLLGASVLGLDDTHRAWRTFVLRAQDPPPELYFVKVDVTGADTI 720
 Db |||||
 Db 661 LFSVLNVERARRRGLLGASVLGLDDTHRAWRTFVLRAQDPPPELYFVKVDVTGADTI 720
 Qy 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMQFVAHL 780
 Db |||||
 Db 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMQFVAHL 780
 Qy 781 QETSPLRDADVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYVQCQGIPOGSIILSTL 840
 Db |||||
 Db 781 QETSPLRDADVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYVQCQGIPOGSIILSTL 840
 Qy 841 LCSLCYGD MENKLPAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGVVNL 900
 Db |||||
 Db 841 LCSLCYGD MENKLPAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGVVNL 900
 Qy 901 RKTVMFPVDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVOQSDYSSYARTSIRASLTF 960
 Db |||||
 Db 901 RKTVMFPVDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVOQSDYSSYARTSIRASLTF 960
 Qy 961 NRGFKAGRNRRKLPVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLOLP 1020
 Db |||||
 Db 961 NRGFKAGRNRRKLPVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLOLP 1020
 Qy 1021 FHQVWKNPTFFLVRISDTSALCVSILKAKNAGMSLGAKGAAGPLPSEAQVWLCHQAPLL 1080
 Db |||||
 Db 1021 FHQVWKNPTFFLVRISDTSALCVSILKAKNAGMSLGAKGAAGPLPSEAQVWLCHQAPLL 1080
 Qy 1081 KLTRHRVTVYVPLGLSLRTAQTLRSKLPGLTTLTALEAAANPALPSPDFKTIID 1132
 Db |||||
 Db 1081 KLTRHRVTVYVPLGLSLRTAQTLRSKLPGLTTLTALEAAANPALPSPDFKTIID 1132

RESULT 33
 US-10-325-810-611
 ; Sequence 611, Application US/10325810
 ; Publication No. US20030204069A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; ; Lingner, Joachim
 ; ; Nakamura, Toru
 ; ; Chapman, Karen B.
 ; ; Morin, Gregg B.
 ; ; Harley, Calvin B.

Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/325,810

FILING DATE: 20-Dec-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181

FILING DATE: 29-Sep-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ausenhus, Scott L.

REGISTRATION NUMBER: 42,271

REFERENCE/DOCKET NUMBER: 015389-002620US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 611:

SEQUENCE CHARACTERISTICS:

LENGTH: 1154 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..1154

OTHER INFORMATION: /note= "fusion protein composed of hTERT
protein sequence, vector sequences, the
Myc epitope and His6 tag"

SEQUENCE DESCRIPTION: SEQ ID NO: 611:

US-10-325-810-611

Query Match 100.0%; Score 5961; DB 15; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCVAVSLRSHREVLPATFVRRLLGQWRLVQRCDPAAAFALVAQCILVCVPM 60
|||||
Db 1 MPAPRCVAVSLRSHREVLPATFVRRLLGQWRLVQRCDPAAAFALVAQCILVCVPM 60
|||||

Qy 61 DARPPPAAPSPQVSCLEKELVARLQRLCERGAKNVLAFGFALLDARGGPEAFTTSVR 120
|||||

Db 61 DARPPPAAPSPQVSCLEKELVARLQRLCERGAKNVLAFGFALLDARGGPEAFTTSVR 120
Qy 121 SYLNTVTDALRGSGAWGLLRLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
|||||
Db 121 SYLNTVTDALRGSGAWGLLRLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
|||||
Qy 181 ATQARPPPHASGPRRRRLGCERAMNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRRR 240
Db 181 ATQARPPPHASGPRRRRLGCERAMNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRRR 240
Qy 241 GAAPERTPVQCGSWAHPCGTRGSDRGFCVWSPARPAEATSLGALSCTRHHSPVSG 300
Db 241 GAAPERTPVQCGSWAHPCGTRGSDRGFCVWSPARPAEATSLGALSCTRHHSPVSG 300
Qy 301 ROHAGPSTSRPPRPMDTPCPVYAEKTHFLYSYGDKQLRPSFLLSLSPSLTGARRL 360
Db 301 ROHAGPSTSRPPRPMDTPCPVYAEKTHFLYSYGDKQLRPSFLLSLSPSLTGARRL 360
Qy 361 VETIFLGSRPWMPGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRPWMPGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKQGSVAAPDEEDTDPRLLVQLLRQHSFVQYGFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKQGSVAAPDEEDTDPRLLVQLLRQHSFVQYGFVRACLRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKTFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCPAAEHLRREI 540
Db 481 RHNERRFLRNTKTFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCPAAEHLRREI 540
Qy 541 LAKEHLMLMSYVVVELLSRFFVTETTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVQLRE 600
Db 541 LAKEHLMLMSYVVVELLSRFFVTETTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVQLRE 600
Qy 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARFRRKRAERLTSRVKA 660
Db 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARFRRKRAERLTSRVKA 660
Qy 661 LFSVLNTERARRPGLLGASVLGDDIHRAWTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGDDIHRAWTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTLDQPYMRQFVAHL 780
Db 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTLDQPYMRQFVAHL 780
Qy 781 QETSPLRDAVVEIOSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYVQCGIPQGSILSTL 840
Db 781 QETSPLRDAVVEIOSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYVQCGIPQGSILSTL 840
Qy 841 LCSLCYGD MENKLPAGIRRDGLLRLVDDFLLVTPHLTHAKTFLRTLVRGPEYGCNVNL 900
Db 841 LCSLCYGD MENKLPAGIRRDGLLRLVDDFLLVTPHLTHAKTFLRTLVRGPEYGCNVNL 900
Qy 901 RKTVNFVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVQSDSYSSYARTSIRASLTF 960
Db 901 RKTVNFVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVQSDSYSSYARTSIRASLTF 960
Qy 961 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNITYKILLQAYRHFACVLQLP 1020
Db 961 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNITYKILLQAYRHFACVLQLP 1020
Qy 1021 FHOQVKNPTFRLVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHOAFLL 1080
Db 1021 FHOQVKNPTFRLVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHOAFLL 1080
Qy 1081 KLTHRRVTYVPLLSLRTAQQLSRKLPGLTTLTALEAAANPALPDSFKTILD 1132
Db 1081 KLTHRRVTYVPLLSLRTAQQLSRKLPGLTTLTALEAAANPALPDSFKTILD 1132

RESULT 34
US-10-877-124-611

; Sequence 611, Application US/10877124
; Publication No. US20040242529A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,124
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 611:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1154
; OTHER INFORMATION: /note= "fusion protein composed of hTERT
; protein sequence, vector sequences, the
; Myc epitope and His6 tag"
; SEQUENCE DESCRIPTION: SEQ ID NO: 611:

Query Match 100.0%; Score 5961; DB 16; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPPLATEFVRLPGQWELVORGDPAAAFRALVAOCLVCVPW 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 DARPPPAAPSFQVSCIKELVARVLQRLCERGANVLAFGFALIDGARGGPPPEAFTTSVR 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 DARPPPAAPSFQVSCIKELVARVLQRLCERGANVLAFGFALLDGARGGPPPEAFTTSVR 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGDVLAHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGDVLAHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 181 ATQARPPPHASGPRRLGRCERANVSHVREAGVPLGLPAGNRRRGGSASRLPLPKPRR 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 181 ATQARPPPHASGPRRLGRCERANVSHVREAGVPLGLPAGNRRRGGSASRLPLPKPRR 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 241 GAAPEPERTVPGQSWAHPGRTGRGFCVVSPPARPAEAEATSEALSGSTRHSHPSVG 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 241 GAAPEPERTVPGQSWAHPGRTGRGFCVVSPPARPAEAEATSEALSGSTRHSHPSVG 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 301 RQHAGPPSTSRPPRMDTPCPVYATKTHPLSYSSGDKEOLRPSFLLSRPSLTGARRL 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 301 RQHAGPPSTSRPPRMDTPCPVYATKTHPLSYSSGDKEOLRPSFLLSRPSLTGARRL 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 361 VETIFLGSREPMPTGTPRLPRLPQRYWQMRPLFLELLGNHAOCYPYGVLLKTHCPLRAVT 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 361 VETIFLGSREPMPTGTPRLPRLPQRYWQMRPLFLELLGNHAOCYPYGVLLKTHCPLRAVT 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 421 PAAGVCAREXPQGSVAAPBEEDTPRLVQLLRQSSPQVYGVFVRACLRLVPPGLWGS 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 421 PAAGVCAREXPQGSVAAPBEEDTPRLVQLLRQSSPQVYGVFVRACLRLVPPGLWGS 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 481 RHNERRFLNKKFISLGKHAQLSLQBLTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 481 RHNERRFLNKKFISLGKHAQLSLQBLTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 541 LAKFLHLMVSVYVVELLSRFYVTTETFOKNRFFYRKSVWSKLOSGIQLKRVOLRE 600
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 541 LAKFLHLMVSVYVVELLSRFYVTTETFOKNRFFYRKSVWSKLOSGIQLKRVOLRE 600
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 601 LSAEVRQHEARPAALITSLRFLPKDGLRPVNMDDYVVGARTFREKRAERLTSRVKA 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 601 LSAEVRQHEARPAALITSLRFLPKDGLRPVNMDDYVVGARTFREKRAERLTSRVKA 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 721 PQDRLTEVIASIIKPQNTYCVRYAVVQKAHGHVKAFKSHVSTLLDLPYMRQFVAHL 780
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Qy 721 PQDRLTEVIASIIKPQNTYCVRYAVVQKAHGHVKAFKSHVSTLLDLPYMRQFVAHL 780
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVYVOCQIPQGSILSTL 840
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVYVOCQIPQGSILSTL 840
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 841 LCSLCYGD MENKLPAGIRRDGLLLRLVDDPFLVTPHLLTHAKTFLRTVLRGVPYGCVVNL 900
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 841 LCSLCYGD MENKLPAGIRRDGLLLRLVDDPFLVTPHLLTHAKTFLRTVLRGVPYGCVVNL 900
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 901 RKTVMNFPVDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVDQSDYSSYARTSIRASLTF 960
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 901 RKTVMNFPVDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVDQSDYSSYARTSIRASLTF 960
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 961 NRGFKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIIKYLLQAYRFHACVLQLP 1020
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 961 NRGFKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIIKYLLQAYRFHACVLQLP 1020
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 1021 FHQVWKNPTFFLRLVISDTASLCYSLKAKNAGMSLGAKGAAGPLPSEAVOMLCHOAFLL 1080
Db 1021 FHQVWKNPTFFLRLVISDTASLCYSLKAKNAGMSLGAKGAAGPLPSEAVOMLCHOAFLL 1080
QY 1081 KLTRHRVTVPLGLSIRTAQTOLSKRLPGTTLTALFAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTVPLGLSIRTAQTOLSKRLPGTTLTALFAANPALPSDFKTILD 1132

RESULT 35

US-10-877-022-611
; Sequence 611, Application US/10877022
; Publication No. US20040247613A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,022
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 611:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 amino acids
; TYPE: amino acid

; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1154
; OTHER INFORMATION: /note= "fusion protein composed of. hTERT
; protein sequence, vector sequences, the
; Myc epitope and His6 tag"
; SEQUENCE DESCRIPTION: SEQ ID NO: 611:
US-10-877-022-611
Query Match 100.0%; Score 5961; DB 16; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPOGWRILVORGDPAAFALVAQCILVCPWM 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPOGWRILVORGDPAAFALVAQCILVCPWM 60
QY 61 DARPPAAPSPROVSKCLKELVARVLORLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
Db 61 DARPPAAPSPROVSKCLKELVARVLORLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
QY 121 SYLNTVTDALRGSGAMGLLLRRVDDVLLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
Db 121 SYLNTVTDALRGSGAMGLLLRRVDDVLLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGGASRSLLPKRPRR 240
Db 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGGASRSLLPKRPRR 240
QY 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEBATSLEGALSGRHSHPSVG 300
Db 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEBATSLEGALSGRHSHPSVG 300
QY 301 RQHHAGPPSTSRPPRMDTPCPVYAEYTKHFLYSSGDKQLRPSFLLSRPSLTGARRL 360
Db 301 RQHHAGPPSTSRPPRMDTPCPVYAEYTKHFLYSSGDKQLRPSFLLSRPSLTGARRL 360
QY 361 VETIFLGSRPWMPGTTPRLPRLPQRYWQMRPLFLELLGNHAQCYPYGVLLKTHCPIRAAVT 420
Db 361 VETIFLGSRPWMPGTTPRLPRLPQRYWQMRPLFLELLGNHAQCYPYGVLLKTHCPIRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSWPQVYGFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSWPQVYGFVRACLRLVPPGLWGS 480
QY 481 RHNERRFLRNTKFTSLGKHAKLSLQELTWKMSVRDCAWLRRSPGVCVPAAEHLRREI 540
Db 481 RHNERRFLRNTKFTSLGKHAKLSLQELTWKMSVRDCAWLRRSPGVCVPAAEHLRREI 540
QY 541 LAKFLHLMMSVYVVELLSRFPYVTTETTPQKURLFPYRKSVMSKLOSIGIRQHLKRVQRE 600
Db 541 LAKFLHLMMSVYVVELLSRFPYVTTETTPQKURLFPYRKSVMSKLOSIGIRQHLKRVQRE 600
QY 601 LSEAEVRQHRARPALLTSRLRFTPKPDGLRPIVNMDDYVVGARTFRERKRAERLTSRVKA 660
Db 601 LSEAEVRQHRARPALLTSRLRFTPKPDGLRPIVNMDDYVVGARTFRERKRAERLTSRVKA 660
QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPQNTYCVRRYAVVQAAAHGVRKAFKSHVSTLTDLQPMROFVAHL 780
Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQAAAHGVRKAFKSHVSTLTDLQPMROFVAHL 780
QY 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLPFMCHHAVIRKSVVQCGIPQGSILSTL 840
Db 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLPFMCHHAVIRKSVVQCGIPQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYGCWNL 900

Db 841 LCSLCYGMENKLFAGIRROGLLRVLDDFLVTPHLTHAKFTLTVRGVPETGCVVNL 900
Qy 901 RKTUVNPFVEALGGTAFAVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRASLTF 960
Db 901 RKTUVNPFVEALGGTAFAVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRASLTF 960
Qy 961 NRGFKAGNRMRKLFVGLRLKCHSLFLLDQVNSLQTVCTNTYKILLQAVRFHACVILQLP 1020
Db 961 NRGFKAGNRMRKLFVGLRLKCHSLFLLDQVNSLQTVCTNTYKILLQAVRFHACVILQLP 1020
Qy 1021 FHQQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTRHRVTYVPLGLSLRTAQOLSRKLPGLTTLTALAANAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLGLSLRTAQOLSRKLPGLTTLTALAANAANPALPSDFKTILD 1132

RESULT 36

US-10-877-146-611

; Sequence 611, Application US/10877146

; Publication No. US20050013825A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Langner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESSES:

ADDRESSES: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/877,146

FILING DATE: 24-Jun-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503

FILING DATE: 02-Nov-1999

APPLICATION NUMBER: 08/974,549

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-Apr-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-Apr-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-May-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-May-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-Oct-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-Oct-1997

; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 611:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1154
; OTHER INFORMATION: /note= "fusion protein composed of hTERT
; protein sequence, vector sequences, the
; Myc epitope and His6 tag"
; SEQUENCE DESCRIPTION: SEQ ID NO: 611:
US-10-877-146-611

Query Match 100.0%; Score 5961; DB 17; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLRGQWRLVQGPAAFPALVAQCLVCPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLRGQWRLVQGPAAFPALVAQCLVCPW 60
Qy 61 DARPPPAAPSFQVSCCLKELVARVQLRCERGANVLAFGFALLDARGGPPPEAFTTSVR 120
Db 61 DARPPPAAPSFQVSCCLKELVARVQLRCERGANVLAFGFALLDARGGPPPEAFTTSVR 120
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Db 121 SYLPNTVTDALRGSGAWGLLRVGGDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180
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Db 361 VETIFLGSRPWMEPTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
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Qy 481 RHNERRFLRNTKKFISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
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Db 541 LAKFLHLMWSVYVVELLRSFFYVTTFTFQKNRLFYFKSVMSKLQSIGIRGHLKRVQLRE 600
Qy 601 LSEAEVRQHREARPALITSRLRTPKDDGLRPVNMMDYVVGARTFREKRAERLTSRVKA 660
Db 601 LSEAEVRQHREARPALITSRLRTPKDDGLRPVNMMDYVVGARTFREKRAERLTSRVKA 660
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLVRRAQDPPPELYFVKVVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLVRRAQDPPPELYFVKVVDVTGAYDTI 720

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QY 721 PODRLTEVIASIIKPNQTYCVRYAVVQAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPNQTYCVRYAVVQAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
QY 781 QETSPRLDAVVIQSSSLNEASSGLFDVFLRFCHHAVIRGKSYVQCQIPOGSIILSTL 840
Db 781 QETSPRLDAVVIQSSSLNEASSGLFDVFLRFCHHAVIRGKSYVQCQIPOGSIILSTL 840
QY 841 LCLSLCYGDMENKLFAGIRGDLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVMNL 900
Db 841 LCLSLCYGDMENKLFAGIRGDLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVMNL 900
QY 901 RKTVMNFPVEDEALGTAFAVQMPAHGLFPWCGLLDTRTLEVSQDYSSYARTSIRASLTF 960
Db 901 RKTVMNFPVEDEALGTAFAVQMPAHGLFPWCGLLDTRTLEVSQDYSSYARTSIRASLTF 960
QY 961 NRGFKAGRNMRRKLFGLVRLKCHSLFGLDQVNSLQVCTNIIYKILLQAYRFHACVQLP 1020
Db 961 NRGFKAGRNMRRKLFGLVRLKCHSLFGLDQVNSLQVCTNIIYKILLQAYRFHACVQLP 1020
QY 1021 FHOQVWKNPTFFLRLVSDTASLCYSTLKAKNAGMSIGAKGAGPLPSEAVQMLCHOAFL 1080
Db 1021 FHOQVWKNPTFFLRLVSDTASLCYSTLKAKNAGMSIGAKGAGPLPSEAVQMLCHOAFL 1080
QY 1081 KLTRHRTVTVPLGLSLRTAQTLQSLRKLPGTTLTALEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRTVTVPLGLSLRTAQTLQSLRKLPGTTLTALEAAANPALPSDFKTILD 1132

RESULT 37

US-10-044-692-325
; Sequence 325, Application US/10044692
; Publication No. US20030096344A1

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0026000S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 325:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 325:
US-10-044-692-325

Query Match 100.0%; Score 5961; DB 14; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLRSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
Db 58 MPAPRCRAVRSLRSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCVPW 117
QY 61 DARPPAAPSPQVSCLEKELVARLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
Db 118 DARPPAAPSPQVSCLEKELVARLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 177
QY 121 SYLPNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYVCPPPLYQLGA 180
Db 178 SYLPNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYVCPPPLYQLGA 237
QY 181 ATQARPPPHASGPRRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSPLPKRPRR 240
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QY 241 GAAPERTPVCGGSAWHGPRTRGSDRGFCVVSAPPAEAEATSLGALSGTHSHPSVG 300
Db 298 GAAPERTPVCGGSAWHGPRTRGSDRGFCVVSAPPAEAEATSLGALSGTHSHPSVG 357
QY 301 RQHAGPSTSPRPDPWDTCPVPVYAEKHFYSSGDKQLRPSFLLSLSRLSLTGARRL 360
Db 358 RQHAGPSTSPRPDPWDTCPVPVYAEKHFYSSGDKQLRPSFLLSLSRLSLTGARRL 417
QY 361 VETIFLGSRPMPGTPRRLPRLPQRYQWQMRPLFLELLGNHACQPYGVLLKTHCPLRAAVT 420
Db 418 VETIFLGSRPMPGTPRRLPRLPQRYQWQMRPLFLELLGNHACQPYGVLLKTHCPLRAAVT 477
QY 421 PAAGVCAREKPGQSVAAPEEEDTDRRLVOLLROHSSPMQVYGFVRACLRLLVPPGLWGS 480
Db 478 PAAGVCAREKPGQSVAAPEEEDTDRRLVOLLROHSSPMQVYGFVRACLRLLVPPGLWGS 537
QY 481 RINERRFLRNTKFTISLGHAKLSLQELTKMSVRDCAWLRSRSPGVCGVPAAEHRLREI 540
Db 538 RINERRFLRNTKFTISLGHAKLSLQELTKMSVRDCAWLRSRSPGVCGVPAAEHRLREI 597
QY 541 LAKFLHMLMSVYVVELLSRFFVYVTTTFOKNRLLFPYKRSVWSKLSQISIGIRQHLKRVLRE 600
Db 598 LAKFLHMLMSVYVVELLSRFFVYVTTTFOKNRLLFPYKRSVWSKLSQISIGIRQHLKRVLRE 657
QY 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRIRIVNMDDYVVGARTFRREKAEERLTSRVKA 660
Db 658 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRIRIVNMDDYVVGARTFRREKAEERLTSRVKA 717
QY 661 LFSVLNYERARRPGLLGASVLGDDIHRWRTFVLVRVRAQDPPELYFVKVDVTGAYDTI 720
Db 718 LFSVLNYERARRPGLLGASVLGDDIHRWRTFVLVRVRAQDPPELYFVKVDVTGAYDTI 777
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Db 778 PODRLTEVIASIIKPONTYCVRRYAVQKAAHGHVRFKAFKSHVSTLTLDLQPMQFVAHL 837
Qy 781 QETSPLRDAVTEQSSSINEASSGLFDVFLRPMCHAVIRKGSYVQCQIPQGSILSTL 840
Db 838 QETSPLRDAVTEQSSSINEASSGLFDVFLRPMCHAVIRKGSYVQCQIPQGSILSTL 897
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Db 898 LCSLCYGMENKLFAGIRDDGLLRLLVDDFLVTLPHLTHAKTFLRLVGRVPEYCVVNL 957
Qy 901 RKTUVNFFVEDEALGCTAFVQMPAHGLFPWCGLLDDTRTLEQSDYSSYARTSIRASLTF 960
Db 958 RKTUVNFFVEDEALGCTAFVQMPAHGLFPWCGLLDDTRTLEQSDYSSYARTSIRASLTF 1017
Qy 961 NRGFKAGNRRKLFVRLKCHSLFLLQVNSLQTVCTNIIKILLQAYRFHACVLQLP 1020
Db 1018 NRGFKAGNRRKLFVRLKCHSLFLLQVNSLQTVCTNIIKILLQAYRFHACVLQLP 1077
Qy 1021 FHQQVWKNPFFLRVISTDASLCYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHOAFL 1080
Db 1078 FHQQVWKNPFFLRVISTDASLCYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHOAFL 1137
Qy 1081 KLTRHRVTYVPLGLSLRTAQTSKLPCTTLTALAAAAANPALPSDFKTILD 1132
Db 1138 KLTRHRVTYVPLGLSLRTAQTSKLPCTTLTALAAAAANPALPSDFKTILD 1189

RESULT 38
US-10-044-539-325
; Sequence 325, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cecch, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.

```

```

;
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 325:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 325:
US-10-044-539-325

Query Match 100.0%; Score 5961; DB 14; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLLGPGQWRLVQRGDPAAAFRALVAQCLVCPWP 60
Db 58 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLLGPGQWRLVQRGDPAAAFRALVAQCLVCPWP 117
Qy 61 DARPPPAAPSPROVSKLKLVARVLQRLCERGAKNVLAFAFLLDGGARGGPEAFTTSVR 120
Db 118 DARPPPAAPSFRQVSKLKLVARVLQRLCERGAKNVLAFAFLLDGGARGGPEAFTTSVR 177
Qy 121 SYLENTVTDALRGSGAMGLLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYLGA 180
Db 178 SYLENTVTDALRGSGAMGLLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYLGA 237
Qy 181 ATQARPPPHASGPRRRRLGCERAWNHSVREAGVPLGAPGARRRGGSASRSLPLPKRRR 240
Db 238 ATQARPPPHASGPRRRRLGCERAWNHSVREAGVPLGAPGARRRGGSASRSLPLPKRRR 297
Qy 241 GAAPERTPVQGSWAHPGRTGRGFCVSPARPAEATSLLEGALSCTRHSHPVSG 300
Db 298 GAAPERTPVQGSWAHPGRTGRGFCVSPARPAEATSLLEGALSCTRHSHPVSG 357
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Qy 361 VETIFLGSRPWMPGTPRRLLPRLPQRYWQMRPLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
Db 418 VETIFLGSRPWMPGTPRRLLPRLPQRYWQMRPLFLELGNHAQCPYGVLLKTHCPLRAAVT 477
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLLVQLLRHSSPWQVYGFVACLRRLVPPGLWGS 480
Db 478 PAAGVCAREKPGQSVAAPEEEDTPRRLLVQLLRHSSPWQVYGFVACLRRLVPPGLWGS 537
Qy 481 RHNERRFLRNTKFTISLGKHAKLSLOELTWQNSVRDCAWLRSSPGVGCVPAEHLRBEI 540
Db 538 RHNERRFLRNTKFTISLGKHAKLSLOELTWQNSVRDCAWLRSSPGVGCVPAEHLRBEI 597
Qy 541 LAKFLHMLMSYVVELLSRFFYVTTFTFQKRLFFYRKSVMWSKLSIGIRHQLKRVQURE 600
Db 598 LAKFLHMLMSYVVELLSRFFYVTTFTFQKRLFFYRKSVMWSKLSIGIRHQLKRVQURE 657
Qy 601 LSEAEVQRHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
Db 658 LSEAEVQRHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 717
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRAMRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
Db 718 LFSVLNYERARRPGLLGASVLGLDDIHRAMRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 777
Qy 721 PQDLRTEVIASIIKPONTYCVRRYAVQKAAHGHVRFKAFKSHVSTLTLDLQPMQFVAHL 780
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Qy 781 QETSPLRDAVTEQSSSINEASSGLFDVFLRPMCHAVIRKGSYVQCQIPQGSILSTL 840

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Db 838 QTSPLRDVAVTEQSSLINEASSGLFDVFLRPMCHHAVRIROKSVQCGIPQGSILSTL 897
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Qy 901 KTVNVPFVEDALGCTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLTF 960
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Qy 961 NRGFKAGNRMRKLGVLRLKCHSLFDLQVNSLQVCTNIYKILLQAYRPHACVLQLP 1020
Db 1018 NRGFKAGNRMRKLGVLRLKCHSLFDLQVNSLQVCTNIYKILLQAYRPHACVLQLP 1077
Qy 1021 FHOQWKNPFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1078 FHOQWKNPFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1137
Qy 1081 KLTRHRVTVPLLSRLTAQOLSRKLPQTTLTALEAANPALPSDFKTILD 1132
Db 1138 KLTRHRVTVPLLSRLTAQOLSRKLPQTTLTALEAANPALPSDFKTILD 1189

RESULT 39
US-10-325-810-613
; Sequence 613, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181
; FILING DATE: 29-Sep-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885

; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-0026200S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 613:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1189
; OTHER INFORMATION: /note= "fusion protein composed of
; melittin signal sequence and full length
; hTERT protein"
; SEQUENCE DESCRIPTION: SEQ ID NO: 613:
; US-10-325-810-613
; Query Match 100.0%; Score 5961; DB 15; Length 1189;
; Best Local Similarity 100.0%; Pred. No. 0;
; Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPAPRCRAVRSLLRSHYREVLPATFVRRILGPGQWRLVQDGDPAAFALVAQCLVCPW 60
Db 58 MPAPRCRAVRSLLRSHYREVLPATFVRRILGPGQWRLVQDGDPAAFALVAQCLVCPW 117
Qy 61 DARPPAAPSPROVSCCLKELVARVLQRLCERAGKNVLAFAFGALLDGGARGGPEAFTTSVR 120
Db 118 DARPPAAPSPROVSCCLKELVARVLQRLCERAGKNVLAFAFGALLDGGARGGPEAFTTSVR 177
Qy 121 SYLENTVTDALRGSGANGLLRLRVGDDVLVHLLARCALFVLVAFSCAYQVCGPPLYQLGA 180
Db 178 SYLENTVTDALRGSGANGLLRLRVGDDVLVHLLARCALFVLVAFSCAYQVCGPPLYQLGA 237
Qy 181 ATQARPPPHASGPRRLGGERAMNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRPRR 240
Db 238 ATQARPPPHASGPRRLGGERAMNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRPRR 297
Qy 241 GAAPERTPVQGSWAHPGRTGCRPSDRGFCVSPAPAEATSLGALSCTRSHSPSVG 300
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Qy 301 RQHAGPPSTSRPPRWDTPCPVYAEYTKHFLYSSGDKQLRPSFLLSLSPSLTGARRL 360
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Qy 361 VETIFLGSRPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 418 VETIFLGSRPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 477
Qy 421 PAAGVCAREKPGQSSVAAPAEEDTDPRLVOLLRQSSFPWQYVGFVACRLRLVPPGLWGS 480
Db 478 PAAGVCAREKPGQSSVAAPAEEDTDPRLVOLLRQSSFPWQYVGFVACRLRLVPPGLWGS 537
Qy 481 RHNERRRFLNTKRFISLGKIAKLSLOELTWKMSVDCAWLRSSPGVGVCPAAEHLRLEE 540
Db 538 RHNERRRFLNTKRFISLGKIAKLSLOELTWKMSVDCAWLRSSPGVGVCPAAEHLRLEE 597
Qy 541 LAKEFLHLMSSVYVVELLRSFFYVTTTFFQKNLFFYRKSVMKLSQSIGIRQHLKRVQRE 600
Db 598 LAKEFLHLMSSVYVVELLRSFFYVTTTFFQKNLFFYRKSVMKLSQSIGIRQHLKRVQRE 657
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Db 658 LSEAEVQREARPAALLTSRLRFPKPDGLRPVNMVYVVGARTFREKRAERLTSRVKA 717
Qy 661 LFSVLNYERARRPCLLGASVLGLDDIHRAWRTFVLVRQAQDPPPELYFKVDVTGAYDTI 720

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Db 778 PQDLTEVIAIIKPONTYCVRRYAVVQAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 837
QY 781 QETSPURDAVWIBOSSSLNEASSGLFDVFLRFMCHHAVIRKGSYVQCGIIPQGSITLSTL 840
Db 838 QETSPURDAVWIBOSSSLNEASSGLFDVFLRFMCHHAVIRKGSYVQCGIIPQGSITLSTL 897
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Db 958 RKTVMNPFVEDEALGTAFOVPAHGLFPWCGLLDTRTLEVSQSDYSSVARTSIRASLTF 1017
QY 961 NRGFKAGRNRRKLFGLRLKCHSLFDLDQVNSLQVCTNIYKILLQAYRHACVQLQP 1020
Db 1018 NRGFKAGRNRRKLFGLRLKCHSLFDLDQVNSLQVCTNIYKILLQAYRHACVQLQP 1077
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Db 1078 FHOQVKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAGPLSEAVQWLCHQAFLL 1137
QY 1081 KLTHRVTVYPLLGSLRTAQTLQSRKLPGLTTLTALEAAANPALPSPDKILD 1132
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RESULT 40
US-10-877-124-613
; Sequence 613, Application US/10877124
; Publication No. US20040242529A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,124
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph, Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 613:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1189
OTHER INFORMATION: /note= "fusion protein composed of
melittin signal sequence and full length
hTERT protein"
SEQUENCE DESCRIPTION: SEQ ID NO: 613:
US-10-877-124-613
Query Match 100.0%; Score 5961; DB 16; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSLLSHRYREVLPPLATFVRRLLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 60
Db 58 MPRAPRCRAVRSLLSHRYREVLPPLATFVRRLLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 117
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Qy 601 LSEAEVQHRARPAALLTSRLRFPKPDGLRPIVNMDDVVGARTFRREKRAERLTSRVKA 660
Db 658 LSEAEVQHRARPAALLTSRLRFPKPDGLRPIVNMDDVVGARTFRREKRAERLTSRVKA 717
Qy 661 LFSVLNTERARRPGLGASVLGLDDIHRATWTEVLVRPAODPPPELVFKVDVTVGAYDTI 720
Db 718 LFSVLNTERARRPGLGASVLGLDDIHRATWTEVLVRPAODPPPELVFKVDVTVGAYDTI 777
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Db 778 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTLQPYMQFVAHL 837
Qy 781 QETSPLRDVAVIEOSSSINEASSGLFDVFLRFMCHAVIRGKSVYVOCQIGIPQGSILSTL 840
Db 838 QETSPLRDVAVIEOSSSINEASSGLFDVFLRFMCHAVIRGKSVYVOCQIGIPQGSILSTL 897
Qy 841 LCSLCYGMENKLFAGIRRDGLLRVDDFLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
Db 898 LCSLCYGMENKLFAGIRRDGLLRVDDFLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 957
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RESULT 41

US-10-877-022-613
; Sequence 613, Application US/10877022
; Publication No. US20040247613A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/877,022

FILING DATE: 24-Jun-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 613:

SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Protein

LOCATION: 1..1189

OTHER INFORMATION: /note= "fusion protein composed of
melittin signal sequence and full length
hTERT protein"

SEQUENCE DESCRIPTION: SEQ ID NO: 613:

US-10-877-022-613

Query Match

Best Local Similarity 100.0%; Score 5961; DB 16; Length 1189;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPRAPCRVRSLLRSHYREVLP	1189
Db	58	MPRAPCRVRSLLRSHYREVLP	1189
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Db	118	DARPPPAAPSFQVSCSKELVARVLR	177
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Db	178	SYLNTVTDALRGSGAWGLLLRRVGD	237
Qy	181	ATQARPPPHASGPRRLGGERAWNHS	240
Db	238	ATQARPPPHASGPRRLGGERAWNHS	297
Qy	241	GAAPERTPVGQSWAHPRTRGPDRCF	300
Db	298	GAAPERTPVGQSWAHPRTRGPDRCF	357
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QY 361 VETIFLGRWPMPTGTPRRRLPRLPQRYQWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 418 VETIFLGRWPMPTGTPRRRLPRLPQRYQWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 477
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Db 478 PAAGVACAREKPGQSVAAPEEEDTDPRLVOLLQHSPPQWYGVFVACLRRLVPPGLMGS 537
QY 481 RHNERFLRNTKFPISGKHAKLSLOELTWKMSVRDCAMLRBSPGVGCVPAAEHRLREEI 540
Db 538 RHNERFLRNTKFPISGKHAKLSLOELTWKMSVRDCAMLRBSPGVGCVPAAEHRLREEI 597
QY 541 LAKFLHLMMSVYVVELLRSFFYTTTFOKNRFFFYRKSWKSLQSIGIRQHILKRVQLRE 600
Db 598 LAKFLHLMMSVYVVELLRSFFYTTTFOKNRFFFYRKSWKSLQSIGIRQHILKRVQLRE 657
QY 601 LSAEVRQHRARPALLTSRLRPIPKDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 660
Db 658 LSAEVRQHRARPALLTSRLRPIPKDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 717
QY 661 LFSVLNAYERARRPGLLGASVLGDDTHRAWRFTFLVRADDPPELYFVKVDVVTGAYDTI 720
Db 718 LFSVLNAYERARRPGLLGASVLGDDTHRAWRFTFLVRADDPPELYFVKVDVVTGAYDTI 777
QY 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTLDLPYMRQFVAHL 780
Db 778 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTLDLPYMRQFVAHL 837
QY 781 QETSPLRDVAVVIEQSSSLNBAASGLFDVFLRPFCHHVRIRGKSVYQCGIPIQGSILSTL 840
Db 838 QETSPLRDVAVVIEQSSSLNBAASGLFDVFLRPFCHHVRIRGKSVYQCGIPIQGSILSTL 897
QY 841 LCSICVGMENKLFAGIRRGGLILRLVDLFLVTPHLLTHAKTFLRLTVRGVPYGCVNIL 900
Db 898 LCSICVGMENKLFAGIRRGGLILRLVDLFLVTPHLLTHAKTFLRLTVRGVPYGCVNIL 957
QY 901 RKTWNVPVDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVOSSYSSVARTSIRASLTF 960
Db 958 RKTWNVPVDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVOSSYSSVARTSIRASLTF 1017
QY 961 NRGFKAGNRMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAVRFHACVQLQP 1020
Db 1018 NRGFKAGNRMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAVRFHACVQLQP 1077
QY 1021 FHOQVKNPTFFLRVSDTASLCYSILKAKNAGMSLGAAGPLSEAVQWILCHOAFLL 1080
Db 1078 FHOQVKNPTFFLRVSDTASLCYSILKAKNAGMSLGAAGPLSEAVQWILCHOAFLL 1137
QY 1081 KLTRHRVTVYVPLGLSLRTAQTLRSKLPGLTTLTALEAANPALPSPDKTILD 1132
Db 1138 KLTRHRVTVYVPLGLSLRTAQTLRSKLPGLTTLTALEAANPALPSPDKTILD 1189

```

RESULT 42

US-10-877-146-613
 ; Sequence 613, Application US/10877146
 ; Publication No. US20050013825A1
 ; GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California

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; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,146
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-Apr-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-Apr-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-May-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-May-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-Oct-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-Oct-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 613:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1189
; OTHER INFORMATION: /note= "fusion protein composed of
; melittin signal sequence and full length
; hirt protein"
; SEQUENCE DESCRIPTION: SEQ ID NO: 613:
; US-10-877-146-613

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Query Match 100.0%; Score 5961; DB 17; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPFLATFVRRLPFGQWRLVQRGDPAAFRALVAQCLVCPW 60
Db 58 MPRAPRCRAVRSLLRSHYREVLPFLATFVRRLPFGQWRLVQRGDPAAFRALVAQCLVCPW 117
QY 61 DARPPPAAPSFQVSCIKELVARVLQRLCERGAKNVLAFGFALLDARGCPPPEAFTTSVR 120
Db 118 DARPPPAAPSFQVSCIKELVARVLQRLCERGAKNVLAFGFALLDARGCPPPEAFTTSVR 177
QY 121 SYLPTNTVTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 178 SYLPTNTVTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 237

```


QY 191 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGSSASRLPLPKPRR 240
 Db 238 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGSSASRLPLPKPRR 297
 QY 241 GAAPEPPTPVGQSWAHPGTRGSDRGFCVSPARPAEATSLGALSGTRSHPSVG 300
 Db 298 GAAPEPPTPVGQSWAHPGTRGSDRGFCVSPARPAEATSLGALSGTRSHPSVG 357
 QY 301 RQHAGPPSTSRPRPMDTPCPVVAETKHFLLYSSGDKQELRPSFLSSLRPSLTGARRL 360
 Db 358 RQHAGPPSTSRPRPMDTPCPVVAETKHFLLYSSGDKQELRPSFLSSLRPSLTGARRL 417
 QY 361 VETIFLGRSPMPGTPRLPLPQRYQWQMRPLFELIGNHAQCPYGVLLKTHCPDRAVT 420
 Db 418 VETIFLGRSPMPGTPRLPLPQRYQWQMRPLFELIGNHAQCPYGVLLKTHCPDRAVT 477
 QY 421 PAAGVCAREKQGSVAAPPEEDTPRRLVQLLRHSSPWYVGFVRACLRELVPGLWGS 480
 Db 478 PAAGVCAREKQGSVAAPPEEDTPRRLVQLLRHSSPWYVGFVRACLRELVPGLWGS 537
 QY 481 RHNERFLRNTKXIFSLGKHAKLSIQELTWKMSVRDCAWLRSSPGVCPVPAEHLREEI 540
 Db 538 RHNERFLRNTKXIFSLGKHAKLSIQELTWKMSVRDCAWLRSSPGVCPVPAEHLREEI 597
 QY 541 LAKFLHMLMSVYVVELLRSFYVTTTPQKNRLFYKSVMSKLSQSIGIRHKLKVQRE 600
 Db 598 LAKFLHMLMSVYVVELLRSFYVTTTPQKNRLFYKSVMSKLSQSIGIRHKLKVQRE 657
 QY 601 LSEAEVQREARPAALLTSRLRFPKPDGLRPIVNMVYVVCARTFREKRAERTLSVKA 660
 Db 658 LSEAEVQREARPAALLTSRLRFPKPDGLRPIVNMVYVVCARTFREKRAERTLSVKA 717
 QY 661 LFSVLNTERARRPGLGASVLGLDDIHRAMWTFVLRVRAQDPPPELVFKVDVDTGAYDTI 720
 Db 718 LFSVLNTERARRPGLGASVLGLDDIHRAMWTFVLRVRAQDPPPELVFKVDVDTGAYDTI 777
 QY 721 PODRLTEVIASIIKPNTYCVRRVAVVQKAAHGHVRKAFKSHVSTLTLQPYMQFVAHL 780
 Db 778 PODRLTEVIASIIKPNTYCVRRVAVVQKAAHGHVRKAFKSHVSTLTLQPYMQFVAHL 837
 QY 781 QETSPLRDADVIEOSSLINEASSGLFDVFLRFPMCHAVIRGKSYVQCGIPQGSILSTL 840
 Db 838 QETSPLRDADVIEOSSLINEASSGLFDVFLRFPMCHAVIRGKSYVQCGIPQGSILSTL 897
 QY 841 LCSICYGDMENKLFAGIRROGLLRLLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
 Db 898 LCSICYGDMENKLFAGIRROGLLRLLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 957
 QY 901 RKTVMNPFVEALGGTAFVQMPAHGLFPWCGLLDTRTLLEVQSDYSYARTSIRASLTF 960
 Db 958 RKTVMNPFVEALGGTAFVQMPAHGLFPWCGLLDTRTLLEVQSDYSYARTSIRASLTF 1017
 QY 961 NRGFKAGNMRKLFVGLRLKCHSLFDLDQVNSLQTVCTNLYKILLQAYRFHACVQLP 1020
 Db 1018 NRGFKAGNMRKLFVGLRLKCHSLFDLDQVNSLQTVCTNLYKILLQAYRFHACVQLP 1077
 QY 1021 FHQOVKNPTEFLRVIDSTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL 1080
 Db 1078 FHQOVKNPTEFLRVIDSTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL 1137
 QY 1081 KLTRHRVTVYVLLGSLRTAQQLSRKLPFGTTLTAAEAAANPALPSPDFTILD 1132
 Db 1138 KLTRHRVTVYVLLGSLRTAQQLSRKLPFGTTLTAAEAAANPALPSPDFTILD 1189

RESULT 43

US-10-044-692-324
 ; Sequence 324, Application US/10044692
 ; Publication No. US20030096344A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; Lingner, Joachim
 ; Nakamura, Toru

Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin
 Andrews, William H.
 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
 NUMBER OF SEQUENCES: 335
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/044,692
 FILING DATE: 11-Jan-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/912,951
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-00260005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 324:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1200 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 324:
 US-10-044-692-324

Query Match 100.0%; Score 5961; DB 14; Length 1200;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPAPRCRAVRSLLRSHRYEVLPLATFVRRLGQWRLVQGDPAAPRALVAQCLVCVPW 60
 Db 69 MPAPRCRAVRSLLRSHRYEVLPLATFVRRLGQWRLVQGDPAAPRALVAQCLVCVPW 128
 QY 61 DARPPPAAPSFQVSCLELVARVQLRCERGAKNVLAFGFALLDGGARGGPPRAFTTSVR 120
 Db 129 DARPPPAAPSFQVSCLELVARVQLRCERGAKNVLAFGFALLDGGARGGPPRAFTTSVR 188
 QY 121 SYLNTVTDALRGSGAWGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 Db 189 SYLNTVTDALRGSGAWGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 248
 QY 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGSSASRLPLPKPRR 240
 Db 249 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGSSASRLPLPKPRR 308

QY 241 GAAPEPERTVPGQSWAHPCRTGSDRGFCVVSPPARPAEATSLGALSCTRHSHPVSG 300
 Db 309 GAAPEPERTVPGQSWAHPCRTGSDRGFCVVSPPARPAEATSLGALSCTRHSHPVSG 368
 QY 301 ROHAGPPSTRPRPMDTPCPVYATKFLYSSGDKQOLRSLFLSSLRPSLTGARRL 360
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 Db 429 VETIFLGSRRPMDCTPRRLRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 488
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 Db 489 PAAGVCAREPQGSVAPEEEDTPRLVLQLLRQHSPPQVYGFVRACLRLRLVPPGLWGS 548
 QY 481 RHNERFLRNTKFIISLGKAKLSQBLTWKMSVRDCAMLRSPGVGCVPAAEHRLREEI 540
 Db 549 RHNERFLRNTKFIISLGKAKLSQBLTWKMSVRDCAMLRSPGVGCVPAAEHRLREEI 608
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 Db 609 LAKFLHLMVSVVVELLSRFPYVTTTFQKNRFLFFYRKSVWSKLQSIGIRQHLKRVQLRE 668
 QY 601 LSAEVRQHRARPALITSRLRFPKPDGLRPIVNMDDYVVGARTFRREKEAERLTSRVKA 660
 Db 669 LSAEVRQHRARPALITSRLRFPKPDGLRPIVNMDDYVVGARTFRREKEAERLTSRVKA 728
 QY 661 LFSVLNTERARRPCLLGASVLGDDIHRWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
 Db 729 LFSVLNTERARRPCLLGASVLGDDIHRWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 788
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 Db 789 PQDLTEVIASIIKPNQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 848
 QY 781 QETSPLRDVAVVIEQSSSLNEASSGLFDVFLRCHHVRIRGKSVYQCQIPOGSIILSTL 840
 Db 849 QETSPLRDVAVVIEQSSSLNEASSGLFDVFLRCHHVRIRGKSVYQCQIPOGSIILSTL 908
 QY 841 LCSLCYGDMMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRLTVRGVPYGCVNL 900
 Db 909 LCSLCYGDMMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRLTVRGVPYGCVNL 968
 QY 901 RKTGVNFPVDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVDYSSYARTSIRASLTF 960
 Db 969 RKTGVNFPVDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVDYSSYARTSIRASLTF 1028
 QY 961 NRGFKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFFHACVLQLP 1020
 Db 1029 NRGFKAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFFHACVLQLP 1088
 QY 1021 FHOQVKNPFFFLRVIDSTASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWILCHOAFL 1080
 Db 1089 FHOQVKNPFFFLRVIDSTASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWILCHOAFL 1148
 QY 1081 KLTRHRVTVYVPLLSLRTAQTOLSRKLPGLTTLTALEAAANPALPSPDKTILD 1132
 Db 1149 KLTRHRVTVYVPLLSLRTAQTOLSRKLPGLTTLTALEAAANPALPSPDKTILD 1200

RESULT 44

US-10-044-539-324

; Sequence 324, Application US/10044539

; Publication No. US2003010093A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
 ; THERAPEUTIC METHODS

; NUMBER OF SEQUENCES: 335

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA: US/10/044,539

; FILING DATE: 11-Jan-2002

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/912,951

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002600US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 324:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1200 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 324:

; US-10-044-539-324

Query Match 100.0%; Score 5961; DB 14; Length 1200;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLRSHYREVLPATFVRRLLGQWRLVQRGDPAAFRALVAQCLVCVPW 60
 Db 69 MPRAPRCRAVRSLRSHYREVLPATFVRRLLGQWRLVQRGDPAAFRALVAQCLVCVPW 128
 QY 61 DARPPAAPSRQVSCLELVARVLQRCERGAKNVLAEGFALLDGCARGGPPFAFTTSVR 120
 Db 129 DARPPAAPSRQVSCLELVARVLQRCERGAKNVLAEGFALLDGCARGGPPFAFTTSVR 188
 QY 121 SYLPTNTVDALRGSGAWGLLLRRVGGDVLVHLIARCAALFVLVAPSCAYQVCGPPLYQLGA 180
 Db 189 SYLPTNTVDALRGSGAWGLLLRRVGGDVLVHLIARCAALFVLVAPSCAYQVCGPPLYQLGA 248
 QY 181 ATQARPPPHASGPRRLRGGERAWNHSVRAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
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 QY 241 GAAPEPERTVPGQSWAHPCRTGSDRGFCVVSPPARPAEATSLGALSCTRHSHPVSG 300
 Db 309 GAAPEPERTVPGQSWAHPCRTGSDRGFCVVSPPARPAEATSLGALSCTRHSHPVSG 368

QY 301 ROHAGPSTGRPRPMDTPCPVVAETKHFYSSGDKQRLRPSFLSSLRPSLTGARRL 360
 Db 369 ROHAGPSTGRPRPMDTPCPVVAETKHFYSSGDKQRLRPSFLSSLRPSLTGARRL 428
 QY 361 VETIFLGSRRPMPGTPRLPRLPORYQWMRPLFLELLGNHAOCYGVLLKTHCPRAVY 420
 Db 429 VETIFLGSRRPMPGTPRLPRLPORYQWMRPLFLELLGNHAOCYGVLLKTHCPRAVY 488
 QY 421 PAAGVCAREKPOGSAPEEDTDPRLVQLLRQHSFPWQYGVFVRACLRLRVPGLWGS 480
 Db 489 PAAGVCAREKPOGSAPEEDTDPRLVQLLRQHSFPWQYGVFVRACLRLRVPGLWGS 548
 QY 481 RHNERFLRNTKFIISLGKHAQLSLOELTWMSVDCAWLRSPGVGCVPAAEHRLREEI 540
 Db 549 RHNERFLRNTKFIISLGKHAQLSLOELTWMSVDCAWLRSPGVGCVPAAEHRLREEI 608
 QY 541 LAKFLHLMMSVYVVELLRSPYVTTETTFQKRLFFYKSVMSKLSQSIGIQLHAKRVOLRE 600
 Db 609 LAKFLHLMMSVYVVELLRSPYVTTETTFQKRLFFYKSVMSKLSQSIGIQLHAKRVOLRE 668
 QY 601 LSEAEVRQHRREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSVKA 660
 Db 669 LSEAEVRQHRREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSVKA 728
 QY 661 LFSVINTERARRPGLLGASVLGLDDIHRAMRTFVLVRAODPPPELVFVKDVTGAYDTI 720
 Db 729 LFSVINTERARRPGLLGASVLGLDDIHRAMRTFVLVRAODPPPELVFVKDVTGAYDTI 788
 QY 721 PODRLTEVIASIIKPNQTYCVRVAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
 Db 789 PODRLTEVIASIIKPNQTYCVRVAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 848
 QY 781 QETSPLRDVAVIEQSSLINEASSGLFDVFLRFMCHHVRIRGKSVQCOGIPQGSILSTL 840
 Db 849 QETSPLRDVAVIEQSSLINEASSGLFDVFLRFMCHHVRIRGKSVQCOGIPQGSILSTL 908
 QY 841 LCSICYGDMENKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFRLTLVRGVPEYGVVNL 900
 Db 909 LCSICYGDMENKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFRLTLVRGVPEYGVVNL 968
 QY 901 RKTVPNPFVEALGGTAFVQMPAHGLFPWCGLLIDRTLEVSQSDYSYARTSIRASLTIF 960
 Db 969 RKTVPNPFVEALGGTAFVQMPAHGLFPWCGLLIDRTLEVSQSDYSYARTSIRASLTIF 1028
 QY 961 NRGFKAGNRWRKLFVGLRLKCHSLFDLDQVNSLQVTCTNLYKILLQAVRFHACVLQLP 1020
 Db 1029 NRGFKAGNRWRKLFVGLRLKCHSLFDLDQVNSLQVTCTNLYKILLQAVRFHACVLQLP 1088
 QY 1021 FHQQWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
 Db 1089 FHQQWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1148
 QY 1081 KLTRHRTVYPLIGSLTAQTLRSKLPGLTTLTALEAAANPALPSDFKTLID 1132
 Db 1149 KLTRHRTVYPLIGSLTAQTLRSKLPGLTTLTALEAAANPALPSDFKTLID 1200

RESULT 45

US-10-325-810-612
 ; Sequence 612, Application US/10325810
 ; Publication No. US20030204069A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 633
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/325,810
 FILING DATE: 20-Dec-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/402,181
 FILING DATE: 29-Sep-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ausenhus, Scott L.
 REGISTRATION NUMBER: 42,271
 REFERENCE/DOCKET NUMBER: 015389-002620US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 612:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1200 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1200
 OTHER INFORMATION: /note= "fusion protein composed of His6
 and Anti-Xpress tags, enterokinase
 cleavage site and full length hTERT
 protein"
 SEQUENCE DESCRIPTION: SEQ ID NO: 612:
 US-10-325-810-612

Query Match 100.0%; Score 5961; DB 15; Length 1200;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPRAPRCRAVRSLRSHYREVLPVPLATFVRRLGQWRLVQRGDPAAFRALVAQCLVCVPW 60
 Db 69 MPRAPRCRAVRSLRSHYREVLPVPLATFVRRLGQWRLVQRGDPAAFRALVAQCLVCVPW 128
 QY 61 DARPPPAAPSFQVSCIKELVARVLQRLCERGAKNVLAFCGALLDARGGPPFAFTTSVR 120
 Db 129 DARPPPAAPSFQVSCIKELVARVLQRLCERGAKNVLAFCGALLDARGGPPFAFTTSVR 188
 QY 121 SYLPTNTVTDALRGSGAWGLLRLRRVGGDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Db 189 SYLPTNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQCGPPLYQLGA 248
Qy 181 ATQARPPPHASGRRRLGCCERANHSVREAGVPLGLPAPCARRGGSASRLPLPKPRR 240
Db 249 ATQARPPPHASGRRRLGCCERANHSVREAGVPLGLPAPCARRGGSASRLPLPKPRR 308
Qy 241 GAAPERTPVGGGSAHAPGRTGPDGFCVSPAPAEATSLGALSGTRHSPSVG 300
Db 309 GAAPERTPVGGGSAHAPGRTGPDGFCVSPAPAEATSLGALSGTRHSPSVG 368
Qy 301 ROHAGPPSTRPPRWDTPCPPIYAEKTHFLYSSGDKQELRPSFLSSLRPLSLTGARRL 360
Db 369 ROHAGPPSTRPPRWDTPCPPIYAEKTHFLYSSGDKQELRPSFLSSLRPLSLTGARRL 428
Qy 361 VETIFLGSREPMECTPRRLPRLPORWYOMEPFLLELGNHAOCYPYVLLKTHCPLRAAVT 420
Db 429 VETIFLGSREPMECTPRRLPRLPORWYOMEPFLLELGNHAOCYPYVLLKTHCPLRAAVT 488
Qy 421 PAAGVCAREKPOGSVAAPBEDDTPRLVQLLRQHSPPWQVYGFVRACLRLVPPGLWGS 480
Db 489 PAAGVCAREKPOGSVAAPBEDDTPRLVQLLRQHSPPWQVYGFVRACLRLVPPGLWGS 548
Qy 481 RHNERPLRNTKPFISLGKHAQLSQELTWKMSVRDCAMLRSPGVCVPAABHRLREEI 540
Db 549 RHNERPLRNTKPFISLGKHAQLSQELTWKMSVRDCAMLRSPGVCVPAABHRLREEI 608
Qy 541 LAKFLHLMVSVVVELLSRFFYTETTFQKNRLFYRKSWKLSQIGIRQHLKRVQLRE 600
Db 609 LAKFLHLMVSVVVELLSRFFYTETTFQKNRLFYRKSWKLSQIGIRQHLKRVQLRE 668
Qy 601 LSAEVRQREARPALITSRLRTPKPDGLRPIVNDYVVGARTFRREKRAELTISRVA 660
Db 669 LSAEVRQREARPALITSRLRTPKPDGLRPIVNDYVVGARTFRREKRAELTISRVA 728
Qy 661 LFSVLNYERARRPGLIGASVLGLDDIHRWRTFVLVRQAOPPELYFVKVDVTGAYDTI 720
Db 729 LFSVLNYERARRPGLIGASVLGLDDIHRWRTFVLVRQAOPPELYFVKVDVTGAYDTI 788
Qy 721 PODRLTEVIASIIKPNQTYCVRYAVVQKAAHGHRKAFKSHVSTLTDLPQYMRQFVAHL 780
Db 789 PODRLTEVIASIIKPNQTYCVRYAVVQKAAHGHRKAFKSHVSTLTDLPQYMRQFVAHL 848
Qy 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQIPQGSILSTL 840
Db 849 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQIPQGSILSTL 908
Qy 841 LCSLCYGDMMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
Db 909 LCSLCYGDMMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 968
Qy 901 RKTVMNPPVDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVDSDYSSVARTSIRASLTF 960
Db 969 RKTVMNPPVDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVDSDYSSVARTSIRASLTF 1028
Qy 961 NRGFKAGNNRRKLFVGLRLKCHSLFLDLQVNSIQVTCTNIYKILLQAYRFHACVQLQP 1020
Db 1029 NRGFKAGNNRRKLFVGLRLKCHSLFLDLQVNSIQVTCTNIYKILLQAYRFHACVQLQP 1088
Qy 1021 FHOQVKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWICHQAFLL 1080
Db 1089 FHOQVKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWICHQAFLL 1148
Qy 1081 KLTRHRVTVYVPLLSLRTAQTQLSRKLPGTTLTALEAAANPALPSPDKTILD 1132
Db 1149 KLTRHRVTVYVPLLSLRTAQTQLSRKLPGTTLTALEAAANPALPSPDKTILD 1200

RESULT 46

US-10-877-124-612
; Sequence 612, Application US/10877124
; Publication No. US20040242529A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.

Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/877,124
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 612:
SEQUENCE CHARACTERISTICS:
LENGTH: 1200 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1200
OTHER INFORMATION: /note= "fusion protein composed of His6
and Anti-Xpress tags, enterokinase
cleavage site and full length hTERT
protein"
SEQUENCE DESCRIPTION: SEQ ID NO: 612:
US-10-877-124-612

Query Match 100.0%; Score 5961; DB 16; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	69	MPRAPRCRAVSLRSHYREVLP	128
Qy	61	DARPPAPSPRQVSCIKELVARVLQRCERGA	120
Db	129	DARPPAPSPRQVSCIKELVARVLQRCERGA	188
Qy	121	SYLPTNTVDALRGSGAGLLRRVDDVLVHLLAR	180
Db	189	SYLPTNTVDALRGSGAGLLRRVDDVLVHLLAR	248
Qy	181	ATQARPPPHASGPRRLRCERAMNHSVREAG	240
Db	249	ATQARPPPHASGPRRLRCERAMNHSVREAG	308
Qy	241	GAAPERTPVQGSWAHPGTRGSDRGFCVSPAR	300
Db	309	GAAPERTPVQGSWAHPGTRGSDRGFCVSPAR	368
Qy	301	QOHAGPSTSRPRPDWTPCPVYAEKHPLYSS	360
Db	369	QOHAGPSTSRPRPDWTPCPVYAEKHPLYSS	428
Qy	361	VETIFLGSRRPMPGTPRRLPRLPORYQMRPL	420
Db	429	VETIFLGSRRPMPGTPRRLPRLPORYQMRPL	488
Qy	421	PAAGVCAREKPGQSVAAPEEDTPRLVQLLRQ	480
Db	489	PAAGVCAREKPGQSVAAPEEDTPRLVQLLRQ	548
Qy	481	RHNERFLRNTKKISLGKHAQLSLOELTWKMS	540
Db	549	RHNERFLRNTKKISLGKHAQLSLOELTWKMS	608
Qy	541	LAKFLHLMMSVYVVELLRSFPYTTFQKRLFF	600
Db	609	LAKFLHLMMSVYVVELLRSFPYTTFQKRLFF	668
Qy	601	LSEAEVQREARPAALLTSRLRPIKPDGLRPI	660
Db	669	LSEAEVQREARPAALLTSRLRPIKPDGLRPI	728
Qy	661	LFSVLNTERARRPGLLGASVLGLDDIHRWRT	720
Db	729	LFSVLNTERARRPGLLGASVLGLDDIHRWRT	788
Qy	721	PODLRLTEVIASIIKPQNTYCVRRYAVVQKA	780
Db	789	PODLRLTEVIASIIKPQNTYCVRRYAVVQKA	848
Qy	781	QETSPLRDVAVIEQSSLINEASSGLFDVFLR	840
Db	849	QETSPLRDVAVIEQSSLINEASSGLFDVFLR	908
Qy	841	LCSLCYGDMENKLPAGIRRDGLLLRLVDDFL	900
Db	909	LCSLCYGDMENKLPAGIRRDGLLLRLVDDFL	968
Qy	901	RKTVNFPEDEALGGTAFVQMPAHGLFPWCG	960
Db	969	RKTVNFPEDEALGGTAFVQMPAHGLFPWCG	1028
Qy	961	NRGFKAGNRMRKLFVGLRLKCHSLFLDLQVNS	1020
Db	1029	NRGFKAGNRMRKLFVGLRLKCHSLFLDLQVNS	1088
Qy	1021	PHQVQWKNPTFFLRVISTASLCYSILKAKNAG	1080
Db	1089	PHQVQWKNPTFFLRVISTASLCYSILKAKNAG	1148

Qy 1081 KLTHRRVTVYVPLIGSLRTAQTOLSRKLP

Db 1149 KLTHRRVTVYVPLIGSLRTAQTOLSRKLP

RESULT 47

US-10-877-022-612

Sequence 612, Application US/10877022

Publication No. US20040247613A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/877,022

FILING DATE: 24-Jun-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503

FILING DATE: 02-Nov-1999

APPLICATION NUMBER: 08/974,549

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 612:

SEQUENCE CHARACTERISTICS:

LENGTH: 1200 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein


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;
;
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
;
; INFORMATION FOR SEQ ID NO: 612:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1200 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1200
; OTHER INFORMATION: /note= "fusion protein composed of His6
; and Anti-Xpress tags, enterokinase
; cleavage site and full length hTBT
; protein"
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 612:
US-10-877-146-612

Query Match 100.0%; Score 5961; DB 17; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCRAVRSLLRSYREVLPLATFVRRLLGPOQWRLVQRGDPAAPRALVAQCLVCVPW 60
Db 69 MPAPRCRAVRSLLRSYREVLPLATFVRRLLGPOQWRLVQRGDPAAPRALVAQCLVCVPW 128

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Db 129 DARPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEAFTTSVR 188

Qy 121 SYLNTVTDALRGSGANGLLRRVDDVLLVHLLARCAFLVLAFCAYQVCGPPLYQLGA 180
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Qy 181 ATQARPPPHASGPRRLRCERAMNHSVREAGVPLGLPAGARRRRGGASRSLLPLPKPRR 240
Db 249 ATQARPPPHASGPRRLRCERAMNHSVREAGVPLGLPAGARRRRGGASRSLLPLPKPRR 308

Qy 241 GAAPEPRTVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSGTRHSPSVG 300
Db 309 GAAPEPRTVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSGTRHSPSVG 368

Qy 301 ROHAGPSTSRPRPMDTPCPVYAEKHLFYSKGDKQLRPSFLLSRLPSLTGARRL 360
Db 369 ROHAGPSTSRPRPMDTPCPVYAEKHLFYSKGDKQLRPSFLLSRLPSLTGARRL 428

Qy 361 VETIFLSRPMWPGTTPRLPLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 429 VETIFLSRPMWPGTTPRLPLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 488

Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRLLVQLLRHSSPWQYGVFVRACLRLVPPGLWGS 480
Db 489 PAAGVCAREKPGQSVAAPEEDTDPRLLVQLLRHSSPWQYGVFVRACLRLVPPGLWGS 548

Qy 481 RHNERRFLNTKKFISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
Db 549 RHNERRFLNTKKFISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 608

Qy 541 LAKFLHLMWSVYVVELLRSFYVTTTFQKNRLFYKSWKLSQSIGRHLKRVQIRE 600
Db 609 LAKFLHLMWSVYVVELLRSFYVTTTFQKNRLFYKSWKLSQSIGRHLKRVQIRE 668

Qy 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFREKKAERLTSRVKA 660
Db 669 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFREKKAERLTSRVKA 728

Qy 661 LFSVLNTERARRPGLGASVLGLDDIHRAWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
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RESULT 49

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US-10-044-692-314
; Sequence 314, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
;
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
;
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
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; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 314:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1285 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 314:
US-10-044-692-314

Query Match 100.0%; Score 5961; DB 14; Length 1285;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGQGWRLVORGDPAAFRALVAOCLVCVPW 60
Db 154 MPAPRCRAVRSLLRSHYREVLPATFVRRLGQGWRLVORGDPAAFRALVAOCLVCVPW 213

QY 61 DARPPPAAPSFROVSCIKELVARVLORLCERGAKNVLATGFALLDGCAGGPPPEAFTTSVR 120
Db 214 DARPPPAAPSFROVSCIKELVARVLORLCERGAKNVLATGFALLDGCAGGPPPEAFTTSVR 273

QY 121 SYLPTNTVDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 274 SYLPTNTVDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 333

QY 181 ATOARPPPHASGRPRRLGCBRAWNHSVREAGVPIGLPAGARRRGSASRSLPLPKRPRR 240
Db 334 ATOARPPPHASGRPRRLGCBRAWNHSVREAGVPIGLPAGARRRGSASRSLPLPKRPRR 393

QY 241 GAAPEPERTPVGGSWAHGRTGSDRGFCVSPARPAAEATSLGALSGTTHSPSVG 300
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QY 301 ROHAGPPSTSPRPMDTPCPVYAEKTHFLYSSGDKQELRPSFLLSLRPSLTGARRL 360
Db 454 ROHAGPPSTSPRPMDTPCPVYAEKTHFLYSSGDKQELRPSFLLSLRPSLTGARRL 513

QY 361 VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 514 VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 573

QY 421 PAAGVCAREKPGQSVAAPEEDTDPRLLVOLLRHSSPMQVYGFVRACLRRLVPPGLWGS 480
Db 574 PAAGVCAREKPGQSVAAPEEDTDPRLLVOLLRHSSPMQVYGFVRACLRRLVPPGLWGS 633

QY 481 RHNERFLRNTKKFISLGKHAKLSLOELTWKMSVRDCAMLRSPGVGCVPAAEHRLREEI 540
Db 634 RHNERFLRNTKKFISLGKHAKLSLOELTWKMSVRDCAMLRSPGVGCVPAAEHRLREEI 693

QY 541 LAKFLHLWLSVYVELLSRFFYTETTFQKNRLFYRKSWSKLQSIGIRQHRLKRVQLRE 600
Db 694 LAKFLHLWLSVYVELLSRFFYTETTFQKNRLFYRKSWSKLQSIGIRQHRLKRVQLRE 753

QY 601 LSAEVRQREARPAALLTSRLRIPKPDGLRPIVNMDDYVVGARTFRRKRAERLTSRVKA 660
Db 754 LSAEVRQREARPAALLTSRLRIPKPDGLRPIVNMDDYVVGARTFRRKRAERLTSRVKA 813

QY 661 LFSVLNYEARRPGCLLGASVLGDDIHRAWRTFVLVRADQPPPELYFVKVDVTGAYDTI 720
Db 814 LFSVLNYEARRPGCLLGASVLGDDIHRAWRTFVLVRADQPPPELYFVKVDVTGAYDTI 873

QY 721 PQDRLTEVIASIIKPNQTYCVRVAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
Db 874 PQDRLTEVIASIIKPNQTYCVRVAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 933

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QY 781 QETSPLRDAVWIEQSSSLEASSGLFDVFLRFWCHHAVRIGKSVYQCOGIPGGSILSTL 840
Db 934 QETSPLRDAVWIEQSSSLEASSGLFDVFLRFWCHHAVRIGKSVYQCOGIPGGSILSTL 993

QY 841 LCSLCYGDMMENKLFAGIRRDGLLLRLVDDFLVTVPHLTHAKTFLRTLVRGVPEYGCVVNL 900
Db 994 LCSLCYGDMMENKLFAGIRRDGLLLRLVDDFLVTVPHLTHAKTFLRTLVRGVPEYGCVVNL 1053

QY 901 RKTIVNFPVEDEALGCTAFVQMPAHLFPWCGLLDTRTLEVSQSDYSSVARTSIRASLTIF 960
Db 1054 RKTIVNFPVEDEALGCTAFVQMPAHLFPWCGLLDTRTLEVSQSDYSSVARTSIRASLTIF 1113

QY 961 NRGFKAGRNMRKLFGLRLKCHSLFLDLQVNSLQVCTNIIYKILLQAYRHFHACVQLQP 1020
Db 1114 NRGFKAGRNMRKLFGLRLKCHSLFLDLQVNSLQVCTNIIYKILLQAYRHFHACVQLQP 1173

QY 1021 FHQQVWKNPTFFELRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQMLCHQAFLL 1080
Db 1174 FHQQVWKNPTFFELRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQMLCHQAFLL 1233

QY 1081 KLTRHRVTYVPLLSLRTAQTOISRLPGTTLTALAAAANPALPSDFKTILD 1132
Db 1234 KLTRHRVTYVPLLSLRTAQTOISRLPGTTLTALAAAANPALPSDFKTILD 1285

RESULT 50
US-10-044-539-314
; Sequence 314, Application US/10044539
; Publication No. US2003010093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429

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REFERENCE/DOCKET NUMBER: 015389-002600US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

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INFORMATION FOR SEQ ID NO: 314:

SEQUENCE CHARACTERISTICS:

LENGTH: 1285 amino acids

TYPE: amino acid

STRADEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 314:

US-10-044-539-314

Query Match	100.0%;	Score	5961;	DB	14;	Length	1285;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	1132;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;

Qy	1	MPRAPRCVAVRSLLRSHYREVLP	PLATFVRR	LGPGQWRLVQRGDPAAF	RAALVAQCLVCVPW	60
Db	154	MPRAPRCVAVRSLLRSHYREVLP	PLATFVRR	LGPGQWRLVQRGDPAAF	RAALVAQCLVCVPW	213
Qy	61	DARPPAPSPROVSCSKELVARVL	QRLCERGA	KNVLAFGALLD	GARGGPEAFTTSVR	120
Db	214	DARPPAPSPROVSCSKELVARVL	QRLCERGA	KNVLAFGALLD	GARGGPEAFTTSVR	273
Qy	121	SYLPTNTVDALRGSGAWGLLRR	VGGDDVLVHLLAR	CALFVLVAPSCAYQVCGP	PLYOLGA	180
Db	274	SYLPTNTVDALRGSGAWGLLRR	VGGDDVLVHLLAR	CALFVLVAPSCAYQVCGP	PLYOLGA	333
Qy	181	ATQARPPHAGSPRRRLGGERAM	NHVSREAGVPLGLPAGARR	GGSGASRS	LPLPKPRR	240
Db	334	ATQARPPHAGSPRRRLGGERAM	NHVSREAGVPLGLPAGARR	GGSGASRS	LPLPKPRR	393
Qy	241	GAAPERTPVQGSWAHPGTRG	PCFVSPARPAEAT	SI	LEGALSGTRSHPSVG	300
Db	394	GAAPERTPVQGSWAHPGTRG	PCFVSPARPAEAT	SI	LEGALSGTRSHPSVG	453
Qy	301	QOHAGPPSTSRPPRMDTCP	PPVYAEKHELYSSG	DKQRLRPSFLSSLRPS	LTGARRL	360
Db	454	QOHAGPPSTSRPPRMDTCP	PPVYAEKHELYSSG	DKQRLRPSFLSSLRPS	LTGARRL	513
Qy	361	VETIFLGSRPMPGTPRRLP	RLPQRYQMRPLFLELLGN	HAQCPYGVLLKTHCFL	RAAVT	420
Db	514	VETIFLGSRPMPGTPRRLP	RLPQRYQMRPLFLELLGN	HAQCPYGVLLKTHCFL	RAAVT	573
Qy	421	PAAGVCAREKPGCSVAAP	EEEDTPRRLVQLLRHSS	FPWQYVGFVRA	CLRRLVPPGLWGS	480
Db	574	PAAGVCAREKPGCSVAAP	EEEDTPRRLVQLLRHSS	FPWQYVGFVRA	CLRRLVPPGLWGS	633
Qy	481	RHNERFLRNTKFTISLGK	HAKLSLOELTWKMS	VRDCAWLRSPGVG	CPVPAEHRLEEI	540
Db	634	RHNERFLRNTKFTISLGK	HAKLSLOELTWKMS	VRDCAWLRSPGVG	CPVPAEHRLEEI	693
Qy	541	LAKFLHLWMSVYVVELLS	RPYVTTETTFQKNRL	FFYKRSVMSKLQSIGIR	QHLKRVQRE	600
Db	694	LAKFLHLWMSVYVVELLS	RPYVTTETTFQKNRL	FFYKRSVMSKLQSIGIR	QHLKRVQRE	753
Qy	601	LSEAEVQHRREAR	PALLTSRLRFTPKDGL	RPINMDYVVGART	FRREKRAERLTSRVKA	660
Db	754	LSEAEVQHRREAR	PALLTSRLRFTPKDGL	RPINMDYVVGART	FRREKRAERLTSRVKA	813
Qy	661	LFSVLYNERARRPG	LIGASVLGLDDIHR	AWRTFVLVRAQDPP	PPELYFVKVDVTGAYDTI	720
Db	814	LFSVLYNERARRPG	LIGASVLGLDDIHR	AWRTFVLVRAQDPP	PPELYFVKVDVTGAYDTI	873
Qy	721	PDRLTEVIASIIK	PONTYCVRRYAVVQKA	AHGHVRFKAFKSHV	STLTDLPYMQFVAHL	780
Db	874	PDRLTEVIASIIK	PONTYCVRRYAVVQKA	AHGHVRFKAFKSHV	STLTDLPYMQFVAHL	933
Qy	781	QETSPLRDVAVIE	QSSSINEASSGLFDV	FLFMCHHAVIRGK	SYVQCQGIPOGSI	840
Db	934	QETSPLRDVAVIE	QSSSINEASSGLFDV	FLFMCHHAVIRGK	SYVQCQGIPOGSI	993

Search completed: August 5, 2005, 14:25:39
Job time : 198 secs

Qy	841	LCSLCYGDMENKLPAGIR	RDGLLRVLVD	DFLLVTPH	LTHAKTFLR	TLVRGVP	EYGC	VNVL	900
Db	994	LCSLCYGDMENKLPAGIR	RDGLLRVLVD	DFLLVTPH	LTHAKTFLR	TLVRGVP	EYGC	VNVL	1053
Qy	901	RKTVVNFVEDEALG	GTAFVQMPAHGL	FPWCGL	LLDTRT	LEVSQ	SDYS	YARTS	960
Db	1054	RKTVVNFVEDEALG	GTAFVQMPAHGL	FPWCGL	LLDTRT	LEVSQ	SDYS	YARTS	1113
Qy	961	NRGFKAGRNMRRL	FGVLR	RLKCHSL	FLDLQVNS	LQVCTN	YKILLQ	AYRHFAC	1020
Db	1114	NRGFKAGRNMRRL	FGVLR	RLKCHSL	FLDLQVNS	LQVCTN	YKILLQ	AYRHFAC	1173
Qy	1021	FHQQVWKNPTFFLR	VISDTAS	LCYSILKAK	NAGMSLGAK	GAAGPLP	SEAVQ	WLCHQAF	1080
Db	1174	FHQQVWKNPTFFLR	VISDTAS	LCYSILKAK	NAGMSLGAK	GAAGPLP	SEAVQ	WLCHQAF	1233
Qy	1081	KLTRHRVTVYVPL	LGSLRTAQ	TQLSRKL	PGTTLT	TALEAAAN	PALP	SDPKT	1132
Db	1234	KLTRHRVTVYVPL	LGSLRTAQ	TQLSRKL	PGTTLT	TALEAAAN	PALP	SDPKT	1285

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